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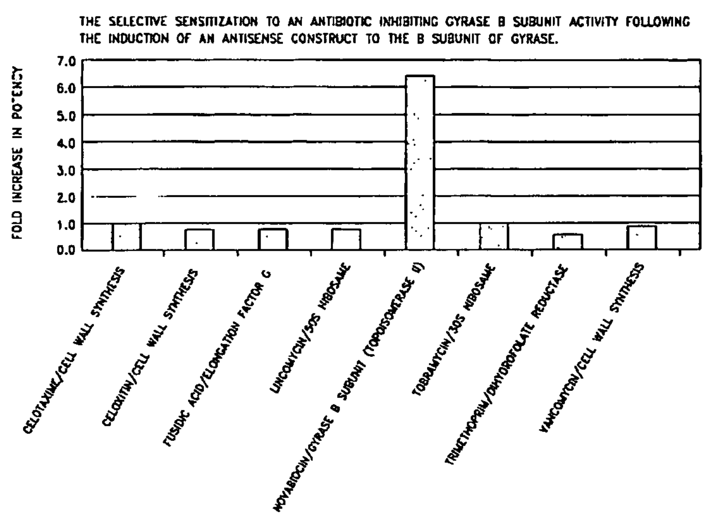
(54) Title: IDENTIFICATION OF ESSENTIAL GENES IN PROKARYOTES



(57) Abstract: The sequences of antisense nucleic acids which inhibit the proliferation of prokaryotes are disclosed. Cell-based assays which employ the antisense nucleic acids to identify and develop antibiotics are also disclosed. The antisense nucleic acids can also be used to identify proteins required for proliferation, express these proteins or portions thereof, obtain antibodies capable of specifically binding to the expressed proteins, and to use those expressed proteins as a screen to isolate candidate molecules for rational drug discovery programs. The nucleic acids can also be used to screen for homologous nucleic acids that are required for proliferation in cells other than *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae,* and *Pseudomonas aeruginosa*. The nucleic acids of the present invention can also be used in various assay systems to screen for proliferation required genes in other organisms.

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IDENTIFICATION OF ESSENTIAL GENES IN PROKARYOTES

Sequence Listing

The present application is being filed along with duplicate copies of a CD-ROM marked "Copy 1" and "Copy 2" containing a Sequence Listing in electronic format. The duplicate copies of the CD-ROM each contain a file entitled SEQLIST_FINAL_9PM created on March 20, 2001 which is 37,487,912 bytes in size.

Background of the Invention

Since the discovery of penicillin, the use of antibiotics to treat the ravages of bacterial infections has saved millions of lives. With the advent of these "miracle drugs," for a time it was popularly believed that humanity might, once and for all, be saved from the scourge of bacterial infections. In fact, during the 1980s and early 1990s, many large pharmaceutical companies cut back or eliminated antibiotics research and development. They believed that infectious disease caused by bacteria finally had been conquered and that markets for new drugs were limited. Unfortunately, this belief was overly optimistic.

The tide is beginning to turn in favor of the bacteria as reports of drug resistant bacteria become more frequent. The United States Centers for Disease Control announced that one of the most powerful known antibiotics, vancomycin, was unable to treat an infection of the common *Staphylococcus aureus* (staph). This organism is commonly found in our environment and is responsible for many nosocomial infections. The import of this announcement becomes clear when one considers that vancomycin was used for years to treat infections caused by *Staphylococcus* species as well as other stubborn strains of bacteria. In short, bacteria are becoming resistant to our most powerful antibiotics. If this trend continues, it is conceivable that we will return to a time when what are presently considered minor bacterial infections are fatal diseases.

Over-prescription and improper prescription habits by some physicians have caused an indiscriminate increase in the availability of antibiotics to the public. The patients are also partly responsible, since they will often improperly use the drug, thereby generating yet another population of bacteria that is resistant, in whole or in part, to traditional antibiotics.

The bacterial pathogens that have haunted humanity remain, in spite of the development of modern scientific practices to deal with the diseases that they cause. Drug resistant bacteria are now an increasing threat to the health of humanity. A new generation of antibiotics is needed to once again deal with the pending health threat that bacteria present.

Discovery of New Antibiotics

As more and more bacterial strains become resistant to the panel of available antibiotics, new antibiotics are required to treat infections. In the past, practitioners of pharmacology would have to rely upon traditional methods of drug discovery to generate novel, safe and efficacious compounds for the treatment of disease. Traditional drug discovery methods involve blindly testing potential drug candidate-molecules, often selected at random, in the hope that one might prove to be an effective treatment for some disease. The process is painstaking and laborious, with no guarantee of success. Today, the average cost to discover and develop a new drug exceeds US $500 million, and the average time from laboratory to patient is 15 years. Improving this process, even incrementally, would represent a huge advance in the generation of novel antimicrobial agents.

Newly emerging practices in drug discovery utilize a number of biochemical techniques to provide for directed approaches to creating new drugs, rather than discovering them at random. For example, gene sequences and proteins encoded thereby that are required for the proliferation of a cell or microorganism make excellent targets since exposure of bacteria to compounds active against these targets would result in the inactivation of the cell or microorganism. Once a target is identified, biochemical analysis of that target can be used to discover or to design molecules that interact with and alter the functions of the target. Use of physical and computational techniques to analyze structural and biochemical properties of targets in order to derive compounds that interact with such targets is called rational drug design and offers great potential. Thus, emerging drug discovery practices use molecular modeling techniques, combinatorial chemistry approaches, and other means to produce and screen and/or design large numbers of candidate compounds.

Nevertheless, while this approach to drug discovery is clearly the way of the future, problems remain. For example, the initial step of identifying molecular targets for investigation can be an extremely time consuming task. It may also be difficult to design molecules that interact with the target by using computer modeling techniques. Furthermore, in cases where the function of the target is not known or is poorly understood, it may be difficult to design assays to detect molecules that interact with and alter the functions of the target. To improve the rate of novel drug discovery and development, methods of identifying important molecular targets in pathogenic cells or microorganisms and methods for identifying molecules that interact with and alter the functions of such molecular targets are urgently required.

Staphylococcus aureus is a Gram positive microorganism which is the causative agent of many infectious diseases. Local infection by *Staphylococcus aureus* can cause abscesses on skin and cellulitis in subcutaneous tissues and can lead to toxin-related diseases such as toxic shock and scalded skin syndromes. *Staphylococcus aureus* can cause serious systemic infections such as osteomyelitis, endocarditis, pneumonia, and septicemia. *Staphylococcus aureus* is also a common cause of food poisoning, often arising from contact between prepared food and infected food industry workers. Antibiotic resistant strains of *Staphylococcus aureus* have recently been

identified, including those that are now resistant to all available antibiotics, thereby severely limiting the options of care available to physicians.

Pseudomonas aeruginosa is an important Gram-negative opportunistic pathogen. It is the most common Gram-negative found in nosocomial infections. *P. aeruginosa* is responsible for 16% of nosocomial pneumonia cases, 12% of hospital-acquired urinary tract infections, 8% of surgical wound infections, and 10% of bloodstream infections. Immunocompromised patients, such as neutropenic cancer and bone marrow transplant patients, are particular susceptible to opportunistic infections. In this group of patients, *P. aeruginosa* is responsible for pneumonia and septicemia with attributable deaths reaching 30%. *P. aeruginosa* is also one of the most common and lethal pathogens responsible for ventilator-associated pneumonia in intubated patients, with directly attributable death rates reaching 38%. Although *P. aeruginosa* outbreaks in burn patients are rare, it is associated with 60% death rates. In the AIDS population, *P. aeruginosa* is associated with 50% of deaths. Cystic fibrosis patients are characteristically susceptible to chronic infection by *P. aeruginosa*, which is responsible for high rates of illness and death. Current antibiotics work poorly for CF infections (Van Delden & Igelwski. 1998. Emerging Infectious Diseases 4:551-560; references therein).

The gram-negative enteric bacterial genus, *Salmonella*, encompasses at least 2 species. One of these, *S. enterica*, is divided into multiple subspecies and thousands of serotypes or serovars (Brenner, et al. 2000 J. Clin. Microbiol. 38:2465-2467). The *S. enterica* human pathogens include serovars Typhi, Paratyphi, Typhimurium, Cholerasuis, and many others deemed so closely related that they are variants of a widespread species. Worldwide, disease in humans caused by *Salmonella* is a very serious problem. In many developing countries, *S. enterica* ser. Typhi still causes often-fatal typhoid fever. This problem has been reduced or eliminated in wealthy industrial states. However, enteritis induced by Salmonella is widespread and is the second most common disease caused by contaminated food in the United States (Edwards, BH 1999 "Salmonella and Shigella species" Clin. Lab Med. 19(3):469-487). Though usually self-limiting in healthy individuals, others such as children, seniors, and those with compromising illnesses can be at much greater risk of serious illness and death.

Some *S. enterica* serovars (e.g. Typhimurium) cause a localized infection in the gastrointestinal tract. Other serovars (i.e. Typhi and Paratyphi) cause a much more serious systemic infection. In animal models, these roles can be reversed which has allowed the use of the relatively safe *S. enterica* ser. Typhimurium as a surrogate in mice for the typhoid fever agent, *S. enterica* ser. Typhi. In mice, *S. enterica* ser Typhimurium causes a systemic infection similar in outcome to typhoid fever. Years of study of the *Salmonella* have led to the identification of many determinants of virulence in animals and humans. *Salmonella* is interesting in its ability to localize to and invade the intestinal epithelium, induce morphologic changes in target cells via injection of certain cell-remodeling proteins, and to reside intracellularly in membrane-bound vesicles (Wallis, TS and

Galyov, EE 2000 "Molecular basis of *Salmonella*-induced enteritis." Molec. Microb. 36:997-1005; Falkow, S "The evolution of pathogenicity in Escherichia, Shigella, and Salmonella," Chap. 149 in Neidhardt, et al. eds pp 2723-2729; Gulig, PA "Pathogenesis of Systemic Disease," Chap. 152 in Neidhardt, et al. ppp 2774-2787). The immediate infection often results in a severe watery diarrhea but *Salmonella* also can establish and maintain a subclinical carrier state in some individuals. Spread is via food contaminated with sewage.

The gene products implicated in *Salmonella* pathogenesis include type three secretion systems (TTSS), proteins affecting cytoplasmic structure of the target cells, many proteins carrying out functions necessary for survival and proliferation of *Salmonella* in the host, as well as "traditional" factors such as endotoxin and secreted exotoxins. Additionally, there must be factors mediating species-specific illnesses. Despite this most of the genomes of *S. enterica* ser. Typhi (see http://www.sanger.ac.uk/Projects/S_typhi/ for the genome database) and *S. enterica* ser. Typhimurium (see http://genome.wustl.edu/gsc/bacterial/salmonella.shtml for the genome database) are highly conserved and are mutually useful for gene identification in multiple serovars. The Salmonella are a complex group of enteric bacteria causing disease similar to but distinct from other gram-negative enterics such as *E. coli* and have been a focus of biomedical research for the last century.

Enterococcus faecalis, a Gram-positive bacterium, is by far the most common member of the enterococci to cause infections in humans. *Enterococcus faecium* generally accounts for less than 20% of clinical isolates. Enterococci infections are mostly hospital-acquired though they are also associated with some community-acquired infections. Of nosocomial infections enterococci account for 12% of bacteremia, 15% of surgical wound infections, 14% of urinary tract infections, and 5 to15% of endocarditis cases (Huycke, M. M., D. F., Sahm and M. S. Gilmore. 1998. Emerging Infectious Diseases 4:239-249). Additionally enterococci are frequently associated with intraabdominal and pelvic infections. Enterococci infections are often hard to treat because they are resistant to a vast array of antimicrobial drugs, including aminoglycosides, penicillin, ampicillin and vancomycin. The development of multiple-drug resistant (MDR) enterococci has made this bacteria a major concern for treating nosocomial infections.

These reasons underscore the urgency of developing new antibiotics that are effective against *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa*, and *Enterococcus faecalis*. Accordingly, there is an urgent need for more novel methods to identify and characterize bacterial genomic sequences that encode gene products involved in proliferation, and are thereby potential new targets for antibiotic development. Prior to the present invention, the discovery of *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae*, and *Pseudomonas aeruginosa* and *Enterococcus faecalis* genes required for proliferation of the microorganism was a painstaking and slow process. While the detection of new cellular drug targets within a *Staphylococcus aureus, Salmonella typhimurium, Klebsiella*

pneumoniae, Pseudomonas aeruginosa or *Enterococcus faecalis* cell is key for novel antibiotic development, the current methods of drug target discovery available prior to this invention have required painstaking processes requiring years of effort.

Summary of the Invention

Some aspects of the present invention are described in the numbered paragraphs below.

1. A purified or isolated nucleic acid sequence comprising a nucleotide sequence consisting essentially of one of SEQ ID NOs: 8-3795, wherein expression of said nucleic acid inhibits proliferation of a cell.

2. The nucleic acid sequence of Paragraph 1, wherein said nucleotide sequence is complementary to at least a portion of a coding sequence of a gene whose expression is required for proliferation of a cell.

3. The nucleic acid of Paragraph 1, wherein said nucleic acid sequence is complementary to at least a portion of a nucleotide sequence of an RNA required for proliferation of a cell.

4. The nucleic acid of Paragraph 3, wherein said RNA is an RNA comprising a sequence of nucleotides encoding more than one gene product.

5. A purified or isolated nucleic acid comprising a fragment of one of SEQ ID NOs.: 8-3795, said fragment selected from the group consisting of fragments comprising at least 10, at least 20, at least 25, at least 30, at least 50 and more than 50 consecutive nucleotides of one of SEQ ID NOs: 8-3795.

6. The fragment of Paragraph 5, wherein said fragment is included in a nucleic acid obtained from an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

7. The fragment of Paragraph 5, wherein said fragment is included in a nucleic acid obtained from an organism other than *Escherichia coli*.

8. A vector comprising a promoter operably linked to the nucleic acid of any one of Paragraphs 1-7.

9. The vector of Paragraph 8, wherein said promoter is active in a microorganism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

10. A host cell containing the vector of Paragraph 8 or Paragraph 9.

11. A purified or isolated antisense nucleic acid comprising a nucleotide sequence complementary to at least a portion of an intragenic sequence, intergenic sequence, sequences spanning at least a portion of two or more genes, 5' noncoding region, or 3' noncoding region within an operon comprising a proliferation-required gene whose activity or expression is inhibited by an antisense nucleic acid comprising the nucleotide sequence of one of SEQ ID NOs.: 8-3795.

12. The purified or isolated antisense nucleic acid of Paragraph 11, wherein said antisense nucleic acid is complementary to a nucleic acid from an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli,*

Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

13. The purified or isolated antisense nucleic acid of Paragraph 11, wherein said nucleotide sequence is complementary to a nucleotide sequence of a nucleic acid from an organism other than *E. coli*.

14. The purified or isolated antisense nucleic acid of Paragraph 11, wherein said proliferation-required gene comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012.

15. A purified or isolated nucleic acid comprising a nucleotide sequence having at least 70% identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, fragments comprising at least 25 consecutive nucleotides of SEQ ID NOs.: 8-3795, the nucleotide sequences complementary to SEQ ID NOs.: 8-3795 and the sequences complementary to fragments comprising at least 25 consecutive nucleotides of SEQ ID NOs.: 8-3795 as determined using BLASTN version 2.0 with the default parameters.

16. The purified or isolated nucleic acid of Paragraph 15, wherein said nucleic acid is obtained from an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus*

pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

17. The nucleic acid of Paragraph 15, wherein said nucleic acid is obtained from an organism other than *E. coli*.

18. A vector comprising a promoter operably linked to a nucleic acid encoding a polypeptide whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence of any one of SEQ ID NOs.: 8-3795.

19. The vector of Paragraph 18, wherein said nucleic acid encoding said polypeptide is obtained from an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

20. The vector of Paragraph 18, wherein said nucleotide sequence encoding said polypeptide is obtained from an organism other than *E. coli*.

21. A host cell containing the vector of Paragraph 18.

22. The vector of Paragraph 18, wherein said polypeptide comprises a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110.

23. The vector of Paragraph 18, wherein said promoter is operably linked to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012.

24. A purified or isolated polypeptide comprising a polypeptide whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence of any one of SEQ ID NOs.: 8-3795, or a fragment selected from the group consisting of fragments comprising at least 5,

at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of one of the said polypeptides.

25. The polypeptide of Paragraph 24, wherein said polypeptide comprises an amino acid sequence of any one of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 or a fragment comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

26. The polypeptide of Paragraph 24, wherein said polypeptide is obtained from an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

27. The polypeptide of Paragraph 24, wherein said polypeptide is obtained from an organism other than *E. coli*.

28. A purified or isolated polypeptide comprising a polypeptide having at least 25% amino acid identity to a polypeptide whose expression is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, or at least 25% amino acid identity to a fragment comprising at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of a polypeptide whose expression is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 as determined using FASTA version 3.0t78 with the default parameters.

29. The polypeptide of Paragraph 28, wherein said polypeptide has at least 25% identity to a polypeptide comprising one of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110 or at least 25% identity to a fragment comprising at least 5, at least 10, at least 20, at least 30, at least 40, at

least 50, at least 60 or more than 60 consecutive amino acids of a polypeptide comprising one of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 as determined using FASTA version 3.0t78 with the default parameters.

30. The polypeptide of Paragraph 28, wherein said polypeptide is obtained from an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

31. The polypeptide of Paragraph 28, wherein said polypeptide is obtained from an organism other than *E. coli*.

32. An antibody capable of specifically binding the polypeptide of one of Paragraphs 28-31.

33. A method of producing a polypeptide, comprising introducing a vector comprising a promoter operably linked to a nucleic acid comprising a nucleotide sequence encoding a polypeptide whose expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 8-3795 into a cell.

34. The method of Paragraph 33, further comprising the step of isolating said polypeptide.

35. The method of Paragraph 33, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

36. The method of Paragraph 33, wherein said nucleic acid encoding said polypeptide is obtained from an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata),*

Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

37. The method of Paragraph 33, wherein said nucleic acid encoding said polypeptide is obtained from an organism other than *E. coli.*

38. The method of Paragraph 33, wherein said promoter is operably linked to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012.

39. A method of inhibiting proliferation of a cell in an individual comprising inhibiting the activity or reducing the amount of a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 or inhibiting the activity or reducing the amount of a nucleic acid encoding said gene product.

40. The method of Paragraph 39, wherein said method comprises inhibiting said activity or reducing said amount of a gene product in an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori,*

Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

41. The method of Paragraph 39, wherein said method comprises inhibiting said activity or reducing said amount of a gene product in an organism other than *E. coli*.

42. The method of Paragraph 39, wherein said gene product is present in an organism other than *E. coli*.

43. The method of Paragraph 39, wherein said gene product comprises a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

44. A method for identifying a compound which influences the activity of a gene product required for proliferation, said gene product comprising a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, said method comprising:

contacting said gene product with a candidate compound; and

determining whether said compound influences the activity of said gene product.

45. The method of Paragraph 44, wherein said gene product is from an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

46. The method of Paragraph 44, wherein said gene product is from an organism other than *E. coli*.

47. The method of Paragraph 44, wherein said gene product is a polypeptide and said activity is an enzymatic activity.

48. The method of Paragraph 44, wherein said gene product is a polypeptide and said activity is a carbon compound catabolism activity.

49. The method of Paragraph 44, wherein said gene product is a polypeptide and said activity is a biosynthetic activity.

50. The method of Paragraph 44, wherein said gene product is a polypeptide and said activity is a transporter activity.

51. The method of Paragraph 44, wherein said gene product is a polypeptide and said activity is a transcriptional activity.

52. The method of Paragraph 44, wherein said gene product is a polypeptide and said activity is a DNA replication activity.

53. The method of Paragraph 44, wherein said gene product is a polypeptide and said activity is a cell division activity.

54. The method of Paragraph 44, wherein said gene product is an RNA.

55. The method of Paragraph 44, wherein said gene product is a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

56. A compound identified using the method of Paragraph 44.

57. A method for identifying a compound or nucleic acid having the ability to reduce the activity or level of a gene product required for proliferation, said gene product comprising a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, said method comprising:

(a) contacting a target gene or RNA encoding said gene product with a candidate compound or nucleic acid; and

(b) measuring an activity of said target.

58. The method of Paragraph 57, wherein said target gene or RNA is from an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus*

faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

59. The method of Paragraph 57, wherein said target gene or RNA is from an organism other than *E. coli*.

60. The method of Paragraph 57, wherein said gene product is from an organism other than *E. coli*.

61. The method of Paragraph 57, wherein said target is a messenger RNA molecule and said activity is translation of said messenger RNA.

62. The method of Paragraph 57, wherein said target is a messenger RNA molecule and said activity is transcription of a gene encoding said messenger RNA.

63. The method of Paragraph 57, wherein said target is a gene and said activity is transcription of said gene.

64. The method of Paragraph 57, wherein said target is a nontranslated RNA and said activity is processing or folding of said nontranslated RNA or assembly of said nontranslated RNA into a protein/RNA complex.

65. The method of Paragraph 57, wherein said target is a messenger RNA molecule encoding a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

66. The method of Paragraph 57, wherein said target comprises a nucleic acid selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012.

67. A compound or nucleic acid identified using the method of Paragraph 57.

68. A method for identifying a compound which reduces the activity or level of a gene product required for proliferation of a cell, wherein the activity or expression of said gene product is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, said method comprising the steps of:

(a) providing a sublethal level of an antisense nucleic acid comprising a nucleotide sequence complementary to a nucleic acid comprising a nucleotide sequence encoding said gene product in a cell to reduce the activity or amount of said gene product in said cell, thereby producing a sensitized cell;

(b) contacting said sensitized cell with a compound; and

(c) determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a cell which does not contain said antisense nucleic acid.

69. The method of Paragraph 68, wherein said determining step comprises determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of a nonsensitized cell.

70. The method of Paragraph 68, wherein said cell is a Gram positive bacterium.

71. The method of Paragraph 68, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

72. The method of Paragraph 68, wherein said bacterium is *Staphylococcus aureus*.

73. The method of Paragraph 72, wherein said *Staphylococcus* species is coagulase negative.

74. The method of Paragraph 72, wherein said bacterium is selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

75. The method of Paragraph 68, wherein said cell is an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

76. The method of Paragraph 68, wherein said cell is not an *E. coli* cell.

77. The method of Paragraph 68, wherein said gene product is from an organism other than *E. coli*.

78. The method of Paragraph 68, wherein said antisense nucleic acid is transcribed from an inducible promoter.

79. The method of Paragraph 68, further comprising the step of contacting said cell with a concentration of inducer which induces transcription of said antisense nucleic acid to a sublethal level.

80. The method of Paragraph 68, wherein growth inhibition is measured by monitoring optical density of a culture growth solution.

81. The method of Paragraph 68, wherein said gene product is a polypeptide.

82. The method of Paragraph 81, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

83. The method of Paragraph 68, wherein said gene product is an RNA.

84. The method of Paragraph 68, wherein nucleic acid encoding said gene product comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012.

85. A compound identified using the method of Paragraph 68.

86. A method for inhibiting cellular proliferation comprising introducing an effective amount of a compound with activity against a gene whose activity or expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 or a compound with activity against the product of said gene into a population of cells expressing said gene.

87. The method of Paragraph 86, wherein said compound is an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, or a proliferation-inhibiting portion thereof.

88. The method of Paragraph 86, wherein said proliferation inhibiting portion of one of SEQ ID NOs.: 8-3795 is a fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 51 consecutive nucleotides of one of SEQ ID NOs.: 8-3795.

89. The method of Paragraph 86, wherein said population is a population of Gram positive bacteria.

90. The method of Paragraph 89, wherein said population of Gram positive bacteria is selected from the group consisting of a population of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

91. The method of Paragraph 86, wherein said population is a population of *Staphylococcus aureus*.

92. The method of Paragraph 91, wherein said population is a population of a bacterium selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

93. The method of Paragraph 86, wherein said population is a population of a bacterium selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus*

anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

94. The method of Paragraph 86, wherein said population is a population of an organism other than *E. coli*.

95. The method of Paragraph 86, wherein said product of said gene is from an organism other than *E. coli*.

96. The method of Paragraph 86, wherein said gene encodes a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

97. The method of Paragraph 86, wherein said gene comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012.

98. A composition comprising an effective concentration of an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, or a proliferation-inhibiting portion thereof in a pharmaceutically acceptable carrier.

99. The composition of Paragraph 98, wherein said proliferation-inhibiting portion of one of SEQ ID NOs.: 8-3795 comprises at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive nucleotides of one of SEQ ID NOs.: 8-3795.

100. A method for inhibiting the activity or expression of a gene in an operon required for proliferation wherein the activity or expression of at least one gene in said operon is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 8-3795, said method comprising contacting a cell in a cell population with an antisense nucleic acid complementary to at least a portion of said operon.

101. The method of Paragraph 100, wherein said antisense nucleic acid comprises a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 or a proliferation-inhibiting portion thereof.

102. The method of Paragraph 100, wherein said cell is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

103. The method of Paragraph 100, wherein said cell is not an *E. coli* cell.

104. The method of Paragraph 100, wherein said gene is from an organism other than *E. coli*.

105. The method of Paragraph 100, wherein said cell is contacted with said antisense nucleic acid by introducing a plasmid which expresses said antisense nucleic acid into said cell population.

106. The method of Paragraph 100, wherein said cell is contacted with said antisense nucleic acid by introducing a phage which encodes said antisense nucleic acid into said cell population.

107. The method of Paragraph 100, wherein said cell is contacted with said antisense nucleic acid by expressing said antisense nucleic acid from the chromosome of cells in said cell population.

108. The method of Paragraph 100, wherein said cell is contacted with said antisense nucleic acid by introducing a promoter adjacent to a chromosomal copy of said antisense nucleic acid such that said promoter directs the transcription of said antisense nucleic acid.

109. The method of Paragraph 100, wherein said cell is contacted with said antisense nucleic acid by introducing a retron which expresses said antisense nucleic acid into said cell population.

110. The method of Paragraph 100, wherein said cell is contacted with said antisense nucleic acid by introducing a ribozyme into said cell-population, wherein a binding portion of said ribozyme comprises said antisense nucleic acid.

111. The method of Paragraph 100, wherein said cell is contacted with said antisense nucleic acid by introducing a liposome comprising said antisense nucleic acid into said cell.

112. The method of Paragraph 100, wherein said cell is contacted with said antisense nucleic acid by electroporation of said antisense nucleic acid into said cell.

113. The method of Paragraph 100, wherein said antisense nucleic acid is a fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive nucleotides of one of SEQ ID NOs.: 8-3795.

114. The method of Paragraph 100 wherein said antisense nucleic acid is a synthetic oligonucleotide.

115. The method of Paragraph 100, wherein said gene comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012.

116. A method for identifying a gene which is required for proliferation of a cell comprising:

(a) contacting a cell with an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, wherein said cell is a cell other than the organism from which said nucleic acid was obtained;

(b) determining whether said nucleic acid inhibits proliferation of said cell; and

(c) identifying the gene in said cell which encodes the mRNA which is complementary to said antisense nucleic acid or a portion thereof.

117. The method of Paragraph 116, wherein said cell is selected from the group consisting of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

118. The method of Paragraph 116 wherein said cell is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae,*

Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

119. The method of Paragraph 116, wherein said cell is not *E. coli*.

120. The method of Paragraph 116, further comprising operably linking said antisense nucleic acid to a promoter which is functional in said cell, said promoter being included in a vector, and introducing said vector into said cell.

121. A method for identifying a compound having the ability to inhibit proliferation of a cell comprising:

(a) identifying a homolog of a gene or gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs. 8-3795 in a test cell, wherein said test cell is not the cell from which said nucleic acid was obtained;

(b) identifying an inhibitory nucleic acid sequence which inhibits the activity of said homolog in said test cell;

(c) contacting said test cell with a sublethal level of said inhibitory nucleic acid, thus sensitizing said cell;

(d) contacting the sensitized cell of step (c) with a compound; and

(e) determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a cell which does not contain said inhibitory nucleic acid.

122. The method of Paragraph 121, wherein said determining step comprises determining whether said compound inhibits proliferation of said sensitized test cell to a greater extent than said compound inhibits proliferation of a nonsensitized test cell.

123. The method of Paragraph 121, wherein step (a) comprises identifying a nucleic acid homologous to a gene or gene product whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs. 8-3795 or a nucleic acid encoding a homologous polypeptide to a polypeptide whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs. 8-3795 by using an algorithm selected from the group consisting of BLASTN version 2.0 with the default parameters and FASTA version 3.0t78 algorithm with the default parameters to identify said homologous nucleic acid or said nucleic acid encoding a homologous polypeptide in a database.

124. The method of Paragraph 121 wherein said step (a) comprises identifying a homologous nucleic acid or a nucleic acid comprising a sequence of nucleotides encoding a homologous polypeptide by identifying nucleic acids which hybridize to said nucleic acid selected from the group consisting of SEQ ID NOs. 8-3795 or the complement of said nucleic acid selected from the group consisting of SEQ ID NOs. 8-3795.

125. The method of Paragraph 121 wherein step (a) comprises expressing a nucleic acid selected from the group consisting of SEQ ID NOs. 8-3795 in said test cell.

126. The method of Paragraph 121, wherein step (a) comprises identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide in a test cell selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

127. The method of Paragraph 121, wherein step (a) comprises identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide in a test cell other than *E. coli*.

128. The method of Paragraph 121, wherein said inhibitory nucleic acid is an antisense nucleic acid.

129. The method of Paragraph 121, wherein said inhibitory nucleic acid comprises an antisense nucleic acid to a portion of said homolog.

130. The method of Paragraph 121, wherein said inhibitory nucleic acid comprises an antisense nucleic acid to a portion of the operon encoding said homolog.

131. The method of Paragraph 121, wherein the step of contacting the cell with a sublethal level of said inhibitory nucleic acid comprises directly contacting the surface of said cell with said inhibitory nucleic acid.

132. The method of Paragraph 121, wherein the step of contacting the cell with a sublethal level of said inhibitory nucleic acid comprises transcribing an antisense nucleic acid complementary to at least a portion of the RNA transcribed from said homolog in said cell.

133. The method of Paragraph 121, wherein said gene product comprises a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

134. The method of Paragraph 121, wherein said gene comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012.

135. A compound identified using the method of Paragraph 121.

136. A method of identifying a compound having the ability to inhibit proliferation comprising:

(a) contacting a test cell with a sublethal level of a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs. 8-3795 or a portion thereof which inhibits the proliferation of the cell from which said nucleic acid was obtained, thus sensitizing said test cell;

(b) contacting the sensitized test cell of step (a) with a compound; and

(c) determining the degree to which said compound inhibits proliferation of said sensitized test cell relative to a cell which does not contain said nucleic acid.

137. The method of Paragraph 136, wherein said determining step comprises determining whether said compound inhibits proliferation of said sensitized test cell to a greater extent than said compound inhibits proliferation of a nonsensitized test cell.

138. A compound identified using the method of Paragraph 136.

139. The method of Paragraph 136, wherein said test cell is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori,*

Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

140. The method of Paragraph 136, wherein the test cell is not *E. coli*.

141. A method for identifying a compound having activity against a biological pathway required for proliferation comprising:

(a) sensitizing a cell by providing a sublethal level of an antisense nucleic acid complementary to a nucleic acid encoding a gene product required for proliferation, wherein the activity or expression of said gene product is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, in said cell to reduce the activity or amount of said gene product;

(b) contacting the sensitized cell with a compound; and

(c) determining the degree to which said compound inhibits the growth of said sensitized cell relative to a cell which does not contain said antisense nucleic acid.

142. The method of Paragraph 141, wherein said determining step comprises determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of a nonsensitized cell.

143. The method of Paragraph 141, wherein said cell is selected from the group consisting of bacterial cells, fungal cells, plant cells, and animal cells.

144. The method of Paragraph 141, wherein said cell is a Gram positive bacterium.

145. The method of Paragraph 144, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

146. The method of Paragraph 145, wherein said Gram positive bacterium is *Staphylococcus aureus*.

147. The method of Paragraph 146, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

148. The method of Paragraph 141, wherein said cell is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli,*

Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

149. The method of Paragraph 141, wherein said cell is not an *E. coli* cell.

150. The method of Paragraph 141, wherein said gene product is from an organism other than *E. coli.*

151. The method of Paragraph 141, wherein said antisense nucleic acid is transcribed from an inducible promoter.

152. The method of Paragraph 141, further comprising contacting the cell with an agent which induces transcription of said antisense nucleic acid from said inducible promoter, wherein said antisense nucleic acid is transcribed at a sublethal level.

153. The method of Paragraph 141, wherein inhibition of proliferation is measured by monitoring the optical density of a liquid culture.

154. The method of Paragraph 141, wherein said gene product comprises a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

155. The method of Paragraph 141, wherein said nucleic acid encoding said gene product comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012.

156. A compound identified using the method of Paragraph 141.

157. A method for identifying a compound having the ability to inhibit cellular proliferation comprising:

(a) contacting a cell with an agent which reduces the activity or level of a gene product required for proliferation of said cell, wherein said gene product is a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795;

(b) contacting said cell with a compound; and

(c) determining whether said compound reduces proliferation of said contacted cell by acting on said gene product.

158. The method of Paragraph 157, wherein said determining step comprises determining whether said compound reduces proliferation of said contacted cell to a greater extent than said compound reduces proliferation of cells which have not been contacted with said agent.

159. The method of Paragraph 157, wherein said cell is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

160. The method of Paragraph 157, wherein said cell is not an *E. coli* cell.

161. The method of Paragraph 157, wherein said gene product is from an organism other than *E. coli.*

162. The method of Paragraph 157, wherein said agent which reduces the activity or level of a gene product required for proliferation of said cell comprises an antisense nucleic acid to a gene or operon required for proliferation.

163. The method of Paragraph 157, wherein said agent which reduces the activity or level of a gene product required for proliferation of said cell comprises a compound known to inhibit growth or proliferation of a cell.

164. The method of Paragraph 157, wherein said cell contains a mutation which reduces the activity or level of said gene product required for proliferation of said cell.

165. The method of Paragraph 157, wherein said mutation is a temperature sensitive mutation.

166. The method of Paragraph 157, wherein said gene product comprises a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

167. A compound identified using the method of Paragraph 157.

168. A method for identifying the biological pathway in which a proliferation-required gene or its gene product lies, wherein said gene or gene product comprises a gene or gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 8-3795, said method comprising:

(a) providing a sublethal level of an antisense nucleic acid which inhibits the activity of said proliferation-required gene or gene product in a test cell;

(b) contacting said test cell with a compound known to inhibit growth or proliferation of a cell, wherein the biological pathway on which said compound acts is known; and

(c) determining the degree to which said proliferation of said test cell is inhibited relative to a cell which was not contacted with said compound.

169. The method of Paragraph 168, wherein said determining step comprises determining whether said test cell has a substantially greater sensitivity to said compound than a cell which does not express said sublethal level of said antisense nucleic acid.

170. The method of Paragraph 168, wherein said gene product comprises a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

171. The method of Paragraph 168, wherein said test cell is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

172. The method of Paragraph 168, wherein said test cell is not an *E. coli* cell.

173. The method of Paragraph 168, wherein said gene product is from an organism other than *E. coli*.

174. A method for determining the biological pathway on which a test compound acts comprising:

(a) providing a sublethal level of an antisense nucleic acid complementary to a proliferation-required nucleic acid in a first cell, wherein the activity or expression of said proliferation-required nucleic acid is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 8-3795 and wherein the biological pathway in which said proliferation-required nucleic acid or a protein encoded by said proliferation-required nucleic acid lies is known,

(b) contacting said first cell with said test compound; and

(c) determining the degree to which said test compound inhibits proliferation of said first cell relative to a cell which does not contain said antisense nucleic acid.

175. The method of Paragraph 174, wherein said determining step comprises determining whether said first cell has a substantially greater sensitivity to said test compound than a cell which does not express said sublethal level of said antisense nucleic acid.

176. The method of Paragraph 174, further comprising:

(d) providing a sublethal level of a second antisense nucleic acid complementary to a second proliferation-required nucleic acid in a second cell, wherein said second proliferation-required nucleic acid is in a different biological pathway than said proliferation-required nucleic acid in step (a); and

(e) determining whether said second cell does not have a substantially greater sensitivity to said test compound than a cell which does not express said sublethal level of said second antisense nucleic acid, wherein said test compound is specific for the biological pathway against which the antisense nucleic acid of step (a) acts if said first cell has a substantially greater sensitivity to said test compound than said second cell.

177. The method of Paragraph 174, wherein said first cell is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella*

typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

178. The method of Paragraph 174, wherein said first cell is not an *E. coli* cell.

179. The method of Paragraph 174, wherein said proliferation-required nucleic acid is from an organism other than *E. coli.*

180. A purified or isolated nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 8-3795.

181. A compound which interacts with a gene or gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence of one of SEQ ID NOs.: 8-3795 to inhibit proliferation.

182. The compound of Paragraph 181, wherein said gene product is a polypeptide comprising one of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

183. The compound of Paragraph 181, wherein said gene comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012.

184. A compound which interacts with a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence of one of SEQ ID NOs.: 8-3795 to inhibit proliferation.

185. A method for manufacturing an antibiotic comprising the steps of:

screening one or more candidate compounds to identify a compound that reduces the activity or level of a gene product required for proliferation, said gene product comprising a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795; and

manufacturing the compound so identified.

186. The method of Paragraph 185, wherein said screening step comprises performing any one of the methods of Paragraphs 44, 68, 121, 136, 141, and 157.

187. The method of Paragraph 185, wherein said gene product is a polypeptide comprising one of SEQ ID NOs:3801-3805, 4861-5915, 10013-14110.

188. A method for inhibiting proliferation of a cell in a subject comprising administering an effective amount of a compound that reduces the activity or level of a gene product required for proliferation of said cell, said gene product comprising a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 to said subject.

189. The method of Paragraph 188 wherein said subject is selected from the group consisting of vertebrates, mammals, avians, and human beings.

190. The method of Paragraph 188, wherein said gene product comprises a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

191. The method of Paragraph 188, wherein said cell is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

192. The method of Paragraph 188, wherein said cell is not *E. coli*.

193. The method of Paragraph 188, wherein said gene product is from an organism other than *E. coli*.

194. A purified or isolated nucleic acid consisting essentially of the coding sequence of one of SEQ ID NOs: 3796-3800, 3806-4860, 5916-10012.

195. A fragment of the nucleic acid of Paragraph 8, said fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive nucleotides of one of SEQ ID NOs: 3796-3800, 3806-4860, 5916-10012.

196. A purified or isolated nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, fragments comprising at least 25 consecutive nucleotides of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, the nucleotide sequences complementary to SEQ ID NOs.:3796-3800, 3806-4860, 5916-10012, and the nucleotide sequences complementary to fragments comprising at least 25 consecutive nucleotides of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012 as determined using BLASTN version 2.0 with the default parameters.

197. The nucleic acid of Paragraph 196, wherein said nucleic acid is from an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

198. The nucleic acid of Paragraph 196, wherein said nucleic acid is from an organism other than *E. coli.*

199. A method of inhibiting proliferation of a cell comprising inhibiting the activity or reducing the amount of a gene product in said cell or inhibiting the activity or reducing the amount of a nucleic acid encoding said gene product in said cell, wherein said gene product is selected from the group consisting of a gene product having having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795

under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 8-3795.

200. The method of Paragraph 199, wherein said method comprises inhibiting said activity or reducing said amount of said gene product or inhibiting the activity or reducing the amount of a nucleic acid encoding said gene product in an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulimum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

201. The method of Paragraph 199, wherein said method comprises inhibiting said activity or reducing said amount of said gene product or inhibiting the activity or reducing the amount of a nucleic acid encoding said gene product in an organism other than *E. coli*.

202. The method of Paragraph 199, wherein said gene product is from an organism other than *E. coli*.

203. The method of Paragraph 199, wherein said gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110.

204. The method of Paragraph 199, wherein said gene product is encoded by a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-

3800, 3806-4860, 5916-10012, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under stringent conditions, and a nucleic acid comprising a nucloetide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under moderate condtions.

205. A method for identifying a compound which influences the activity of a gene product required for proliferation comprising:

contacting a candidate compound with a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795; and

determining whether said candidate compound influences the activity of said gene product.

206. The method of Paragraph 205, wherein said gene product is from an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori,*

Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

207. The method of Paragraph 205, wherein said gene product is from an organism other than *E. coli*.

208. The method of Paragraph 205, wherein said gene product is a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110.

209. The method of Paragraph 205, wherein said gene product is encoded by a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under stringent conditions, and a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under moderate condtions.

210. A compound identified using the method of Paragraph 205.

211. A method for identifying a compound or nucleic acid having the ability to reduce the activity or level of a gene product required for proliferation comprising:

(a) providing a target that is a gene or RNA, wherein said target comprises a nucleic acid that encodes a gene product selected from the group consisting of a gene product having having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleic acid identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group

consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795;

(b) contacting said target with a candidate compound or nucleic acid; and

(c) measuring an activity of said target.

212. The method of Paragraph 211, wherein said target gene or RNA is from an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

213. The method of Paragraph 211, wherein said target gene or RNA is from an organism other than *E. coli*.

214. The method of Paragraph 211, wherein said gene product is from an organism other than *E. coli*.

215. The method of Paragraph 211, wherein said target is a messenger RNA molecule and said activity is translation of said messenger RNA.

216. The method of Paragraph 211, wherein said compound is a nucleic acid and said activity is translation of said gene product.

217. The method of Paragraph 211, wherein said target is a gene and said activity is transcription of said gene.

218. The method of Paragraph 211, wherein said target is a nontranslated RNA and said activity is processing or folding of said nontranslated RNA or assembly of said nontranslated RNA into a protein/RNA complex.

219. The method of Paragraph 211, wherein said target gene is a messenger RNA molecule encoding a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110.

220. The method of Paragraph 11, wherein said target gene comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under stringent conditions, and a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under moderate condtions.

221. A compound or nucleic acid identified using the method of Paragraph 211.

222. A method for identifying a compound which reduces the activity or level of a gene product required for proliferation of a cell comprising:

(a) providing a sublethal level of an antisense nucleic acid complementary to a nucleic acid encoding said gene product in a cell to reduce the activity or amount of said gene product in said cell, thereby producing a sensitized cell, wherein said gene product is selected from the group consisting of a gene product having having at least 70% nucleic acid identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited

by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795;

(b) contacting said sensitized cell with a compound; and

(c) determining the degree to which said compound inhibits the growth of said sensitized cell relative to a cell which does not contain said antisense nucleic acid.

223. The method of Paragraph 222, wherein said determining step comprises determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of a nonsensitized cell.

224. The method of Paragraph 222, wherein said sensitized cell is a Gram positive bacterium.

225. The method of Paragraph 224, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

226. The method of Paragraph 225, wherein said bacterium is *Staphylococcus aureus*.

227. The method of Paragraph 224, wherein said *Staphylococcus* species is coagulase negative.

228. The method of Paragraph 226, wherein said bacterium is selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

229. The method of Paragraph 222, wherein said sensitized cell is an organism selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris,*

Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

230. The method of Paragraph 222, wherein said cell is an organism other than *E. coli*.

231. The method of Paragraph 222, wherein said gene product is from an organism other than *E. coli*.

232. The method of Paragraph 222, wherein said antisense nucleic acid is transcribed from an inducible promoter.

233. The method of Paragraph 222, further comprising the step of contacting said cell with a concentration of inducer which induces transcription of said antisense nucleic acid to a sublethal level.

234. The method of Paragraph 222, wherein growth inhibition is measured by monitoring optical density of a culture medium.

235. The method of Paragraph 222, wherein said gene product is a polypeptide.

236. The method of Paragraph 235, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110.

237. The method of Paragraph 222, wherein said gene product is an RNA.

238. The method of Paragraph 222, wherein said nucleic acid encoding said gene product comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleic acid identity as determined using BLASTN version 2.0 with the default parameters to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under stringent conditions, and a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under moderate condtions.

239. A compound identified using the method of Paragraph 222.

240. A method for inhibiting cellular proliferation comprising introducing a compound with activity against a gene product or a compound with activity against a gene encoding said gene product into a population of cells expressing said gene product, wherein said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence

identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795.

241. The method of Paragraph 240, wherein said compound is an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, or a proliferation-inhibiting portion thereof.

242. The method of Paragraph 240, wherein said proliferation inhibiting portion of one of SEQ ID NOs.: 8-3795 is a fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 51 consecutive nucleotides of one of SEQ ID NOs.: 8-3795.

243. The method of Paragraph 240, wherein said population is a population of Gram positive bacteria.

244. The method of Paragraph 243, wherein said population of Gram positive bacteria is selected from the group consisting of a population of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

245. The method of Paragraph 243, wherein said population is a population of *Staphylococcus aureus*.

246. The method of Paragraph 245, wherein said population is a population of a bacterium selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

247. The method of Paragraph 240, wherein said population is a population of a bacterium selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr*

(also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

248. The method of Paragraph 240, wherein said population is a population of an organism other than *E. coli*.

249. The method of Paragraph 240, wherein said product of said gene is from an organism other than *E. coli*.

250. The method of Paragraph 240, wherein said gene product is selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110.

251. The method of Paragraph 240, wherein said gene comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under moderate condtions.

252. A preparation comprising an effective concentration of an antisense nucleic acid in a pharmaceutically acceptable carrier wherein said antisense nucleic acid is selected from the group consisting of a nucleic acid comprising a sequence having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 or a proliferation-inhibiting portion

thereof, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions.

253. The preparation of Paragraph 252, wherein said proliferation-inhibiting portion of one of SEQ ID NOs.: 8-3795 comprises at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive nucleotides of one of SEQ ID NOs.: 8-3795.

254. A method for inhibiting the activity or expression of a gene in an operon which encodes a gene product required for proliferation comprising contacting a cell in a cell population with an antisense nucleic acid comprising at least a proliferation-inhibiting portion of said operon in an antisense orientation, wherein said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795.

255. The method of Paragraph 254, wherein said antisense nucleic acid comprises a nucleotide sequence having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide seqence selected from the group consisting of SEQ ID NOs.: 8-3795, a proliferation inhibiting portion thereof, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, and a nucleic acid which comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions.

256. The method of Paragraph 254, wherein said cell is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis*

Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

257. The method of Paragraph 254, wherein said cell is not an *E. coli* cell.

258. The method of Paragraph 254, wherein said gene is from an organism other than *E. coli*.

259. The method of Paragraph 254, wherein said cell is contacted with said antisense nucleic acid by introducing a plasmid which transcribes said antisense nucleic acid into said cell population.

260. The method of Paragraph 254, wherein said cell is contacted with said antisense nucleic acid by introducing a phage which transcribes said antisense nucleic acid into said cell population.

261. The method of Paragraph 254, wherein said cell is contacted with said antisense nucleic acid by transcribing said antisense nucleic acid from the chromosome of cells in said cell population.

262. The method of Paragraph 254, wherein said cell is contacted with said antisense nucleic acid by introducing a promoter adjacent to a chromosomal copy of said antisense nucleic acid such that said promoter directs the synthesis of said antisense nucleic acid.

263. The method of Paragraph 254, wherein said cell is contacted with said antisense nucleic acid by introducing a retron which expresses said antisense nucleic acid into said cell population.

264. The method of Paragraph 254, wherein said cell is contacted with said antisense nucleic acid by introducing a ribozyme into said cell-population, wherein a binding portion of said ribozyme is complementary to said antisense oligonucleotide.

265. The method of Paragraph 254, wherein said cell is contacted with said antisense nucleic acid by introducing a liposome comprising said antisense oligonucleotide into said cell.

266. The method of Paragraph 254, wherein said cell is contacted with said antisense nucleic acid by electroporation of said antisense nucleic acid into said cell.

267. The method of Paragraph 254, wherein said antisense nucleic acid has at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive nucleotides of one of SEQ ID NOs.: 8-3795.

268. The method of Paragraph 254 wherein said antisense nucleic acid is a synthetic oligonucleotide.

269. The method of Paragraph 254, wherein said gene comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under moderate condtions.

270. A method for identifying a gene which is required for proliferation of a cell comprising:

(a) contacting a cell with an antisense nucleic acid selected from the group consisting of a nucleic acid at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 or a proliferation-inhibiting portion thereof, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, wherein said cell is a cell other than the organism from which said nucleic acid was obtained;

(b) determining whether said nucleic acid inhibits proliferation of said cell; and

(c) identifying the gene in said cell which encodes the mRNA which is complementary to said antisense nucleic acid or a portion thereof.

271. The method of Paragraph 270, wherein said cell is selected from the group consisting of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

272. The method of Paragraph 270 wherein said cell is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulimum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

273. The method of Paragraph 270, wherein said cell is not *E. coli*.

274. The method of Paragraph 270, further comprising operably linking said antisense nucleic acid to a promoter which is functional in said cell, said promoter being included in a vector, and introducing said vector into said cell.

275. A method for identifying a compound having the ability to inhibit proliferation of a cell comprising:

(a) identifying a homolog of a gene or gene product whose activity or level is inhibited by an antisense nucleic acid in a test cell, wherein said test cell is not the microorgaism from which the antisense nucleic acid was obtained, wherein said antisense nucleic acid is selected from the group consisting of a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs. 8-3795, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions;

(b) identifying an inhibitory nucleic acid sequence which inhibits the activity of said homolog in said test cell;

(c) contacting said test cell with a sublethal level of said inhibitory nucleic acid, thus sensitizing said cell;

(d) contacting the sensitized cell of step (c) with a compound; and

(e) determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a cell which does not express said inhibitory nucleic acid.

276. The method of Paragraph 275, wherein said determining step comprises determining whether said compound inhibits proliferation of said sensitized test cell to a greater extent than said compound inhibits proliferation of a nonsensitized test cell.

277. The method of Paragraph 275, wherein step (a) comprises identifying a homologous nucleic acid to a gene or gene product whose activity or level is inhibited by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs. 8-3795 or a nucleic acid encoding a homologous polypeptide to a polypeptide whose activity or level is inhibited by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs. 8-3795 by using an algorithm selected from the group consisting of BLASTN version 2.0 with the default parameters and FASTA version 3.0t78 algorithm with the default parameters to identify said homologous nucleic acid or said nucleic acid encoding a homologous polypeptide in a database.

278. The method of Paragraph 275 wherein said step (a) comprises identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide by identifying nucleic acids comprising nucleotide sequences which hybridize to said nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs. 8-3795 or the complement of the nucleotide sequence of said nucleic acid selected from the group consisting of SEQ ID NOs. 8-3795.

279. The method of Paragraph 275 wherein step (a) comprises expressing a nucleic acid having at least 70% nucleic acid identity as determined using BLASTN version 2.0 with the default parameters to a sequence selected from the group consisting of SEQ ID NOs. 8-3795 in said test cell.

280. The method of Paragraph 275, wherein step (a) comprises identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide in an test cell selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus*

faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

281. The method of Paragraph 275, wherein step (a) comprises identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide in a test cell other than *E. coli.*

282. The method of Paragraph 275, wherein said inhibitory nucleic acid is an antisense nucleic acid.

283. The method of Paragraph 275, wherein said inhibitory nucleic acid comprises an antisense nucleic acid to a portion of said homolog.

284. The method of Paragraph 275, wherein said inhibitory nucleic acid comprises an antisense nucleic acid to a portion of the operon encoding said homolog.

285. The method of Paragraph 275, wherein the step of contacting the cell with a sublethal level of said inhibitory nucleic acid comprises directly contacting said cell with said inhibitory nucleic acid.

286. The method of Paragraph 275, wherein the step of contacting the cell with a sublethal level of said inhibitory nucleic acid comprises expressing an antisense nucleic acid to said homolog in said cell.

287. The method of Paragraph 275, wherein said gene product comprises a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

288. The method of Paragraph 275, wherein said gene comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under moderate condtions.

289. A compound identified using the method of Paragraph 275.

290. A method of identifying a compound having the ability to inhibit proliferation comprising:

(a) sensitizing a test cell by contacting said test cell with a sublethal level of an antisense nucleic acid, wherein said antisense nucleic acid is selected from the group consisting of a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs. 8-3795 or a portion thereof which inhibits the proliferation of the cell from which said nucleic acid was obtained, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditionst;

(b) contacting the sensitized test cell of step (a) with a compound; and

(c) determining the degree to which said compound inhibits proliferation of said sensitized test cell relative to a cell which does not contain said antisense nucleic acid.

291. The method of Paragraph 290, wherein said determining step comprises determining whether said compound inhibits proliferation of said sensitized test cell to a greater extent than said compound inhibits proliferation of a nonsensitized test cell.

292. A compound identified using the method of Paragraph 290.

293. The method of Paragraph 290, wherein said test cell is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

294. The method of Paragraph 290, wherein the test cell is not *E. coli*.

295. A method for identifying a compound having activity against a biological pathway required for proliferation comprising:

(a) sensitizing a cell by providing a sublethal level of an antisense nucleic acid complementary to a nucleic acid encoding a gene product required for proliferation, wherein said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795;

(b) contacting the sensitized cell with a compound; and

(c) determining the extent to which said compound inhibits the growth of said sensitized cell relative to a cell which does not contain said antisense nucleic acid.

296. The method of Paragraph 295, wherein said determining step comprises determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of a nonsensitized cell.

297. The method of Paragraph 295, wherein said cell is selected from the group consisting of bacterial cells, fungal cells, plant cells, and animal cells.

298. The method of Paragraph 295, wherein said cell is a Gram positive bacterium.

299. The method of Paragraph 298, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

300. The method of Paragraph 299, wherein said Gram positive bacterium is *Staphylococcus aureus*.

301. The method of Paragraph 298, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

302. The method of Paragraph 295, wherein said cell is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulimum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

303. The method of Paragraph 295, wherein said cell is not an *E. coli* cell.

304. The method of Paragraph 295, wherein said gene product is from an organism other than *E. coli*.

305. The method of Paragraph 295, wherein said antisense nucleic acid is transcribed from an inducible promoter.

306. The method of Paragraph 305, further comprising contacting the cell with an agent which induces expression of said antisense nucleic acid from said inducible promoter, wherein said antisense nucleic acid is expressed at a sublethal level.

307. The method of Paragraph 295, wherein inhibition of proliferation is measured by monitoring the optical density of a liquid culture.

308. The method of Paragraph 295, wherein said gene product comprises a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

309. The method of Paragraph 295, wherein said nucleic acid encoding said gene product comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting

of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under moderate condtions.

310. A compound identified using the method of Paragraph 295.

311. A method for identifying a compound having the ability to inhibit cellular proliferation comprising:

(a) contacting a cell with an agent which reduces the activity or level of a gene product required for proliferation of said cell, wherein said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795;

(b) contacting said cell with a compound; and

(c) determining the degree to which said compound reduces proliferation of said contacted cell relative to a cell which was not contacted with said agent.

312. The method of Paragraph 311, wherein said determining step comprises determining whether said compound reduces proliferation of said contacted cell to a greater extent than said compound reduces proliferation of cells which have not been contacted with said agent.

313. The method of Paragraph 311, wherein said cell is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida*

glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

314. The method of Paragraph 311, wherein said cell is not an *E. coli* cell.

315. The method of Paragraph 311, wherein said gene product is from an organism other than *E. coli*.

316. The method of Paragraph 311, wherein said agent which reduces the activity or level of a gene product required for proliferation of said cell comprises an antisense nucleic acid to a gene or operon required for proliferation.

317. The method of Paragraph 311, wherein said agent which reduces the activity or level of a gene product required for proliferation of said cell comprises a compound known to inhibit growth or proliferation of a cell.

318. The method of Paragraph 311, wherein said cell contains a mutation which reduces the activity or level of said gene product required for proliferation of said cell.

319. The method of Paragraph 311, wherein said mutation is a temperature sensitive mutation.

320. The method of Paragraph 311, wherein said gene product comprises a gene product comprises a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

321. A compound identified using the method of Paragraph 311.

322. A method for identifying the biological pathway in which a proliferation-required gene product or a gene encoding a proliferation-required gene product lies comprising:

(a) providing a sublethal level of an antisense nucleic acid which inhibits the activity or reduces the level of said gene encoding a proliferation-required gene product or said said proliferation-required gene product in a test cell, wherein said proliferation-

required gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795;

(b) contacting said test cell with a compound known to inhibit growth or proliferation of a cell, wherein the biological pathway on which said compound acts is known; and

(c) determining the degree to which said compound inhibits proliferation of said test cell relative to a cell which does not contain said antisense nucleic acid.

323. The method of Paragraph 322, wherein said determining step comprises determining whether said test cell has a substantially greater sensitivity to said compound than a cell which does not express said sublethal level of said antisense nucleic acid.

324. The method of Paragraph 322, wherein said gene product comprises a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

325. The method of Paragraph 322, wherein said test cell is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus*

neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

326. The method of Paragraph 322, wherein said test cell is not an *E. coli* cell.

327. The method of Paragraph 322, wherein said gene product is from an organism other than *E. coli.*

328. A method for determining the biological pathway on which a test compound acts comprising:

(a) providing a sublethal level of an antisense nucleic acid complementary to a proliferation-required nucleic acid in a cell, thereby producing a sensitized cell, wherein said antisense nucleic acid is selected from the group consisting of a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795 or a proliferation-inhibiting portion thereof,a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions and wherein the biological pathway in which said proliferation-required nucleic acid or a protein encoded by said proliferation-required polypeptide lies is known,

(b) contacting said cell with said test compound; and

(c) determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a cell which does not contain said antisense nucleic acid.

329. The method of Paragraph 328, wherein said determining step comprises determining whether said sensitized cell has a substantially greater sensitivity to said test compound than a cell which does not express said sublethal level of said antisense nucleic acid.

330. The method of Paragraph 328, further comprising:

(d) providing a sublethal level of a second antisense nucleic acid complementary to a second proliferation-required nucleic acid in a second cell, wherein said second

proliferation-required nucleic acid is in a different biological pathway than said proliferation-required nucleic acid in step (a); and

(e) determining whether said second cell does not have a substantially greater sensitivity to said test compound than a cell which does not express said sublethal level of said second antisense nucleic acid, wherein said test compound is specific for the biological pathway against which the antisense nucleic acid of step (a) acts if said sensitized cell has substantially greater sensitivity to said test compound than said second cell.

331. The method of Paragraph 328, wherein said sensitized cell is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

332. The method of Paragraph 328, wherein said sensitized cell is not an *E. coli* cell.

333. The method of Paragraph 328, wherein said proliferation-required nucleic acid is from an organism other than *E. coli.*

334. A compound which inhibits proliferation by interacting with a gene encoding a gene product required for proliferation or with a gene product required for proliferation, wherein said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from

the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795.

335. The compound of Paragraph 334, wherein said gene product comprises a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

336. The compound of Paragraph 334, wherein said gene comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 under moderate condtions.

337. A method for manufacturing an antibiotic comprising the steps of:

screening one or more candidate compounds to identify a compound that reduces the activity or level of a gene product required for proliferation wherein said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence

which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795 ; and

manufacturing the compound so identified.

338. The method of Paragraph 337, wherein said screening step comprises performing any one of the methods of Paragraphs 205, 211, 222, 275, 290, 295, 311.

339. The method of Paragraph 337, wherein said gene product comprises a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

340. A method for inhibiting proliferation of a cell in a subject comprising administering an effective amount of a compound that reduces the activity or level of a gene product required for proliferation of said cell, wherein said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795.

341. The method of Paragraph 340 wherein said subject is selected from the group consisting of vertebrates, mammals, avians, and human beings.

342. The method of Paragraph 340, wherein said gene product comprises a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default

parameters to an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110.

343. The method of Paragraph 340, wherein said cell is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

344. The method of Paragraph 340, wherein said cell is not *E. coli.*

345. The method of Paragraph 340, wherein said gene product is from an organism other than *E. coli.*

Definitions

By "biological pathway" is meant any discrete cell function or process that is carried out by a gene product or a subset of gene products. Biological pathways include anabolic, catabolic, enzymatic, biochemical and metabolic pathways as well as pathways involved in the production of cellular structures such as cell walls. Biological pathways that are usually required for proliferation of cells or microorganisms include, but are not limited to, cell division, DNA synthesis and replication, RNA synthesis (transcription), protein synthesis (translation), protein processing, protein transport, fatty acid biosynthesis, electron transport chains, cell wall synthesis, cell membrane production, synthesis and maintenance, and the like.

By "inhibit activity of a gene or gene product" is meant having the ability to interfere with the function of a gene or gene product in such a way as to decrease expression of the gene, in such a way as to reduce the level or activity of a product of the gene or in such a way as to inhibit the interaction of the gene or gene product with other biological molecules required for its activity. Agents which inhibit the activity of a gene include agents that inhibit transcription of the gene, agents that inhibit processing of the transcript of the gene, agents that reduce the stability of the

transcript of the gene, and agents that inhibit translation of the mRNA transcribed from the gene. In microorganisms, agents which inhibit the activity of a gene can act to decrease expression of the operon in which the gene resides or alter the folding or processing of operon RNA so as to reduce the level or activity of the gene product. The gene product can be a non-translated RNA such as ribosomal RNA, a translated RNA (mRNA) or the protein product resulting from translation of the gene mRNA. Of particular utility to the present invention are antisense RNAs that have activities against the operons or genes to which they specifically hybridze.

By "activity against a gene product" is meant having the ability to inhibit the function or to reduce the level or activity of the gene product in a cell. This includes, but is not limited to, inhibiting the enzymatic activity of the gene product or the ability of the gene product to interact with other biological molecules required for its activity, including inhibiting the gene product's assembly into a multimeric structure.

By "activity against a protein" is meant having the ability to inhibit the function or to reduce the level or activity of the protein in a cell. This includes, but is not limited to, inhibiting the enzymatic activity of the protein or the ability of the protein to interact with other biological molecules required for its activity, including inhibiting the protein's assembly into a multimeric structure.

By "activity against a nucleic acid" is meant having the ability to inhibit the function or to reduce the level or activity of the nucleic acid in a cell. This includes, but is not limited to, inhibiting the ability of the nucleic acid interact with other biological molecules required for its activity, including inhibiting the nucleic acid's assembly into a multimeric structure.

By "activity against a gene" is meant having the ability to inhibit the function or expression of the gene in a cell. This includes, but is not limited to, inhibiting the ability of the gene to interact with other biological molecules required for its activity.

By "activity against an operon" is meant having the ability to inhibit the function or reduce the level of one or more products of the operon in a cell. This includes, but is not limited to, inhibiting the enzymatic activity of one or more products of the operon or the ability of one or more products of the operon to interact with other biological molecules required for its activity.

By "antibiotic" is meant an agent which inhibits the proliferation of a cell or microorganism.

By "*E. coli or Escherichia coli*" is meant *Escherichia coli* or any organism previously categorized as a species of *Shigella* including *Shigella boydii, Shigella flexneri, Shigella dysenteriae, Shigella sonnei, Shigella 2A*.

By "homologous coding nucleic acid" is meant a nucleic acid homologous to a nucleic acid encoding a gene product whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 or a portion thereof. In some embodiments, the homologous coding nucleic acid may have at least 97%, at least 95%, at least 90%, at least 85%, at

least 80%, or at least 70% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 and fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof. In other embodiments the homologous coding nucleic acids may have at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, or at least 70% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of the nucleotide sequences complementary to one of SEQ ID NOs.: 8-3795 and fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof. Identity may be measured using BLASTN version 2.0 with the default parameters or tBLASTX with the default parameters. (Altschul, S.F. et al. Gapped BLAST and PSI-BLAST: A New Generation of Protein Database Search Programs, Nucleic Acid Res. 25: 3389-3402 (1997)) Alternatively a "homologuous coding nucleic acid" could be identified by membership of the gene of interest to a functional orthologue cluster. All other members of that orthologue cluster would be considered homologues. Such a library of functional orthologue clusters can be found at http://www.ncbi.nlm.nih.gov/COG. A gene can be classified into a cluster of orthologous groups or COG by using the COGNITOR program available at the above web site, or by direct BLASTP comparison of the gene of interest to the members of the COGs and analysis of these results as described by Tatusov, R.L., Galperin, M.Y., Natale, D. A. and Koonin, E.V. (2000) The COG database: a tool for genome-scale analysis of protein functions and evolution. Nucleic Acids Research v. 28 n. 1, pp33-36.

The term "homologous coding nucleic acid" also includes nucleic acids comprising nucleotide sequences which encode polypeptides having at least 99%, 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40% or at least 25% maino acid identity or similarity to a polypeptide comprising the amino acid sequence of one of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110 or to a polypeptpide whose expression is inhibited by a nucleic acid comprising a nucleotide sequence of one of SEQ ID NOs: 8-3795 or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof as determined using the FASTA version 3.0t78 algorithm with the default parameters. Alternatively, protein identity or similarity may be identified using BLASTP with the default parameters, BLASTX with the default parameters, TBLASTN with the default parameters, or tBLASTX with the default parameters. (Altschul, S.F. et al. Gapped BLAST and PSI-BLAST: A New Generation of Protein Database Search Programs, Nucleic Acid Res. 25: 3389-3402 (1997)).

The term "homologous coding nucleic acid" also includes coding nucleic acids which hybridize under stringent conditions to a nucleic acid selected from the group consisting of the nucleotide sequences complementary to one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 and coding nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the sequences complementary to one of SEQ ID NOS.:

3796-3800, 3806-4860, 5916-10012 As used herein, "stringent conditions" means hybridization to filter-bound nucleic acid in 6xSSC at about 45°C followed by one or more washes in 0.1xSSC/0.2% SDS at about 68°C. Other exemplary stringent conditions may refer, *e.g.*, to washing in 6xSSC/0.05% sodium pyrophosphate at 37°C, 48°C, 55°C, and 60°C as appropriate for the particular probe being used.

The term "homologous coding nucleic acid" also includes coding nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a nucleotide sequence selected from the group consisting of the sequences complementary to one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 and coding nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the sequences complementary to one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012. As used herein, "moderate conditions" means hybridization to filter-bound DNA in 6x sodium chloride/sodium citrate (SSC) at about 45°C followed by one or more washes in 0.2xSSC/0.1% SDS at about 42-65°C.

The term "homologous coding nucleic acids" also includes nucleic acids comprising nucleotide sequences which encode a gene product whose activity may be complemented by a gene encoding a gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795. In some embodiments, the homologous coding nucleic acids may encode a gene product whose activity is complemented by the gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012. In other embodiments, the homologous coding nucleic acids may comprise a nucleotide sequence encode a gene product whose activity is complemented by one of the polypeptides of SEQ ID NOs. 3745-4773.

The term "homologous antisense nucleic acid" includes nucleic acids comprising a nucleotide sequence having at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, or at least 70% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of one of the sequences of SEQ ID NOS. 8-3795 and fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof. Homologous antisense nucleic acids may also comprising nucleotide sequences which have at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, or at least 70% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of the sequences complementary to one of sequences of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 and fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof. Nucleic acid identity may be determined as described above.

The term "homologous antisense nucleic acid" also includes antisense nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a nucleotide sequence complementary to one of SEQ ID NOs.: 8-3795 and antisens nucleic acids comprising

nucleotide sequences which hybridize under stringent conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the sequence complementary to one of SEQ ID NOs. 8-3795. Homologous antisense nucleic acids also include antisense nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 and antisense nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012.

The term "homologous antisense nucleic acid" also includes antisense nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a nucleotide sequence complementary to one of SEQ ID NOs.: 8-3795 and antisens nucleic acids comprising nucleotide seuqences which hybridize under moderate conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the sequence complementary to one of SEQ ID NOs. 8-3795. Homologous antisense nucleic acids also include antisense nucleic acids comprising nucleotide seuqences which hybridize under moderate conditions to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 and antisense nucleic acids which comprising nucleotide sequences hybridize under moderate conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012.

By "homologous polypeptide" is meant a polypeptide homologous to a polypeptide whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 or by a homologous antisense nucleic acid. The term "homologous polypeptide" includes polypeptides having at least 99%, 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40% or at least 25% amino acid identity or similarity to a polypeptide whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795 or by a homologous antisense nucleic acid, or polypeptides having at least 99%, 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40% or at least 25% amino acid identity or similarity to a polypeptide to a fragment comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of a polypeptide whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 or by a homologous antisense nucleic acid. Identity or similarity may be determined using the FASTA version 3.0t78 algorithm with the default parameters. Alternatively, protein identity or similarity may be identified using BLASTP with the default parameters, BLASTX with the default parameters, or TBLASTN with the default

parameters. (Altschul, S.F. et al. Gapped BLAST and PSI-BLAST: A New Generation of Protein Database Search Programs, Nucleic Acid Res. 25: 3389-3402 (1997).

The term homologous polypeptide also includes polypeptides having at least 99%, 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40% or at least 25% amino acid identity or similarity to a polypeptide selected from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110 and polypeptides having at least 99%, 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40% or at least 25% amino acid identity or similarity to a fragment comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of a polypeptide selected from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110.

The invention also includes polynucleotides, preferably DNA molecules, that hybridize to one of the nucleic acids of SEQ ID NOs.: 8-3795, SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012 or the complements of any of the preceding nucleic acids. Such hybridization may be under stringent or moderate conditions as defined above or under other conditions which permit specific hybridization. The nucleic acid molecules of the invention that hybridize to these DNA sequences include oligodeoxynucleotides ("oligos") which hybridize to the target gene under highly stringent or stringent conditions. In general, for oligos between 14 and 70 nucleotides in length the melting temperature (Tm) is calculated using the formula:

$$Tm\ (^\circ C) = 81.5 + 16.6(\log[\text{monovalent cations (molar)}] + 0.41\ (\%\ G{+}C) - (500/N)$$

where N is the length of the probe. If the hybridization is carried out in a solution containing formamide, the melting temperature may be calculated using the equation:

$$Tm(^\circ C) = 81.5 + 16.6(\log[\text{monovalent cations (molar)}] + 0.41(\%\ G{+}C) - (0.61)\ (\%\ \text{formamide}) - (500/N)$$

where N is the length of the probe. In general, hybridization is carried out at about 20-25 degrees below Tm (for DNA-DNA hybrids) or about 10-15 degrees below Tm (for RNA-DNA hybrids).

Other hybridization conditions are apparent to those of skill in the art (see, for example, Ausubel, F.M. *et al.*, eds., 1989, *Current Protocols in Molecular Biology*, Vol. I, Green Publishing Associates, Inc. and John Wiley & Sons, Inc., New York, at pp. 6.3.1-6.3.6 and 2.10.3.

The term, *Salmonella*, is the generic name for a large group of gram-negative enteric bacteria that are closely related to *Escherichia coli*. The diseases caused by *Salmonella* are often due to contamination of foodstuffs or the water supply and affect millions of people each year. Traditional methods of *Salmonella* taxonomy were based on assigning a separate species name to

each serologically distinguishable strain (Kauffmann, F 1966 The bacteriology of the *Enterobacteriaceae*. Munksgaard, Copenhagen). Serology of *Salmonella* is based on surface antigens (O [somatic] and H [flagellar]). Over 2,400 serotypes or serovars of *Salmonella* are known (Popoff, et al. 2000 Res. Microbiol. 151:63-65). Therefore, each serotype was considered to be a separate species and often given names, accordingly (e.g. *S. paratyphi, S. typhimurium, S. typhi, S. enteriditis,* etc.).

However, by the 1970s and 1980s it was recognized that this system was not only cumbersome, but also inaccurate. Then, many *Salmonella* species were lumped into a single species (all serotypes and subgenera I, II, and IV and all serotypes of *Arizona*) with a second subspecies, *S. bongorii* also recognized (Crosa, et al., 1973, J. Bacteriol. 115:307-315). Though species designations are based on the highly variable surface antigens, the *Salmonella* are very similar otherwise with a major exception being pathogenicity determinants.

There has been some debate on the correct name for the *Salmonella* species. Currently (Brenner, et al. 2000 J. Clin. Microbiol. 38:2465-2467), the accepted name is *Salmonella enterica*. *S. enterica* is divided into six subspecies (I, *S. enterica* subsp. *enterica*; II, *S. enterica*, subsp. *salamae*; IIIa, *S. enterica* subsp. *arizonàe*; IIIb, *S. enterica* subsp. *diarizonae*; IV, *S. enterica* subsp. *houtenae*; and VI, *S. enterica* subsp. *indica*). Within subspecies I, serotypes are used to distinguish each of the serotypes or serovars (e.g. *S. enterica* serotype Enteriditis, *S. enterica* serotype Typhimurium, *S. enterica* serotype Typhi, and *S. enterica* serotype Choleraesuis, etc.). Current convention is to spell this out on first usage (*Salmonella enterica* ser. Typhimurium) and then use an abbreviated form (*Salmonella* Typhimurium or *S.* Typhimurium). Note, the genus and species names (*Salmonella enterica*) are italicized but not the serotype/serovar name (Typhimurium). Because the taxonomic committees have yet to officially approve of the actual species name, this latter system is what is employed by the CDC (Brenner, et al. 2000 J. Clin. Microbiol. 38:2465-2467). Due to the concerns of both taxonomic priority and medical importance, some of these serotypes might ultimately receive full species designations (*S. typhi* would be the most notable).

Therefore, as used herein "*Salmonella enterica* or *S. enterica*" includes serovars Typhi, Typhimurium, Paratyphi, Choleraesuis, etc." However, appeals of the "official" name are in process and the taxonomic designations may change (*S. choleraesuis* is the species name that could replace *S. enterica* based solely on priority).

By "identifying a compound" is meant to screen one or more compounds in a collection of compounds such as a combinatorial chemical library or other library of chemical compounds or to characterize a single compound by testing the compound in a given assay and determining whether it exhibits the desired activity.

By "inducer" is meant an agent or solution which, when placed in contact with a cell or microorganism, increases transcription, or inhibitor and/or promoter clearance/fidelity, from a desired promoter.

As used herein, "nucleic acid" means DNA, RNA, or modified nucleic acids. Thus, the terminology "the nucleic acid of SEQ ID NO: X" or "the nucleic acid comprising the nucleotide sequence" includes both the DNA sequence of SEQ ID NO: X and an RNA sequence in which the thymidines in the DNA sequence have been substituted with uridines in the RNA sequence and in which the deoxyribose backbone of the DNA sequence has been substituted with a ribose backbone in the RNA sequence. Modified nucleic acids are nucleic acids having nucleotides or structures which do not occur in nature, such as nucleic acids in which the internucleotide phosphate residues with methylphosphonates, phosphorothioates, phosphoramidates, and phosphate esters. Nonphosphate internucleotide analogs such as siloxane bridges, carbonate brides, thioester bridges, as well as many others known in the art may also be used in modified nucleic acids. Modified nucleic acids may also comprise, α-anomeric nucleotide units and modified nucleotides such as 1,2-dideoxy-d-ribofuranose, 1,2-dideoxy-1-phenylribofuranose, and N^4, N^4-ethano-5-methyl-cytosine are contemplated for use in the present invention. Modified nucleic acids may also be peptide nucleic acids in which the entire deoxyribose-phosphate backbone has been exchanged with a chemically completely different, but structurally homologous, polyamide (peptide) backbone containing 2-aminoethyl glycine units.

As used herein, "sub-lethal" means a concentration of an agent below the concentration required to inhibit all cell growth.

Brief Description of the Drawings

Figure 1 is an IPTG dose response curve in *E. coli* transformed with an IPTG-inducible plasmid containing either an antisense clone to the *E. coli* ribosomal protein *rpl*W (AS-*rplW*) which is required for protein synthesis and essential for cell proliferation, or an antisense clone to the *elaD* (AS-*elaD*) gene which is not known to be involved in protein synthesis and which is also essential for proliferation.

Figure 2A is a tetracycline dose response curve in *E. coli* transformed with an IPTG-inducible plasmid containing antisense to *rplW* (AS-*rplW*) in the absence (0) or presence of IPTG at concentrations that result in 20% and 50% growth inhibition.

Figure 2B is a tetracycline dose response curve in *E. coli* transformed with an IPTG-inducible plasmid containing antisense to *elaD* (AS-*elaD*)in the absence (0) or presence of IPTG at concentrations that result in 20% and 50% growth inhibition.

Figure 3 is a graph showing the fold increase in tetracycline sensitivity of *E. coli* transfected with antisense clones to essential ribosomal proteins *L23* (AS-*rplW*) and *L7/L12* and *L10* (AS-*rplLrplJ*). Antisense clones to genes known to not be directly involved in protein synthesis, *atpB/E* (AS-*atpB/E*), *visC* (AS-*visC*), *elaD* (AS-*elaD*), *yohH* (AS-*yohH*), are much less sensitive to tetracycline.

Figure 4 illustrates the results of an assay in which *Staphylococcus aureus* cells transcribing an antisense nucleic acid complementary to the *gyrB* gene encoding the β subunit of gyrase were contacted with several antibiotics whose targets were known.

Detailed Description of the Preferred Embodiments

The present invention describes a group of prokaryotic genes and gene families required for cellular proliferation. Exemplary genes and gene families from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* and *Salmonella typhi* are provided. A proliferation-required gene or gene family is one where, in the absence or substantial reduction of a gene transcript and/or gene product, growth or viability of the cell or microorganism is reduced or eliminated. Thus, as used herein, the terminology "proliferation-required" or "required for proliferation" encompasses instances where the absence or substantial reduction of a gene transcript and/or gene product completely eliminates cell growth as well as instances where the absence of a gene transcript and/or gene product merely reduces cell growth. These proliferation-required genes can be used as potential targets for the generation of new antimicrobial agents. To achieve that goal, the present invention also encompasses assays for analyzing proliferation-required genes and for identifying compounds which interact with the gene and/or gene products of the proliferation-required genes. In addition, the present invention contemplates the expression of genes and the purification of the proteins encoded by the nucleic acid sequences identified as required proliferation genes and reported herein. The purified proteins can be used to generate reagents and screen small molecule libraries or other candidate compound libraries for compounds that can be further developed to yield novel antimicrobial compounds.

The present invention also describes methods for identification of nucleotide sequences homologous to these genes and polypeptides described herein, including nucleic acids comprising nucleotide sequences homologous to the nucleic acids of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 and polypeptides homologous to the polypeptides of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110. For example, these sequences may be used to identify homologous coding nucleic acids, homologous antisense nucleic acids, or homologous polypeptides in microorganisms such as *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli,*

Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis or any species falling within the genera of any of the above species. In some embodiments, the homologous coding nucleic acids, homologus antisense nucleic acids, or homologous polypeptides are identified in an organism other than *E. coli.*

The homologous coding nucleic acids, homologous antisense nucleic acids, or homologous polypeptides, may then be used in each of the methods described herein, including methods to identify compounds which inhibit the proliferation of the organism containing the homologous coding nucleic acid, homologous antisense nucleic acid or homologous polypeptide, methods of inhibiting the growth of the organism containing the homologous coding nucleic acid, homologus antisense nucleic acid or homologous polypeptide, methods of identifying compounds which influence the activity or level of a gene product required for proliferation of the organism containing the homologous coding nucleic acid, homologous antisense nucleic acid or homologous polypeptide, methods for identifying compounds or nucleic acids having the ability to reduce the level or activity of a gene product required for proliferation of the organism containing the homologous coding nucleic acid, homologous antisense nucleic acid or homologous polypeptide, methods of inhibiting the activity or expression of a gene in an operon required for proliferation of the organism containing the homologous coding nucleic acid, homologous antisense nucleic acid or homologous polypeptide, methods for identifying a gene required proliferation of the organism containing the homologous coding nucleic acid, homologous antisense nucleic acid or homologous polypeptide, methods for identifying the biological pathway in which a gene or gene product required for proliferation of the organism containing the homologous coding nucleic acid, homologous antisense nucleic acid or homologous polypeptide lies, methods for identifying compounds having activity against biological pathway required for proliferation of the organism containing the homologous coding nucleic acid, homologous antisense nucleic acid or homologous polypeptide, methods for determining the biological pathway on which a test compound acts, and methods of inhibiting the proliferation of the organism containing the homologous coding nucleic acid, homologous antisense nucleic acid or homologous polypeptide in a subject. In some embodiments of the present invention, the methods are performed using an organism, other than *E. coli* or a gene or gene product from an organism other than *E. coli.*

The present invention utilizes a novel method to identify proliferation-required sequences. Generally, a library of nucleic acid sequences from a given source are subcloned or otherwise inserted immediately downstream of an inducible promoter on an appropriate vector, such as a *Staphylococcus aureus*/*E. coli* or *Pseudomonas aeruginosa*/*E. coli* shuttle vector, or a vector which will replicate in both *Salmonella typhimurium* and *Klebsiella pneumoniae*, or other vector or shuttle vector capable of functioning in the intended organism., thus forming an expression library. It is generally preferred that expression is directed by a regulatable promoter sequence such that expression level can be adjusted by addition of variable concentrations of an inducer molecule or of an inhibitor molecule to the medium. Temperature activated promoters, such as promoters regulated by temperature sensitive repressors, such as the lambda C_{I857} repressor, are also envisioned. Although the insert nucleic acids may be derived from the chromosome of the cell or microorganism into which the expression vector is to be introduced, because the insert is not in its natural chromosomal location, the insert nucleic acid is an exogenous nucleic acid for the purposes of the discussion herein. The term "expression" is defined as the production of a sense or antisense RNA molecule from a gene, gene fragment, genomic fragment, chromosome, operon or portion thereof. Expression can also be used to refer to the process of peptide or polypeptide synthesis. An expression vector is defined as a vehicle by which a ribonucleic acid (RNA) sequence is transcribed from a nucleic acid sequence carried within the expression vehicle. The expression vector can also contain features that permit translation of a protein product from the transcribed RNA message expressed from the exogenous nucleic acid sequence carried by the expression vector. Accordingly, an expression vector can produce an RNA molecule as its sole product or the expression vector can produce a RNA molecule that is ultimately translated into a protein product.

Once generated, the expression library containing the exogenous nucleic acid sequences is introduced into a population of cells (such as the organism from which the exogenous nucleic acid sequences were obtained) to search for genes that are required for bacterial proliferation. Because the library molecules are foreign, in context, to the population of cells, the expression vectors and the nucleic acid segments contained therein are considered exogenous nucleic acid.

Expression of the exogenous nucleic acid fragments in the test population of cells containing the expression library is then activated. Activation of the expression vectors consists of subjecting the cells containing the vectors to conditions that result in the expression of the exogenous nucleic acid sequences carried by the expression library. The test population of cells is then assayed to determine the effect of expressing the exogenous nucleic acid fragments on the test population of cells. Those expression vectors that negatively impacted the growth of the cells upon induction of expression of the random sequences contained therein were identified, isolated, and purified for further study.

A variety of assays are contemplated to identify nucleic acid sequences that negatively impact growth upon expression. In one embodiment, growth in cultures expressing exogenous nucleic acid sequences and growth in cultures not expressing these sequences is compared. Growth measurements

are assayed by examining the extent of growth by measuring optical densities. Alternatively, enzymatic assays can be used to measure bacterial growth rates to identify exogenous nucleic acid sequences of interest. Colony size, colony morphology, and cell morphology are additional factors used to evaluate growth of the host cells. Those cultures that fail to grow or grow at a reduced rate under expression conditions are identified as containing an expression vector encoding a nucleic acid fragment that negatively affects a proliferation-required gene.

Once exogenous nucleic acids of interest are identified, they are analyzed. The first step of the analysis is to acquire the nucleotide sequence of the nucleic acid fragment of interest. To achieve this end, the insert in those expression vectors identified as containing a nucleotide sequence of interest is sequenced, using standard techniques well known in the art. The next step of the process is to determine the source of the nucleotide sequence. As used herein "source" means the genomic region containing the cloned fragment.

Determination of the gene(s) corresponding to the nucleotide sequence was achieved by comparing the obtained sequence data with databases containing known protein and nucleotide sequences from various microorganisms. Thus, initial gene identification was made on the basis of significant sequence similarity or identity to either characterized or predicted *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* or *Enterococcus faecalis* genes or their encoded proteins and/or homologues in other species.

The number of nucleotide and protein sequences available in database systems has been growing exponentially for years. For example, the complete nucleotide sequences of *Caenorhabditis elegans* and several bacterial genomes, including *E. coli, Aeropyrum pernix, Aquifex aeolicus, Archaeoglobus fulgidus, Bacillus subtilis, Borrelia burgdorferi, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium tetani, Corynebacterium diptheria, Deinococcus radiodurans, Haemophilus influenzae, Helicobacter pylori 26695, Helicobacter pylori J99, Methanobacterium thermoautotrophicum, Methanococcus jannaschii, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Pseudomonas aeruginosa, Pyrococcus abyssi, Pyrococcus horikoshii, Rickettsia prowazekii, Synechocystis PCC6803, Thermotoga maritima, Treponema pallidum, Bordetella pertussis, Campylobacter jejuni, Clostridium acetobutylicum, Mycobacterium tuberculosis CSU#93, Neisseria gonorrhoeae, Neisseria meningitidis, Pseudomonas aeruginosa, Pyrobaculum aerophilum, Pyrococcus furiosus, Rhodobacter capsulatus, Salmonella typhimurium, Streptococcus mutans, Streptococcus pyogenes, Ureaplasma urealyticum* and *Vibrio cholera* are available. This nucleotide sequence information is stored in a number of databanks, such as GenBank, the National Center for Biotechnology Information (NCBI), the Genome Sequencing Center (http://genome.wustl.edu/gsc/salmonella.shtml),and the Sanger Centre (http://www.sanger.ac.uk/projects/S___typhi)which are publicly available for searching. A variety of computer programs are available to assist in the analysis of the sequences stored within these databases. FASTA, (W. R. Pearson (1990) "Rapid and Sensitive Sequence Comparison with

FASTP and FASTA" Methods in Enzymology 183:63- 98), Sequence Retrieval System (SRS), (Etzold & Argos, SRS an indexing and retrieval tool for flat file data libraries. Comput. Appl. Biosci. 9:49-57, 1993) are two examples of computer programs that can be used to analyze sequences of interest. In one embodiment of the present invention, the BLAST family of computer programs, which includes BLASTN version 2.0 with the default parameters, or BLASTX version 2.0 with the default parameters, is used to analyze nucleotide sequences.

BLAST, an acronym for "Basic Local Alignment Search Tool," is a family of programs for database similarity searching. The BLAST family of programs includes: BLASTN, a nucleotide sequence database searching program, BLASTX, a protein database searching program where the input is a nucleic acid sequence; and BLASTP, a protein database searching program. BLAST programs embody a fast algorithm for sequence matching, rigorous statistical methods for judging the significance of matches, and various options for tailoring the program for special situations. Assistance in using the program can be obtained by e-mail at blast@ncbi.nlm.nih.gov. tBLASTX can be used to translate a nucleotide sequence in all three potential reading frames into an amino acid sequence.

Bacterial genes are often transcribed in polycistronic groups. These groups comprise operons, which are a collection of genes and intergenic sequences under common regulation. The genes of an operon are transcribed on the same mRNA and are often related functionally. Given the nature of the screening protocol, it is possible that the identified exogenous nucleic acid corresponds to a gene or portion thereof with or without adjacent noncoding sequences, an intragenic sequence (i.e. a sequence within a gene), an intergenic sequence (i.e. a sequence between genes), a nucleotide sequence spanning at least a portion of two or more genes, a 5' noncoding region or a 3' noncoding region located upstream or downstream from the actual nucleotide sequence that is required for bacterial proliferation. Accordingly, it is often desirable to determine which gene(s) that is encoded within the operon is individually required for proliferation.

In one embodiment of the present invention, an operon is identified and then dissected to determine which gene or genes are required for proliferation. Operons can be identified by a variety of means known to those in the art. For example, the RegulonDB DataBase described by Huerta et al. (*Nucl. Acids Res.* 26:55-59, 1998), which may also be found on the website http://www.cifn.unam.mx/Computational_Biology/regulondb/, provides information about operons in *Escherichia coli*. The Subtilist database (http://bioweb.pasteur.fr/GenoList/SubtiList), (Moszer, I., Glaser, P. and Danchin, A. (1995) Microbiology 141: 261-268 and Moszer, I (1998) FEBS Letters 430: 28-36), may also be used to predict operons. This database lists genes from the fully sequenced, Gram-positive bacteria, *Bacillus subtilis*, together with predicted promoters and terminator sites. This information can be used in conjunction with the *Staphylococcus aureus* genomic sequence data to predict operons and thus produce a list of the genes affected by the antisense nucleic acids of the present invention. The *Pseudomonas aeruginosa* web site (http://www.pseudomonas.com) can be used to help predict operon organization in this bacterium.

The databases available from the Genome Sequencing Center (http://genome.wustl.edu/gsc/salmonella.shtml), and the Sanger Centre (http://www.sanger.ac.uk/projects/S___typhi) may be used to predict operons in *Salmonella typhimurium*. The TIGR microbial database has an incomplete version of the *E. faecalis* genome http://www.tigr.org/cgi-bin/BlastSearch/blast.cgi?organism=e_faecalis. One can take a nucleotide sequence and BLAST it for homologs.

A number of techniques that are well known in the art can be used to dissect the operon. Analysis of RNA transcripts by Northern blot or primer extension techniques are commonly used to analyze operon transcripts. In one aspect of this embodiment, gene disruption by homologous recombination is used to individually inactivate the genes of an operon that is thought to contain a gene required for proliferation.

Several gene disruption techniques have been described for the replacement of a functional gene with a mutated, non-functional (null) allele. These techniques generally involve the use of homologous recombination. One technique using homologous recombination in *Staphylococcus aureus* is described in Xia et a.. 1999, Plasmid 42: 144-149. This technique uses crossover PCR to create a null allele with an in-frame deletion of the coding region of a target gene. The null allele is constructed in such a way that nucleotide sequences adjacent to the wild type gene are retained. These homologous sequences surrounding the deletion null allele provide targets for homologous recombination so that the wild type gene on the *Staphylococcus aureus* chromosome can be replaced by the constructed null allele. This method can be used with other bacteria as well, including *Salmonella* and *Klebsiella* species. Similar gene disruption methods that employ the counter selectable marker *sacB* (Schweizer, H. P., Klassen, T. and Hoang, T. (1996) Mol. Biol. of *Pseudomonas*. ASM press, 229-237 are available for *Pseudomonas, Salmonella* and *Klebsiella* species. *E. faecalis* genes can be disrupted by recombining in a non-replicating plasmid that contains an internal fragment to that gene (Leboeuf, C., L. Leblanc, Y. Auffray and A. Hartke. 2000. J. Bacteriol. 182:5799-5806).

The crossover PCR amplification product is subcloned into a suitable vector having a selectable marker, such as a drug resistance marker. In some embodiments the vector may have an origin of replication which is functional in *E. coli* or another organism distinct from the organism in which homologous recombination is to occur, allowing the plasmid to be grown in *E. coli* or the organism other than that in which homologous recombination is to occur, but may lack an origin of replication functional in *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhi* such that selection of the selectable marker requires integration of the vector into the homologous region of the *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis,*

Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus, or *Salmonella typhi* chromosome. Usually a single crossover event is responsible for this integration event such that the *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhi* chromosome now contains a tandem duplication of the target gene consisting of one wild type allele and one deletion null allele separated by vector sequence. Subsequent resolution of the duplication results in both removal of the vector sequence and either restoration of the wild type gene or replacement by the in-frame deletion. The latter outcome will not occur if the gene should prove essential. A more detailed description of this method is provided in Example 5 below. It will be appreciated that this method may be practiced with any of the nucleic acids or organisms described herein.

Recombinant DNA techniques can be used to express the entire coding sequences of the gene identified as required for proliferation, or portions thereof. The over-expressed proteins can be used as reagents for further study. The identified exogenous sequences are isolated, purified, and cloned into a suitable expression vector using methods well known in the art. If desired, the nucleic acids can contain the nucleotide sequences encoding a signal peptide to facilitate secretion of the expressed protein.

Expression of fragments of the bacterial genes identified as required for proliferation is also contemplated by the present invention. The fragments of the identified genes can encode a polypeptide comprising at least 5, at least 10, at least 15, at least 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 75, or more than 75 consecutive amino acids of a gene complementary to one of the identified sequences of the present invention. The nucleic acids inserted into the expression vectors can also contain endogenous sequences upstream and downstream of the coding sequence.

When expressing the encoded protien of the idnetified required for bacterial proliferation or a fragment thereof, the nucleotide sequence to be expressed is operably linked to a promoter in an expression vector using conventional cloning technology. The expression vector can be any of the bacterial, insect, yeast, or mammalian expression systems known in the art. Commercially available vectors and expression systems are available from a variety of suppliers including Genetics Institute (Cambridge, MA), Stratagene (La Jolla, California), Promega (Madison, Wisconsin), and Invitrogen (San Diego, California). If desired, to enhance expression and facilitate proper protein folding, the codon usage and codon bias of the sequence can be optimized for the particular expression organism in which the expression vector is introduced, as explained by Hatfield, et al., U.S. Patent No. 5,082,767. Fusion protein expression systems are also contemplated by the present invention.

Following expression of the protein encoded by the identified exogenous nucleic acid, the protein may be purified. Protein purification techniques are well known in the art. Proteins encoded and expressed from identified exogenous nucleic acids can be partially purified using precipitation techniques, such as precipitation with polyethylene glycol. Alternatively, epitope tagging of the protein can be used to allow simple one step purification of the protein. In addition, chromatographic methods such as ion-exchange chromatography, gel filtration, use of hydroxyapaptite columns, immobilized reactive dyes, chromatofocusing, and use of high-performance liquid chromatography, may also be used to purify the protein. Electrophoretic methods such as one-dimensional gel electrophoresis, high-resolution two-dimensional polyacrylamide electrophoresis, isoelectric focusing, and others are contemplated as purification methods. Also, affinity chromatographic methods, comprising antibody columns, ligand presenting columns and other affinity chromatographic matrices are contemplated as purification methods in the present invention.

The purified proteins produced from the gene coding sequences identified as required for proliferation can be used in a variety of protocols to generate useful antimicrobial reagents. In one embodiment of the present invention, antibodies are generated against the proteins expressed from the identified exogenous nucleic acids. Both monoclonal and polyclonal antibodies can be generated against the expressed proteins. Methods for generating monoclonal and polyclonal antibodies are well known in the art. Also, antibody fragment preparations prepared from the produced antibodies discussed above are contemplated.

In addition, the purified protein, fragments thereof, or derivatives thereof may be administered to an individual in a pharmaceutically acceptable carrier to induce an immune response against the protein. Preferably, the immune response is a protective immune response which protects the individual. Methods for determining appropriate dosages of the protein and pharmaceutically acceptable carriers may be determined empiracally and are familiar to those skilled in the art.

Another application for the purified proteins of the present invention is to screen small molecule libraries for candidate compounds active against the various target proteins of the present invention. Advances in the field of combinatorial chemistry provide methods, well known in the art, to produce large numbers of candidate compounds that can have a binding, or otherwise inhibitory effect on a target protein. Accordingly, the screening of small molecule libraries for compounds with binding affinity or inhibitory activity for a target protein produced from an identified gene is contemplated by the present invention.

The present invention further contemplates utility against a variety of other pathogenic microorganisms in addition to *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhi*. For example, homologous coding nucleic acids, homologous antisense nucleic acids or homologous polypeptides from other pathogenic

microorganisms (including nucleic acids homologous to the nucleic acids of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, nucleic acids homologous to the antisense nucleic acids of SEQ ID NOs.: 8-3795, and polypeptides homologous to the polypeptides of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110) may be identified using methods such as those described herein. The homologous coding nucleic acids, homologous antisense nucleic acids or homologous polypeptides may be used to identify compounds which inhibit the proliferation of these other pathogenic microorganisms using methods such as those described herein.

For example, the proliferation-required nucleic acids, antisense nucleic acids, and polypeptides from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhi* described herein (including the nucleic acids of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, the antisense nucleic acids of SEQ ID NOs: 8-3795, and the polypeptides of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110) may be used to identify homologous coding nucleic acids, homologous antisense nucleic acids or homologous polypeptides required for proliferation in prokaryotes and eukaryotes. For example, nucleic acids or polypeptides required for the proliferation of protists, such as *Plasmodium* spp.; plants; animals, such as *Entamoeba* spp. *and Contracaecum* spp; and fungi including *Candida* spp., (e.g., *Candida albicans*), *Cryptococcus neoformans*, and *Aspergillus fumigatus* may be identified. In one embodiment of the present invention, monera, specifically bacteria, including both Gram positive and Gram negative bacteria, are probed in search of novel gene sequences required for proliferation. Likewise, homologous antisense nucleic acids which may be used to inhibit growth of these organisms or to identify antibiotics may also be identified. These embodiments are particularly important given the rise of drug resistant bacteria.

The number of bacterial species that are becoming resistant to existing antibiotics is growing. A partial list of these microorganisms includes: *Escherichia* spp., such as *E. coli, Enterococcus* spp, such as *E. faecalis*; *Pseudomonas* spp., *such as P. aeruginosa, Clostridium* spp., such as *C. botulinum, Haemophilus* spp., such as *H. influenzae, Enterobacter* spp., such as *E. cloacae, Vibrio* spp., such as *V. cholera; Moraxala* spp., such as *M. catarrhalis*; *Streptococcus* spp., such as *S. pneumoniae, Neisseria* spp., such as *N. gonorrhoeae; Mycoplasma* spp., such as *Mycoplasma pneumoniae; Salmonella typhimurium*; *Helicobacter pylori*; *Escherichia coli;* and *Mycobacterium tuberculosis*. The genes and polypeptides identified as required for the proliferation of *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhi* (including the nucleic acids of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, the sequences complementary to the nucleic acids of SEQ ID NOs.: 3796-3800, 3806-4860,

5916-10012, and the polypeptides of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110) can be used to identify homologous coding nucleic acids or homologous polypeptides required for proliferation from these and other organisms using methods such as nucleic acid hybridization and computer database analysis. Likewise, the antisense nucleic acids which inhibit proliferation of *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhi* (including the antisense nucleic acids of SEQ ID NOs.: 8-3795 or the sequences complementary thereto) may also be used to identify antisense nucleic acids which inhibit proliferation of these and other microorganisms or cells using nucleic acid hybridization or computer database analysis.

In one embodiment of the present invention, the nucleic acid sequences from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhii* (including the nucleic acids of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012 and the antisense nucleic acids of SEQ ID NOs. 8-3795) are used to screen genomic libraries generated from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhi* and other bacterial species of interest. For example, the genomic library may be from Gram positive bacteria, Gram negative bacteria or other organisms including *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica,*

Yersinia pestis or any species falling within the genera of any of the above species, including coagulase negative species of *Staphylococcus*. In some embodiments, the genomic library may be from an organism other than *E. coli*. Standard molecular biology techniques are used to generate genomic libraries from various cells or microorganisms. In one aspect, the libraries are generated and bound to nitrocellulose paper. The identified exogenous nucleic acid sequences of the present invention can then be used as probes to screen the libraries for homologous sequences.

For example, the libraries may be screened to identify homologous coding nucleic acids or homologous antisense nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795, nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of one of SEQ ID NOs. 8-3795, nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a nucleic acid complementary to one of SEQ ID NOs. 8-3795, nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the sequence complementary to one of SEQ ID NOs. 8-3795, nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a nucleic acid selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a nucleic acid complementary to one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the sequence complementary to one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a nucleic acid selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012.

The libraries may also be screened to identify homologous nucleic coding nucleic acids or homologous antisense nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795, nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of one of SEQ ID NOs. 8-3795, nucleic acids comprising nucleotide

sequences which hybridize under moderate conditions to a nucleic acid complementary to one of SEQ ID NOs. 8-3795, nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the sequence complementary to one of SEQ ID NOs. 8-3795, nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a nucleic acid selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, nucleic acids comprising nucleic acid sequences which hybridize under moderate conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a nucleic acid complementary to one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 and nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the sequence complementary to one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012.

The homologous nucleic coding nucleic acids, homologous antisense nucleic acids or homologous polypeptides identified as above can then be used as targets or tools for the identification of new, antimicrobial compounds using methods such as those described herein. In some embodiments, the homologous coding nucleic acids, homologous antisense nucleic acids, or homologous polypeptides may be used to identify compounds with activity against more than one microorganism.

For example, the preceding methods may be used to isolate homologous coding nucleic acids or homologous antisense nucleic acids comprising a nucleotide sequence with at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, or at least 70% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of one of the sequences of SEQ ID NOS. 8-3795, fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof, and the sequences complementary thereto. The preceding methods may also be used to isolate homologous coding nucleic acids or homologous antisense nucleic acids comprising a nucleotide sequence with at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, or at least 70% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of one of the nucleotide sequences of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof, and the sequences complementary thereto. In some embodiments, the preceding methods may be used to isolate homologous coding nucleic acids or homologous antisense nucleic acids comprising a nucleotide sequence with at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, or at least 70% nucleotide sequence identity to a nucleic acid sequence selected from the group consisting of one of the sequences of SEQ ID NOS.

3796-3800, 3806-4860, 5916-10012, fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof, and the sequences complementary thereto. Identity may be measured using BLASTN version 2.0 with the default parameters. (Altschul, S.F. et al. Gapped BLAST and PSI-BLAST: A New Generation of Protein Database Search Programs, Nucleic Acid Res. 25: 3389-3402 (1997)). For example, the homologous polynucleotides may comprise a coding sequence which is a naturally occurring allelic variant of one of the coding sequences described herein. Such allelic variants may have a substitution, deletion or addition of one or more nucleotides when compared to the nucleic acids of SEQ ID NOs: 8-3795, SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 or the nucleotide sequences complementary thereto.

Additionally, the above procedures may be used to isolate homologous coding nucleic acids which encode polypeptides having at least 99%, 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40% or at least 25% amino acid identity or similarity to a polypeptide comprising the sequence of one of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110 or to a polypeptpide whose expression is inhibited by a nucleic acid of one of SEQ ID NOs: 8-3795 or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof as determined using the FASTA version 3.0t78 algorithm with the default parameters. Alternatively, protein identity or similarity may be identified using BLASTP with the default parameters, BLASTX with the default parameters, or TBLASTN with the default parameters. (Altschul, S.F. et al. Gapped BLAST and PSI-BLAST: A New Generation of Protein Database Search Programs, Nucleic Acid Res. 25: 3389-3402 (1997)).

Alternatively, homologous coding nucleic acids, homologous antisense nucleic acids or homologous polypeptides may be identified by searching a database to identify sequences having a desired level of nucleotide or amino acid sequence homology to a nucleic acid or polypeptide involved in proliferation or an antisense nucleic acid to a nucleic acid involved in microbial proliferation. A variety of such databases are available to those skilled in the art, including GenBank and GenSeq. In some embodiments, the databases are screened to identify nucleic acids with at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, or at least 70% nucleotide sequence identity to a nucleic acid required for proliferation, an antisense nucleic acid which inhibits proliferation, or a portion of a nucleic acid required for proliferation or a portion of an antisense nucleic acid which inhibits proliferation. For example, homologous coding sequences may be identified by using a database to identify nucleic acids homologous to one of SEQ ID Nos. 8-3795, homologous to fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof, nucleic acids homologous to one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, homologous to fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, nucleic acids homologous to one of SEQ ID Nos. 8-

3795, homologous to fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof or nucleic acids homologous to the sequences complementary to any of the preceding nucleic acids. In other embodiments, the databases are screened to identify polypeptides having at least 99%, 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40% or at least 25% amino acid sequence identity or similarity to a polypeptide involved in proliferation or a portion thereof. For example, the database may be screened to identify polypeptides homologous to a polypeptide comprising one of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110, a polypeptide whose expression is inhibited by a nucleic acid of one of SEQ ID NOs: 8-3795 or homologous to fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of any of the preceding polypeptides. In some embodiments, the database may be screened to identify homologous coding nucleic acids, homologous antisense nucleic acids or homologous polypeptides from cells or microorganisms other than the *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhi* species from which they were obtained. For example the database may be screened to identify homologous coding nucleic acids, homologous antisense nucleic acids or homologous polypeptides from microorganisms such as *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, .Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* or any species falling within the genera of any of the above species, including coagulase negative *Staphylococcus*. In some embodiments, the homologous coding nucleic acids, homologous antisense nucleic acids, or homologous polypeptides are from an organism other than *E. coli*.

In another embodiment, gene expression arrays and microarrays can be employed. Gene expression arrays are high density arrays of DNA samples deposited at specific locations on a glass chip, nylon membrane, or the like. Such arrays can be used by researchers to quantify relative gene expression under different conditions. Gene expression arrays are used by researchers to help identify optimal drug targets, profile new compounds, and determine disease pathways. An example of this technology is found in U.S. Patent No. 5807522.

It is possible to study the expression of all genes in the genome of a particular microbial organism using a single array. For example, the arrays may consist of 12 x 24 cm nylon filters containing PCR products corresponding to ORFs from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhi* (including the nucleic acids of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012). 10 ngs of each PCR product are spotted every 1.5 mm on the filter. Single stranded labeled cDNAs are prepared for hybridization to the array (no second strand synthesis or amplification step is done) and placed in contact with the filter. Thus the labeled cDNAs are of "antisense" orientation. Quantitative analysis is done by phosphorimager.

Hybridization of cDNA made from a sample of total cell mRNA to such an array followed by detection of binding by one or more of various techniques known to those in the art results in a signal at each location on the array to which cDNA hybridized. The intensity of the hybridization signal obtained at each location in the array thus reflects the amount of mRNA for that specific gene that was present in the sample. Comparing the results obtained for mRNA isolated from cells grown under different conditions thus allows for a comparison of the relative amount of expression of each individual gene during growth under the different conditions.

Gene expression arrays may be used to analyze the total mRNA expression pattern at various time points after induction of an antisense nucleic acid complementary to a proliferation-required gene. Analysis of the expression pattern indicated by hybridization to the array provides information on other genes whose expression is influenced by antisense expression. For example, if the antisense is complementary to a gene for ribosomal protein L7/L12 in the 50S subunit, levels of other mRNAs may be observed to increase, decrease or stay the same following expression of antisense to the L7/L12 gene. If the antisense is complementary to a different 50S subunit ribosomal protein mRNA (e.g. L25), a different mRNA expression pattern may result. Thus, the mRNA expression pattern observed following expression of an antisense nucleic acid comprising a nucleotide sequence complementary to a proliferation required gene may identify other proliferation-required nucleic acids. In addition, the mRNA expression patterns observed when the bacteria are exposed to candidate drug compounds or known antibiotics may be compared to those observed with antisense nucleic acids comprising a nucleotide sequence complementary to a

proliferation-required nucleic acid. If the mRNA expression pattern observed with the candidate drug compound is similar to that observed with the antisense nucleic acid, the drug compound may be a promising therapeutic candidate. Thus, the assay would be useful in assisting in the selection of promising candidate drug compounds for use in drug development.

In cases where the source of nucleic acid deposited on the array and the source of the nucleic acid being hybridized to the array are from two different cells or microorganisms, gene expression arrays can identify homologous nucleic acids in the two cells or microorganisms.

The present invention also contemplates additional methods for screening other microorganisms for proliferation-required genes. In one aspect of this embodiment, an antisense nucleic acid comprising a nucleotide sequence complementary to the proliferation-required sequences from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhi* or a portion thereof is transcribed in an antisense orientation in such a way as to alter the level or activity of a nucleic acid required for proliferation of an autologous or heterologous cell or microorganism. For example, the antisense nucleic acid may be a homologous antisense nucleic acid such as an antisense nucleic acid homologous to the nucleotide sequence complementary to one of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, an antisense nucleic acid comprising a nucleotide sequence homologous to one of SEQ ID Nos.: 8-3795, or an antisense nucleic acid comprising a nucleotide sequence complementary to a portion of any of the preceding nucleic acids. The cell or microorganism transcribing the homologous antisense nucleic acid may be used in a cell-based assay, such as those described herein, to identify candidate antibiotic compounds. In another embodiment, the conserved portions of nucleotide sequences identified as proliferation-required can be used to generate degenerate primers for use in the polymerase chain reaction (PCR). The PCR technique is well known in the art. The successful production of a PCR product using degenerate probes generated from the nucleotide sequences identified herein indicates the presence of a homologous gene sequence in the species being screened. This homologous gene is then isolated, expressed, and used as a target for candidate antibiotic compounds. In another aspect of this embodiment, the homologous gene (for example a homologous coding nucleic acid)thus identified, or a portion thereof, is transcribed in an autologous cell or microorganism or in a heterologous cell or microorganism in an antisense orientation in such a way as to alter the level or activity of a homologous gene required for proliferation in the autologous or heterologous cell or microorganism. Alternatively, a homologous antisense nucleic acid may be transcribed in an autologous or heterologous cell or microorganism in such a way as to alter the level or activity of a gene product required for proliferation in the autologous or heterologous cell or microorganism.

The nucleic acids homologous to the genes required for the proliferation of *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and

Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus, or *Salmonella typhi* or the sequences complementary thereto may be used to identify homologous coding nucleic acids or homologous antisense nucleic acids from cells or microorganisms other than *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus*, or *Salmonella typhi* to inhibit the proliferation of cells or microorganisms other than *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus*, or *Salmonella typhi* by inhibiting the activity or reducing the amount of the identified homologous coding nucleic acid or homologous polypeptide in the cell or microorganism other than *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa Enterococcus faecalis,Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* or to identify compounds which inhibit the growth of cells or microorganisms other than *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* as described below. For example, the nucleic acids homologous to proliferation-required genes from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhi* or the sequences complementary thereto may be used to identify compounds which inhibit the growth of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella*

boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species. In some embodiments of the present invention, the nucleic acids homologous to proliferation-required sequences from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhi* (including nucleic acids homologous to one of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012) or the sequences complementary thereto (including nucleic acids homologous to one of SEQ ID NOs.: 8-3795) are used to identify proliferation-required sequences in an organism other than *E. coli.*

In another embodiment of the present invention, antisense nucleic acids complementary to the sequences identified as required for proliferation or portions thereof (including antisense nucleic acids comprising a nucleotide sequence complementary to one of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012 or portions thereof, such as the nucleic acids of SEQ ID NOs.: 8-3795) are transferred to vectors capable of function within a species other than the species from which the sequences were obtained. For example, the vector may be functional in *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* or any species falling within the genera of any of the above species. In some embodiments of the present invention, the vector may be functional in an organism other than *E. coli.* As would be appreciated by one of ordinary skill in the art, vectors may contain certain elements that are species specific. These elements can include promoter sequences, operator sequences, repressor genes, origins of replication, ribosomal binding sequences, termination sequences, and others. To use the

antisense nucleic acids, one of ordinary skill in the art would know to use standard molecular biology techniques to isolate vectors containing the sequences of interest from cultured bacterial cells, isolate and purify those sequences, and subclone those sequences into a vector adapted for use in the species of bacteria to be screened.

Vectors for a variety of other species are known in the art. For example, numerous vectors which function in *E. coli* are known in the art. Also, Pla et al. have reported an expression vector that is functional in a number of relevant hosts including: *Salmonella typhimurium, Pseudomonas putida, and Pseudomonas aeruginosa.* **J. Bacteriol.** 172(8):4448-55 (1990). Brunschwig and Darzins (Gene (1992) 111:35-4) described a shuttle expression vector for *Pseudomonas aeruginosa*. Similarly many examples exist of expression vectors that are freely transferable among various Gram-positive microorganisms. Expression vectors for *Enterococcus faecalis* may be engineered by incorporating suitable promoters into a pAK80 backbone (Israelsen, H., S. M. Madsen, A. Vrang, E. B. Hansen and E. Johansen. 1995. Appl. Environ. Microbiol. 61:2540-2547).

Following the subcloning of the antisense nucleic acids complementary to proliferation-required sequences from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhi* or portions thereof into a vector functional in a second cell or microorganism of interest (i.e. a cell or microorganism other than the one from which the identified nucleic acids were obtained), the antisense nucleic acids are conditionally transcribed to test for bacterial growth inhibition. The nucleotide sequences of the nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* that, when transcribed, inhibit growth of the second cell or microorganism are compared to the known genomic sequence of the second cell or microorganism to identify the homologous gene from the second organism. If the homologous sequence from the second cell or microorganism is not known, it may be identified and isolated by hybridization to the proliferation-required *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalisEscherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* sequence of interest or by amplification using PCR primers based on the proliferation-required nucleotide sequence of interest as described above. In this way, sequences which may be required for the proliferation of the second cell or microorganism may be identified. For example, the second microorganism may be *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis,*

Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis or any species falling within the genera of any of the above species. In some embodiments of the present invention, the second microorganism is an organism other than *E. coli*.

The homologous nucleic acid sequences from the second cell or microorganism which are identified as described above may then be operably linked to a promoter, such as an inducible promoter, in an antisense orientation and introduced into the second cell or microorganism. The techniques described herein for identifying *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* or *Salmonella typhi* genes required for proliferation may thus be employed to determine whether the identified nucleotide sequences from a second cell or microorganism inhibit the proliferation of the second cell or microorganism. For example, the second microorganism may be *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans,*

Treponema pallidum, Yersinia enterocolitica, Yersinia pestis or any species falling within the genera of any of the above species. In some embodiments of the present invention, the second microorganism may be an organism other than *E. coli*.

Antisense nucleic acids required for the proliferation of microorganisms other than *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* or the genes corresponding thereto, may also be hybridized to a microarray containing the *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis* ORFs, *Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* and *Salmonella typhi* (including the nucleic acids of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012) to gauge the homology between the *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* sequences and the proliferation-required nucleic acids from other cells or microorganisms. For example, the proliferation-required nucleic acid may be from *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* or any species falling within the genera of any of the above species. In some embodiments of the present invention, the proliferation-required nucleotide sequences from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, Salmonella typhi* or homologous nucleic acids are used to identify proliferation-required sequences in an organism other than *E. coli*. In some embodiments of the present invention, the proliferation-required sequences

may be from an organism other than *E. coli*. The proliferation-required nucleic acids from a cell or microorganism other than *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* may be hybridized to the array under a variety of conditions which permit hybridization to occur when the probe has different levels of homology to the nucleotide sequence on the microarray. This would provide an indication of homology across the cells or microorganisms as well as clues to other possible essential genes in these cells or microorganisms.

In still another embodiment, the antisense nucleic acids of the present invention (including the antisense nucelic acids of SEQ ID NOs. 8-3795 or homologous antisense nucleic acids) that inhibit bacterial growth or proliferation can be used as antisense therapeutics for killing bacteria. The antisense sequences can be complementary to one of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, homologous nucleic acids, or portions thereof. Alternatively, antisense therapeutics can be complementary to operons in which proliferation-required genes reside (i.e. the antisense nucleic acid may hybridize to a nucleotide sequence of any gene in the operon in which the proliferation-required genes reside). Further, antisense therapeutics can be complementary to a proliferation-required gene or portion thereof with or without adjacent noncoding sequences, an intragenic sequence (i.e. a sequence within a gene), an intergenic sequence (i.e. a sequence between genes), a sequence spanning at least a portion of two or more genes, a 5' noncoding region or a 3' noncoding region located upstream or downstream from the actual sequence that is required for bacterial proliferation or an operon containing a proliferation-required gene.

In addition to therapeutic applications, the present invention encompasses the use of nucleic acids complementary to nucleic acids required for proliferation as diagnostic tools. For example, nucleic acid probes comprising nucleotide sequences complementary to proliferation-required sequences that are specific for particular species of cells or microorganisms can be used as probes to identify particular microorganism species or cells in clinical specimens. This utility provides a rapid and dependable method by which to identify the causative agent or agents of a bacterial infection. This utility would provide clinicians the ability to accurately identify the species responsible for the infection and amdminister a compound effective against it. In an extension of this utility, antibodies generated against proteins translated from mRNA transcribed from proliferation-required sequences can also be used to screen for specific cells or microorganisms that produce such proteins in a species-specific manner.

Other embodiments of the present invention include methods of identifying compounds which inhibit the activity of gene products required for cellular proliferation using rational drug design. As discussed in more detail below, in such methods, the structure of the gene product is determined using techniques such as x-ray crystallography or computer modeling. Compounds are screened to identify those which have a structure which would allow them to interact with the gene product or a portion

thereof to inhibit its activity. The compounds may be obtained using any of a variety of methods familiar to those skilled in the art, including combinatorial chemistry. In some embodiments, the compounds may be obtained from a natural product library. In some embodiments, compounds having a structure which allows them to interact with the active site of a gene product, such as the active site of an enzyme, or with a portion of the gene product which interacts with another biomolecule to form a complex are identified. If desired, lead compounds may be identified and further optimized to provide compounds which are highly effective against the gene product.

The following examples teach the genes of the present invention and a subset of uses for the genes identified as required for proliferation. These examples are illustrative only and are not intended to limit the scope of the present invention.

EXAMPLES

The following examples are directed to the identification and exploitation of genes required for proliferation. Methods of gene identification are discussed as well as a variety of methods to utilize the identified sequences. It will be appreciated that any of the antisense nucleic acids, proliferartion-required genes or proliferation-required gene products described herein, or portions thereof, may be used in the procedures described below, including the antisense nucleic acids of SEQ ID NOs.: 8-3795, the nucleic acids of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, or the polypeptides of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110. Likewise, homologous coding nucleic acids or portions thereof, may be used in any of the procedures described below.

Genes Identified as Required for Proliferation of *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* or *Enterococcus faecalis*

Genomic fragments were operably linked to an inducible promoter in a vector and assayed for growth inhibition activity. Example 1 describes the examination of a library of genomic fragments cloned into vectors comprising inducible promoters. Upon induction with xylose or IPTG, the vectors produced an RNA molecule corresponding to the subcloned genomic fragments. In those instances where the genomic fragments were in an antisense orientation with respect to the promoter, the transcript produced was complementary to at least a portion of an mRNA (messenger RNA) encoding a *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* or *Enterococcus faecalis* gene product such that they interacted with sense mRNA produced from various *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* or *Enterococcus faecalis* genes and thereby decreased the translation efficiency or the level of the sense messenger RNA thus decreasing production of the protein encoded by these sense mRNA molecules. In cases where the sense mRNA encoded a protein required for proliferation, bacterial cells containing a vector from which transcription from the promoter had been induced failed to grow or grew at a substantially reduced rate. Additionally, in cases where the transcript produced was complementary to at least a portion of a non-translated RNA and where that

non-translated RNA was required for proliferation, bacterial cells containing a vector from which transcription from the promoter had been induced also failed to grow or grew at a substantially reduced rate.

EXAMPLE 1

Inhibition of Bacterial Proliferation after Induction of Antisense Expression

Nucleic acids involved in proliferation of *Staphylococcus aureus, Salmonella typhimurium,* and *Klebsiella pneumoniae* were identified as follows. Randomly generated fragments of *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* or *Enterococcus faecalis* genomic DNA were transcribed from inducible promoters.

In the case of *Staphylococcus aureus,* a novel inducible promoter system, XylT5, comprising a modified T5 promoter fused to the *xylO* operater from the *xylA* promoter of *Staphylococcus aureus* was used. The promoter is described in U.S. Provisional Patent Application Serial Number 60/259,434. Transcription from this hybrid promoter is inducible by xylose.

Randomly generated fragments of *Salmonella typhimurium* genomic DNA were transcribed from an IPTG inducible promoter in pLEX5BA (Krause et al., J. Mol. Biol. 274: 365 (1997) or a derivative thereof. Randomly generated fragements of *Klebsiella pneumoniae* genomic DNA were expressed from an IPTG inducible promoter in pLEX5BA-Kan. To construct pLEX5BA-kan, pLEX5BA was digested to completion with *ClaI* in order to remove the *bla* gene. Then the plasmid was treated with a partial *NotI* digestion and blunted with T4 DNA polymerase. A 3.2 kbp fragment was then gel purified and ligated to a blunted 1.3 kbp kan gene from pKanπ. Kan resistant transformants were selected on Kan plates. Orientation of the kan gene was checked by *SmaI* digestion. A clone, which had the kan gene in the same orientation as the bla gene, was used to identify genes required for proliferation of *Klebsiella pneumoniae*.

Randomly generated fragments of *Pseudomonas aeruginosa* genomic DNA were trancribed from a two-component inducible promoter system. Integrated on the chromosome was the T7 RNA polymerase gene regulated by *lac*UV5/ *lac*O (Brunschwig, E. and Darzins, A. 1992. Gene 111:35-41). On a separate plasmid, a T7 gene 10 promoter, which is transcribed by T7 RNA polymerase, was fused with a *lac*O operator followed by a multiple cloning site.

Should the genomic DNA downstream of the promoter contain, in an antisense orientation, at least a portion of an mRNA or a non-translated RNA encoding a gene product involved in proliferation, then induction of transcription from the promoter will result in detectable inhibition of proliferation.

In the case of *Staphylococcus aureus,* a shotgun library of *Staphylococcus aureus* genomic fragments was cloned into the vector pXylT5-P15a, which harbors the XylT5 inducible promoter. The vector was linearized at a unique *Bam*HI site immediately downstream of the XylT5 promoter/operator. The linearized vector was treated with shrimp alkaline phosphatase to prevent reclosure of the linearized ends. Genomic DNA isolated from *Staphylococcus aureus* strain RN450

was fully digested with the restriction enzyme *Sau*3A , or , alternatively, partially digested with DNase I and "blunt-ended" by incubating with T4 DNA polymerase. Random genomic fragments between 200 and 800 base pairs in length were selected by gel purification. The size-selected genomic fragments were added to the linearized and dephosphorylated vector at a molar ratio of 0.1 to 1, and ligated to form a shotgun library.

The ligated products were transformed into electrocompetent *E. coli* strain XL1-Blue MRF' (Stratagene) and plated on LB medium with supplemented with carbenicillin at 100 μg/ml. Resulting colonies numbering 5 x 10^5 or greater were scraped and combined, and were then subjected to plasmid purification.

The purified library was then transformed into electrocompetent *Staphylococcus aureus* RN4220. Resulting transformants were plated on agar containing LB + 0.2% glucose (LBG medium) + chloramphenicol at 15 μg/ml (LBG+CM15 medium) in order to generate 100 to 150 platings at 500 colonies per plating. The colonies were subjected to robotic picking and arrayed into wells of 384 well culture dishes. Each well contained 100μl of LBG + CM15 liquid medium. Inoculated 384 well dishes were incubated 16 hours at 37°C, and each well was robotically gridded onto solid LBG + CM15 medium with or without 2% xylose. Gridded plates were incubated 16 hours at 37°C, and then manually scored for arrayed colonies that were growth-compromised in the presence of xylose.

Arrayed colonies that were growth-sensitive on medium containing 2% xylose, yet were able to grow on similar medium lacking xylose, were subjected to further growth sensitivity analysis as follows: Colonies from the plate lacking xylose were manually picked and inoculated into individual wells of a 96 well culture dish containing LBG + CM15, and were incubated for 16 hours at 37°C. These cultures were robotically diluted 1/100 into fresh medium and allowed to incubate for 4 hours at 37°C, after which they were subjected to serial dilutions in a 384 well array and then gridded onto media containing 2% xylose or media lacking xylose. After growth for 16 hours at 37°C, the arrays that resulted on the two media were compared to each other. Clones that grew similarly at all dilutions on both media were scored as a negative and were no longer considered. Clones that grew on xylose medium but failed to grow at the same serial dilution on the non-xylose plate were given a score based on the differential, i.e. should the clone grow at a serial dilution of 10^4 or less on the xylose plate and grow at a serial dilution of 10^8 or less on the non-xylose plate, then the corresponding clone received a score of "4" representing the log difference in growth observed.

For *Salmonella typhimurium* and *Klebsiella pneumoniae* growth curves were carried out by back diluting cultures 1:200 into fresh media containing 1 mM IPTG or media lacking IPTG and measuring the OD_{450} every 30 minutes (min). To study the effects of transcriptional induction on solid medium, 10^2, 10^3, 10^4, 10^5, 10^6, 10^7 and 10^8 fold dilutions of overnight cultures were prepared.

Aliquots of from 0.5 to 3 µl of these dilutions were spotted on selective agar plates with or without 1 mM IPTG. After overnight incubation, the plates were compared to assess the sensitivity of the clones to IPTG.

Nucleic acids involved in proliferation of *Pseudomonas aeruginosa* were identified as follows. Randomly generated fragments of *Pseudomonas aeruginosa* genomic DNA were transcribed from a two-component inducible promoter system. Integrated on the chromosome was the T7 RNA polymerase gene regulated by *lac*UV5/ *lac*O (Brunschwig, E. and Darzins, A. 1992. Gene 111:35-41). On an expression plasmid there was a T7 gene 10 promoter, which is transcribed by T7 RNA polymerase, fused with a *lac*O operator followed by a multiple cloning site. Transcription from this hybrid promoter is inducible by IPTG. Should the genomic DNA downstream of the promoter contain, in an antisense orientation, at least a portion of an mRNA encoding a gene product involved in proliferation, then induction of expression from the promoter will result in detectable inhibition of proliferation.

A shotgun library of *Pseudomonas aeruginosa* genomic fragments was cloned into the vectors pEP5, pEP5S, or other similarly constructed vectors which harbor the T7*lac*O inducible promoter. The vector was linearized at a unique *Sma*I site immediately downstream of the T7*lac*O promoter/operator. The linearized vector was treated with shrimp alkaline phosphatase to prevent reclosure of the linearized ends. Genomic DNA isolated from *Pseudomonas aeruginosa* strain PAO1 was partially digested with DNase I and "blunt-ended" by incubating with T4 DNA polymerase. Random genomic fragments between 200 and 800 base pairs in length were selected by gel purification. The size-selected genomic fragments were added to the linearized and dephosphorylated vector at a molar ratio of 2 to 1, and ligated to form a shotgun library.

The ligated products were transformed into electrocompetent *E. coli* strain XL1-Blue MRF' (Stratagene) and plated on LB medium with carbenicillin at 100 g/ml or Streptomycin 100 g/ml. Resulting colonies numbering 5 x 10^5 or greater were scraped and combined, and were then subjected to plasmid purification.

The purified library was then transformed into electrocompetent *Pseudomonas aeruginosa* strain PAO1. Resulting transformants were plated on LB agar with carbenicillin at 100 g/ml or Streptomycin 40 g/ml in order to generate 100 to 150 platings at 500 colonies per plating. The colonies were subjected to robotic picking and arrayed into wells of 384 well culture dishes. Each well contained 100 l of LB + CB 100 or Streptomycin 40 liquid medium. Inoculated 384 well dishes were incubated 16 hours at room temperature, and each well was robotically gridded onto solid LB + CB100 or Streptomycin 40 medium with or without 1 mM IPTG. Gridded plates were incubated 16 hours at 37°C, and then manually scored for arrayed colonies that were growth-compromised in the presence of IPTG.

Arrayed colonies that were growth-sensitive on medium containing 1 mM IPTG, yet were able to grow on similar medium lacking IPTG, were subjected to further growth sensitivity analysis

as follows: Colonies from the plate lacking IPTG were manually picked and inoculated into individual wells of a 96 well culture dish containing LB + CB100 or Streptomycin 40, and were incubated for 16 hours at 30°C. These cultures were robotically diluted 1/100 into fresh medium and allowed to incubate for 4 hours at 37°C, after which they were subjected to serial dilutions in a 384 well array and then gridded onto media with and without 1 mM IPTG. After growth for 16 hours at 37°C, the arrays of serially diluted spots that resulted were compared between the two media. Clones that grew similarly at all dilutions on both media were scored as a negative and were no longer considered. Clones that grew on IPTG medium but failed to grow at the same serial dilution on the non-IPTG plate were given a score based on the differential, i.e. should the clone grow at a serial dilution of 10^4 or less on the IPTG plate and grow at a serial dilution of 10^8 or less on the IPTG plate, then the corresponding clone received a score of "4" representing the log difference in growth observed.

Following the identification of those vectors that, upon induction, negatively impacted *Pseudomonas aeruginosa* growth or proliferation, the inserts or nucleic acid fragments contained in those vectors were isolated for subsequent characterization. Vectors of interest were subjected to nucleic acid sequence determination.

Nucleic acids involved in proliferation of *E. faecalis* were identified as follows. Randomly generated fragments of genomic DNA were expressed from the vectors pEPEF3 or pEPEF14, which contain the CP25 or P59 promoter, respectively, regulated by the xyl operator/repressor. Should the genomic DNA downstream of the promoter contain, in an antisense orientation, at least a portion of a mRNA encoding a gene product involved in proliferation, then induction of expression from the promoter will result in detectable inhibition of proliferation.

A shotgun library of *E. faecalis* genomic fragments was cloned into the vector pEPEF3 or pEPEF14, which harbor xylose inducible promoters. The vector was linearized at a unique *Sma*I site immediately downstream of the promoter/operator. The linearized vector was treated with alkaline phosphatase to prevent reclosure of the linearized ends. Genomic DNA isolated from *E. faecalis* strain OG1RF was partially digested with DNase I and "blunt-ended" by incubating with T4 DNA polymerase. Random genomic fragments between 200 and 800 base pairs in length were selected by gel purification. The size-selected genomic fragments were added to the linearized and dephosphorylated vector at a molar ratio of 2 to 1, and ligated to form a shotgun library.

The ligated products were transformed into electrocompetent *E. coli* strain TOP10 cells (Invitrogen) and plated on LB medium with erythromycin (Erm) at 150 μg/ml. Resulting colonies numbering 5 x 10^5 or greater were scraped and combined, and were then subjected to plasmid purification.

The purified library was then transformed into electrocompetent *E. faecalis* strain OG1RF. Resulting transformants were plated on Todd-Hewitt (TH) agar with erythromycin at 10 μg/ml in

order to generate 100 to 150 platings at 500 colonies per plating. The colonies were subjected to robotic picking and arrayed into wells of 384 well culture dishes. Each well contained 100 μl of THB + Erm 10 μg/ml. Inoculated 384 well dishes were incubated 16 hours at room temperature, and each well was robotically gridded onto solid TH agar + Erm with or without 5% xylose. Gridded plates were incubated 16 hours at 37°C, and then manually scored for arrayed colonies that were growth-compromised in the presence of xylose.

Arrayed colonies that were growth-sensitive on medium containing 5% xylose, yet were able to grow on similar medium lacking xylose, were subjected to further growth sensitivity analysis. Colonies from the plate lacking xylose were manually picked and inoculated into individual wells of a 96 well culture dish containing THB + Erm 10, and were incubated for 16 hours at 30°C. These cultures were robotically diluted 1/100 into fresh medium and allowed to incubate for 4 hours at 37°C, after which they were subjected to serial dilution on plates containing 5% xylose or plates lacking xylose. After growth for 16 hours at 37°C, the arrays of serially diluted spots that resulted were compared between the two media. Colonies that grew similarly on both media were scored as a negative and corresponding colonies were no longer considered. Colonies on xylose medium that failed to grow to the same serial dilution compared to those on the non-xylose plate were given a score based on the differential. For example, colonies on xylose medium that only grow to a serial dilution of -4 while they were able to grow to -8 on the non-xylose plate, then the corresponding transformant colony received a score of "4" representing the log difference in growth observed.

Following the identification of those vectors that, upon induction, negatively impacted *E. faecalis* growth or proliferation, the inserts or nucleic acid fragments contained in those expression vectors were isolated for subsequent characterization. The inserts in the vectors of interest were subjected to nucleotide sequence determination.

It will be appreciated that other restriction enzymes and other endonucleases or methodologies may be used to generate random genomic fragments. In addition, random genomic fragments may be generated by mechanical shearing. Sonication and nebulization are two such techniques commonly used for mechanical shearing of DNA.

EXAMPLE 2

Nucleotide Sequence Determination of Identified Clones Transribing Nucleic Acid Fragments with Detrimental Effects on *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* or *Enterococcus faecalis* Proliferation

Plasmids from clones that received a dilution plating score of "2" or greater were isolated to obtain the genomic DNA insert responsible for growth inhibition as follows. *Staphylococcus aureus* were grown in standard laboratory media (LB or TB with 15 ug/ml Chloramphenicol to select for the plasmid). Growth was carried out at 37°C overnight in culture tubes or 2 ml deep well microtiter plates.

Lysis of *Staphylococcus aureus* was performed as follows. Cultures (2-5 ml) were centrifuged and the cell pellets resuspended in 1.5 mg/ml solution of lysostaphin (20 μl/ml of original culture) followed by addition of 250 μl of resuspension buffer (Qiagen). Alternatively, cell pellets were resuspended directly in 250 μl of resuspension buffer (Qiagen) to which 5-20 μl of a 1 mg/ml lysostaphin solution were added.

DNA was isolated using Qiagen miniprep kits or Wizard (Qiagen) miniprep kits according to the instructions provided by the manufacturer.

The genomic DNA inserts were amplified from the purified plasmids by PCR as follows.

1 μl of Qiagen purified plasmid was put into a total reaction volume of 25 μl Qiagen Hot Start PCR mix. For *Staphylococcus aureus*, the following primers were used in the PCR reaction:

pXylT5F: CAGCAGTCTGAGTTATAAAATAG (SEQ ID NO: 1)

LexL TGTTTTATCAGACCGCTT (SEQ ID NO: 2)

Similar methods were conducted for *Salmonella typhimurium* and *Klebsiella pneumoniae*. For *Salmonella typhimurium* and *Klebsiella pneumoniae* the following primers were used:

5' - TGTTTTATCAGACCGCTT- 3' (SEQ ID NO: 2) and

5'-ACAATTTCACACAGCCTC-3' (SEQ ID NO: 4)

PCR was carried out in a PE GenAmp with the following cycle times:

Step 1. 95° C 15 min

Step 2. 94° C 45 sec

Step 3. 54° C 45 sec

Step 4. 72° C 1 minute

Step 5. Return to step 2, 29 times

Step 6. 72° C 10 minutes

Step 7. 4° C hold

The PCR products were cleaned using Qiagen Qiaquick PCR plates according to the manufacturer's instructions.

For *Pseudomonas aeruginosa,* plasmids from transformant colonies that received a dilution plating score of "2" or greater were isolated to obtain the genomic DNA insert responsible for growth inhibition as follows. *Pseudomonas aeruginosa* were grown in standard laboratory media (LB with carbenicillin at 100 g/ml or Streptomycin 40 g/ml to select for the plasmid). Growth was carried out at 30°C overnight in 100 ul culture wells in microtiter plates. To amplify insert DNA 2 ul of culture were placed into 25 ul Qiagen Hot Start PCR mix. PCR reactions were in 96 well microtiter plates. For plasmid pEP5S the following primers were used in the PCR reaction:

T7L1+: GTCGGCGATATAGGCGCCAGCAACCG (SEQ ID NO: 5)

pStrA3: ATAATCGAGCATGAGTATCATACG (SEQ ID NO: 6)

PCR was carried out in a PE GenAmp with the following cycle times:

Step 1. 95° C 15 min

Step 2. 94° C 45 sec

Step 3. 54° C 45 sec

Step 4. 72° C 1 minute

Step 5. Return to step 2, 29 times

Step 6. 72° C 10 minutes

Step 7. 4° C hold

The PCR products were cleaned using Qiagen Qiaquick PCR plates according to the manufacturer's instructions.

The purified PCR products were then directly cycle sequenced with Qiagen Hot Start PCR mix. The following primers were used in the sequencing reaction:

T7/L2: ATGCGTCCGGCGTAGAGGAT (SEQ ID NO: 7)

PCR was carried out in a PE GenAmp with the following cycle times:

Step 1. 94° C 15 min

Step 2. 96° C 10 sec

Step 3. 50° C 5 sec

Step 4. 60 C 4 min

Step 5. Return to step 2, 24 times

Step 6. 4° C hold

The PCR products were cleaned using Qiagen Qiaquick PCR plates according to the manufacturer's instructions.

For *E. faecalis,* plasmids from transformant colonies that received a dilution plating score of "2" or greater were isolated to obtain the genomic DNA insert responsible for growth inhibition as follows. *E. faecalis* were grown in THB 10 μg/ml Erm at 30°C overnight in 100 ul culture wells in microtiter plates. To amplify insert DNA 2 ul of culture were placed into 25 μl Qiagen Hot Start

PCR mix. PCR reactions were in 96 well microtiter plates. The following primers were used in the PCR reaction:

pXylT5: CAGCAGTCTGAGTTATAAAATAG (SEQ ID NO: 1) and the

pEP/pAK1 primer.

PCR was carried out in a PE GenAmp with the following cycle times:

Step 1. 95° C 15 min

Step 2. 94° C 45 sec

Step 3. 54° C 45 sec

Step 4. 72° C 1 minute

Step 5. Return to step 2, 29 times

Step 6. 72° C 10 minutes

Step 7. 4° C hold

The PCR products were cleaned using Qiagen Qiaquick PCR plates according to the manufacturer's instructions.

The purified PCR products were then directly cycle sequenced with Qiagen Hot Start PCR mix. The following primers were used in the PCR reaction:

pXylT5: CAGCAGTCTGAGTTATAAAATAG (SEQ ID NO: 1)

PCR was carried out in a PE GenAmp with the following cycle times:

Step 1. 94° C 15 min

Step 2. 96° C 10 sec

Step 3. 50° C 5 sec

Step 4. 60° C 4 min

Step 5. Return to step 2, 24 times

Step 6. 4° C hold

The PCR products were cleaned using Qiagen Qiaquick PCR plates according to the manufacturer's instructions.

The amplified genomic DNA inserts from each of the above procedures were subjected to automated sequencing. Sequence identification numbers (SEQ ID NOs) and clone names for the identified inserts are listed in Table IA and discussed below.

EXAMPLE 3

Comparison Of Isolated Nucleic Acids to Known Sequences

The nucleotide sequences of the subcloned fragments from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* or *Enterococcus faecalis* obtained from the expression vectors discussed above were compared to known sequences from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* or *Enterococcus faecalis* and other microorganisms as follows. First, to confirm that

each clone originated from one location on the chromosome and was not chimeric, the nucleotide sequences of the selected clones were compared against the *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* or *Enterococcus faecalis* genomic sequences to align the clone to the correct position on the chromosome. The NCBI BLASTN v 2.0.9 program was used for this comparison, and the incomplete *Staphylococcus aureus* genomic sequences licensed from TIGR, as well as the NCBI nonredundant GenBank database were used as the source of genomic data. *Salmonella typhimurium* sequences were compared to sequences available from the Genome Sequencing Center (http://genome.wustl.edu/gsc/salmonella.shtml),and the Sanger Centre (http://www.sanger.ac.uk/projects/S___typhi). *Pseudomonas aeruginosa* sequences were compared to a proprietary database and the NCBI GenBank database. The *E. faecalis* sequences were compared to a proprietary database.

The BLASTN analysis was performed using the default parameters except that the filtering was turned off. No further analysis was performed on inserts which resulted from the ligation of multiple fragments.

In general, antisense molecules and their complementary genes are identified as follows. First, all possible full length open reading frames (ORFs) are extracted from available genomic databases. Such databases include the GenBank nonredundant (nr) database, the unfinished genome database available from TIGR and the PathoSeq database developed by Incyte Genomics. The latter database comprises over 40 annotated bacterial genomes including complete ORF analysis. If databases are incomplete with regard to the bacterial genome of interest, it is not necessary to extract all ORFs in the genome but only to extract the ORFs within the portions of the available genomic sequences which are complementary to the clones of interest. Computer algorithms for identifying ORFs, such as GeneMark, are available and well known to those in the art. Comparison of the clone DNA to the complementary ORF(s) allows determination of whether the clone is a sense or antisense clone. Furthermore, each ORF extracted from the database can be compared to sequences in well annotated databases including the GenBank (nr) protein database, SWISSPROT and the like. A description of the gene or of a closely related gene in a closely related microorganism is often available in these databases. Similar methods are used to identify antisense clones corresponding to genes encoding non-translated RNAs.

In order to generate the gene identification data compiled in Table IB, each of the cloned nucleic acid sequences discussed above corresponding to SEQ ID NO.s 8-3795 was used to identify the corresponding *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* or *Enterococcus faecalis* ORFs in the PathoSeq v.4.1 (March 2000 release) database of microbial genomic sequences. For this purpose, the NCBI BLASTN 2.0.9 computer algorithm was used. The default parameters were used except that filtering was turned off. The default parameters for the BLASTN and BLASTX analyses were:

Expectation value (e)=10

Alignment view options: pairwise
Filter query sequence (DUST with BLASTN, SEG with others)=T
Cost to open a gap (zero invokes behavior)=0
Cost to extend a gap (zero invokes behavior)=0
X dropoff value for gapped alignment (in bits) (zero invokes behavior)=0
Show GI's in deflines=F
Penalty for a nucleotide mismatch (BLASTN only)=-3
Reward for a nucleotide match (BLASTN only)=1
Number of one-line descriptions (V)=500
Number of alignments to show (B)=250
Threshold for extending hits=default
Perform gapped alignment (not available with BLASTX)=T
Query Genetic code to use=1
DB Genetic code (for TBLAST[nx] only=1
Number of processors to use=1
SeqAlign file
Believe the query defline=F
Matrix=BLOSUM62
Word Size= default
Effective length of the database (use zero for the real size)=0
Number of best hits from a region to keep=100
Length of region used to judge hits=20
Effective length of the search space (use zero for the real size)=0
Query strands to search against database (for BLAST[nx] and TBLASTX), 3 is both, 1 is top, 2 is bottom=3
Produce HTML output=F

Alternatively, ORFs were identified and refined by conducting a survey of the public and private data sources. Full-length gene protein and nucleotide sequences for these organisms were assembled from various sources. For *Pseudomonas aeruginosa*, gene sequences were adopted from the Pseudomonas genome sequencing project (downloaded from http://www.pseudomonas.com). For *Klebsiella pneumoniae, Staphylococcus aureus, Streptococcus pneumoniae* and *Salmonella typhi,* genomic sequences from PathoSeq v 4.1 (Mar 2000 release) was reanalyzed for ORFs using the gene finding software GeneMark v 2.4a, which was purchased from GenePro Inc. 451 Bishop St., N.W., Suite B, Atlanta, GA, 30318, USA.

Antisense clones were identified as those clones for which transcription from the inducible promoter would result in the expression of an RNA antisense to a complementary ORF, intergenic or intragenic sequence. Those clones containing single inserts and that caused growth sensitivity upon induction are listed in Table IA. ORFs complementary to the antisense nucleic acids, and their encoded polypeptides, are listed in Table IB.

The gene descriptions in the PathoSeq database derive from annotations available in the public sequence databases described above. Where a clone was found to share significant sequence identity to two or more adjacent ORFs, it was listed once for each ORF and the PathoSeq information for each ORF was compiled in Table IB.

Table IA lists the SEQ ID NOs. and clone names of the inserts which inhibited proliferation and the organism in which the clone was identified. This information was used to identify the

ORFs (SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012) whose gene products (SEQ ID NOs. 3801-3805, 4861-5915, 10013-14110) were inhibited by the nucleic acids comprising the nucleotide sequences of SEQ ID NOs. 8-3795. Table IB lists the clone name, the SEQ ID NO. of the antisense clone (in the column labelled Clone SEQ ID), the PathoSeq Locus containing the clone, the SEQ ID of the ORF identified in PathoSeq (in the column labelled Gene Seq ID (protein), the refined full length gene (column labelled genemarked gene), and the SEQ ID NO of the protein encoded by the refined full length gene (column labelled full length ORF protein SEQ ID).

Table IC provides a cross reference between PathoSeq Gene Locus listed in Table IB, the SEQ ID NOs. of the PathoSeq proteins and the SEQ ID NOs. of the nucleic acids which encode them.

It will be appreciated that ORFs may also be identified using databases other than PathoSeq. For example, the ORFs may be identified using the methods described in U.S. Provisional Patent Application Serial Number 60/191,078, filed March 21, 2000.

EXAMPLE 4

Identification of Genes and their Corresponding Operons Affected by Antisense Inhibition

Once the genes involved in *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* or *Enterococcus faecalis* proliferation are identified as described above, the operons in which these genes lie may be identified by comparison with known microbial genomes. Since bacterial genes are transcribed in a polycistronic manner, the antisense inhibition of a single gene in an operon might affect the expression of all the other genes on the operon or the genes downstream from the single gene identified. Accordingly, each of the genes contained within an operon may be analyzed for their effect on proliferation.

Operons are predicted by looking for all adjacent genes in a genomic region that lie in the same orientation with no large noncoding gaps in between. First, full-length ORFs complementary to the antisense molecules are identified as described above. Adjacent ORFs are then identified and their relative orientation determined either by directly analyzing the genomic sequences surrounding the ORFs complementary to the antisense clones or by extracting adjacent ORFs from the collection obtained through whole genome ORF analysis described above followed by ORF alignment. Operons predicted in this way may be confirmed by comparison to the arrangement of the homologous nucleic acids in the *Bacillus subtilis* complete genome sequence, as reported by the genome database compiled at Institut Pasteur Subtilist Release R15.1 (June 24, 1999) which can be found at http://bioweb.pasteur.fr/GenoList/SubtiList/. The *Bacillus subtilis* genome is the only fully sequenced and annotated genome from a Gram-positive microorganism, and appears to have a high level of similarity to *Staphylococcus aureus* both at the level of conservation of gene sequence and genomic organization including operon structure. Operons for *Salmonella typhimurium* and *Klebsiella pneumoniae* may be identified by comparison with *E. coli, Haemophilus,* or

Pseudomonas sequences. The *Pseudomonas aeruginosa* web site (http://www.pseudomonas.com) can also be used to help predict operon organization in this bacterium.

Extensive DNA sequences of *Salmonella typhimurium* are available through the Salmonella Genome Center (Washington University, St. Louis, MO) the Sanger Centre (United Kingdom) and the PathoSeq database (Incyte). Annotation of some of the DNA sequences in some of the aforementioned databases is lacking, but comparisons may be made to *E. coli* using tools such as BLASTX.

Public or proprietary databases may be used to analyzed *E. faecalis* sequences as well as sequences from the organisms listed above.

The results of such an analysis as applied to clone number S1M10000001A05 from *Staphylococcus aureus* are listed in Table II. Table II lists the SEQ ID NOs. of the *Staphylococcus aureus* genes involved in proliferation, the SEQ ID NOs. of the proteins encoded by these genes, and the clone name containing the nucleic acid which inhibits *Staphylococcus aureus* proliferation. In addition, Table II lists those other genes located on the operon included in the *Staphylococcus aureus* genomic sequence determined as described above. For each of the genes described in Table II, the microorganism containing the most closely related homolog, identified in one of the public databases, is also indicated in Table II.

TABLE II

DNA Seq ID	Protein Seq ID	Molecule number	Clone name	Gene	Organism used for identification of gene
3796	3801	SaXA001	S1M10000001A05	ytmI	*B. subtilis*
3797	3802			nirR	*S. carnosus*
3798	3803			nirB	*S. carnosus*
3799	3804			nirD	*S. carnosus*
3800	3805			sirB	*S. carnosus*

The preceding analyses may be conducted for each of the sequences which are listed in Table IA which inhibit proliferation and the ORFs listed in Table IB and Table IC. Once the full length ORFs and/or the operons containing them have been identified using the methods described above, they can be obtained from a genomic library by performing a PCR amplification using primers at each end of the desired sequence. Those skilled in the art will appreciate that a comparison of the ORFs to homologous sequences in other cells or microorganisms will facilitate confirmation of the start and stop codons at the ends of the ORFs.

In some embodiments, the primers may contain restriction sites which facilitate the insertion of the gene or operon into a desired vector. For example, the gene may be inserted into an expression vector and used to produce the proliferation-required protein as described below. Other methods for obtaining the full length ORFs and/or operons are familiar to those skilled in the art.

For exmaple, natural restriction sites may be employed to insert the full length ORFs and/or operons into a desired vector.

EXAMPLE 5

Identification of Individual Genes within an Operon Required for Proliferation

The following example illustrates a method for determining if a targeted gene within an operon is required for cell proliferation by replacing the targeted allele in the chromosome with an in-frame deletion of the coding region of the targeted gene.

Deletion inactivation of a chromosomal copy of a gene in *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori*, or *Salmonella typhi* can be accomplished by integrative gene replacement. The principles of this method were described in Xia, M., et al. 1999 Plasmid 42:144-149 and Hamilton, C. M., et al 1989. *J. Bacteriol.* 171: 4617-4622. A similar gene disruption method is available for *Pseudomonas aeruginosa*, except the counter selectable marker is *sacB* (Schweizer, H. P., Klassen, T. and Hoang, T. (1996) Mol. Biol. of *Pseudomonas*. ASM press, 229-237). In this approach, a mutant allele of the targeted gene is constructed by way of an in-frame deletion and introduced into the chromosome using a suicide vector. This results in a tandem duplication comprising a deleted (null) allele and a wild type allele of the target gene. Cells in which the vector sequences have been deleted are isolated using a counter-selection technique. Removal of the vector sequence from the chromosomal insertion results in either restoration of the wild-type target sequence or replacement of the wild type sequence with the deletion (null) allele. *E. faecalis* genes can be disrupted using a suicide vector that contains an internal fragment to a gene of interest. With the appropriate selection this plasmid will homologously recombine into the chromosome (Nallapareddy, S. R., X. Qin, G. M. Weinstock, M. Hook, B. E. Murray. 2000. Infect. Immun. 68:5218-5224).

The resultant population of *Staphylococcus aureus; Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori*, or *Salmonella typhi* colonies can then be evaluated to determine whether the target sequence is required for proliferation by PCR amplification of the affected target sequence. If the targeted gene is not required for proliferation, then PCR analysis will show that roughly equal numbers of colonies have retained either the wild-type or the mutant allele. If the targeted gene is required for proliferation, then only wild-type alleles will be recovered in the PCR analysis.

The method of cross-over PCR is used to generate the mutant allele by amplification of nucleotide sequences flanking but not including the coding region of the gene of interest, using specifically designed primers such that overlap between the resulting two PCR amplification products allows them to hybridize. Further PCR amplification of this hybridization product using

primers representing the extreme 5' and 3' ends can produce an amplification product containing an in-frame deletion of the coding region but retaining substantial flanking sequences.

For *Staphylococcus aureus*, this amplification product is subcloned into the suicide vector pSA3182 (Xia, M., et al. 1999 Plasmid 42:144-149) which is host-dependent for autonomous replication. This vector includes a *tetC* tetracycline-resistance marker and the origin of replication of the well-known *Staphylococcus aureus* plasmid pT181 (Mojumdar, M and Kahn, S.A., Characterisation of the Tetracycline Resistance Gene of Plasmid pT181, J. Bacteriol. 170: 5522 (1988)). The vector lacks the *repC* gene which is required for autonomous replication of the vector at the pT181 origin. This vector can be propagated in a *Staphylococcus aureus* host strain such as SA3528, which expresses *repC* in trans. Once the amplified truncated target gene sequence is cloned and propagated in the pSA3182 vector, it can then be introduced into a *repC* minus strain such as RN4220 (Kreiswirth, B.N. et al., The Toxic Shock Syndrome Exotoxin Structural Gene is Not Detectably Transmitted by a Prophage, Nature 305:709-712 (1983)) by electroporation with selection for tetracycline resistance. In this strain, the vector must integrate by homologous recombination at the targeted gene in the chromosome to impart drug resistance. This results in a inserted truncated copy of the allele, followed by pSA3182 vector sequence, and finally an intact and functional allele of the targeted gene.

Once a tetracycline resistant *Staphylococcus aureus* strain is isolated using the above technique and shown to include truncated and wild-type alleles of the targeted gene as described above, a second plasmid, pSA7592 (Xia, M., et al. 1999 Plasmid 42:144-149) is introduced into the strain by electroporation. This gene includes an erythromycin resistance gene and a *repC* gene that is expressed at high levels. Expression of *repC* in these transformants is toxic due to interference of normal chromosomal replication at the integrated pT181 origin of replication. This selects for strains that have removed the vector sequence by homologous recombination, resulting in either of two outcomes: The selected cells either possess a wild-type allele of the targeted gene or a gene in which the wild-type allele has been replaced by the engineered in-frame deletion of the truncated allele.

PCR amplification can be used to determine the genetic outcome of the above process in the resulting erythromycin resistant, tet sensitive transformant colonies. If the targeted gene is not required for cellular replication, then PCR evidence for both wild-type and mutant alleles will be found among the population of resultant transformants. However, if the targeted gene is required for cellular proliferation, then only the wild-type form of the gene will be evident among the resulting transformants.

Similarly, for *Salmonella typhimurium*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* or *Enterococcus faecalis*, *Escherichia coli*, *Enterococcus faecalis*, *Haemophilus influenzae*, *Helicobacter pylori*, or *Salmonella typhi* the PCR products containing the mutant allele of the

target sequence may be introduced into an appropriate knockout vector and cells in which the wild type target has been disrupted are selected using the appropriate methodology.

The above methods have the advantage that insertion of an in-frame deletion mutation is far less likely to cause downstream polar effects on genes in the same operon as the targeted gene. However, it will be appreciated that other methods for disrupting *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* genes which are familiar to those skilled in the art may also be used.

Each gene in the operon may be disrupted using the methodology above to determine whether it is required for proliferation.

EXAMPLE 6

Expression of the Proteins Encoded by Genes Identified as Required for *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* Proliferation

The following is provided as one exemplary method to express the proliferation-required proteins idenfied as described above. The proliferation-required proteins may be expressed using any of the bacterial, insect, yeast, or mammalian expression systems known in the art. In some embodiments, the proliferation-required proteins encoded by the identified nucleotide sequences described above (including the proteins of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 encoded by the nucleic acids of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012 are expressed using expression systems designed either for *E. coli* or for *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi*. First, the initiation and termination codons for the gene are identified. If desired, methods for improving translation or expression of the protein are well known in the art. For example, if the nucleic acid encoding the polypeptide to be expressed lacks a methionine codon to serve as the initiation site, a strong Shine-Delgarno sequence, or a stop codon, these nucleotide sequences can be added. Similarly, if the identified nucleic acid lacks a transcription termination signal, this nucleotide sequence can be added to the construct by, for example, splicing out such a sequence from an appropriate donor sequence. In addition, the coding sequence may be operably linked to a strong constitutive promoter or an inducible promoter if desired. The identified nucleic acid or portion thereof encoding the polypeptide to be expressed is obtained by, for example, PCR from the bacterial expression vector or genome using oligonucleotide primers complementary to the identified nucleic acid or portion thereof and containing restriction endonuclease sequences appropriate for inserting the coding sequences into the vector such that the coding sequences can be expressed from the vector's promoter. Alternatively, other conventional cloning techniques may be used to place the coding sequence under the control of

the promoter. In some embodiments, a termination signal may be located downstream of the coding sequence such that transcription of the coding sequence ends at an appropriate position.

Several expression vector systems for protein expression in *E. coli* are well known and available to those knowledgeable in the art. The coding sequence may be inserted into any of these vectors and placed under the control of the promoter. The expression vector may then be transformed into DH5α or some other *E. coli* strain suitable for the over expression of proteins.

Alternatively, an expression vector encoding a protein required for proliferation of *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae,Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* may be introduced into *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa,Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi*. Protocols for introducing nucleic acids into these organisms are well known in the art. For example, the protocols described in J.C.Lee "Electroporation of Staphylococci" from Methods in Molecular Biology vol 47: Electroporation Protocols for Microorganisms Edited by : J.A. Nickoloff Humana Press Inc., Totowa, NJ. pp209-216, may be used to introduce nucleic acids into *Staphylococcus aureus*. Nucleic acids may also be introduced into *Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* or *Enterococcus faecalis* using methods familiar to those skilled in the art. Positive transformants are selected after growing the transformed cells on plates containing an antibiotic to which the vector confers resistance. In one embodiment, *Staphylococcus aureus* is transformed with an expression vector in which the coding sequence is operably linked to the T5 promoter containing a xylose operator such that expression of the encoded protein is inducible with xylose.

In one embodiment, the protein is expressed and maintained in the cytoplasm as the native sequence. In an alternate embodiment, the expressed protein can be modified to include a protein tag that allows for differential cellular targeting, such as to the periplasmic space of Gram-negative or Gram-positive expression hosts or to the exterior of the cell (i.e., into the culture medium). In some embodiments, the osmotic shock cell lysis method described in Chapter 16 of **Current Protocols in Molecular Biology,** Vol. 2, (Ausubel, et al., Eds.) John Wiley & Sons, Inc. (1997) may be used to liberate the polypeptide from the cell. In still another embodiment, such a protein tag could also facilitate purification of the protein from either fractionated cells or from the culture medium by affinity chromatography. Each of these procedures can be used to express a proliferation-required protein.

Expressed proteins, whether in the culture medium or liberated from the periplasmic space or the cytoplasm, are then purified or enriched from the supernatant using conventional techniques such as ammonium sulfate precipitation, standard chromatography, immunoprecipitation, immunochromatography, size exclusion chromatography, ion exchange chromatography, and HPLC.

Alternatively, the polypeptide may be secreted from the host cell in a sufficiently enriched or pure state in the supernatant or growth media of the host cell to permit it to be used for its intended purpose without further enrichment. The purity of the protein product obtained can be assessed using techniques such as SDS PAGE, which is a protein resolving technique well known to those skilled in the art. Coomassie, silver staining or staining with an antibody are typical methods used to visualize the protein of interest.

Antibodies capable of specifically recognizing the protein of interest can be generated using synthetic peptides using methods well known in the art. See, **Antibodies: A Laboratory Manual**, (Harlow and Lane, Eds.) Cold Spring Harbor Laboratory (1988). For example, 15-mer peptides having an amino acid sequence encoded by the appropriate identified gene sequence of interest or portion thereof can be chemically synthesized. The synthetic peptides are injected into mice to generate antibodies to the polypeptide encoded by the identified nucleic acid sequence of interest or portion thereof. Alternatively, samples of the protein expressed from the expression vectors discussed above can be purified and subjected to amino acid sequencing analysis to confirm the identity of the recombinantly expressed protein and subsequently used to raise antibodies. An Example describing in detail the generation of monoclonal and polyclonal antibodies appears in Example 7.

The protein encoded by the identified nucleic acid of interest or portion thereof can be purified using standard immunochromatography techniques. In such procedures, a solution containing the secreted protein, such as the culture medium or a cell extract, is applied to a column having antibodies against the secreted protein attached to the chromatography matrix. The secreted protein is allowed to bind the immunochromatography column. Thereafter, the column is washed to remove non-specifically bound proteins. The specifically-bound secreted protein is then released from the column and recovered using standard techniques. These procedures are well known in the art.

In an alternative protein purification scheme, the identified nucleic acid of interest or portion thereof can be incorporated into expression vectors designed for use in purification schemes employing chimeric polypeptides. In such strategies the coding sequence of the identified nucleic acid of interest or portion thereof is inserted in-frame with the gene encoding the other half of the chimera. The other half of the chimera can be maltose binding protein (MBP) or a nickel binding polypeptide encoding sequence. A chromatography matrix having maltose or nickel attached thereto is then used to purify the chimeric protein. Protease cleavage sites can be engineered between the MBP gene or the nickel binding polypeptide and the identified expected gene of interest, or portion thereof. Thus, the two polypeptides of the chimera can be separated from one another by protease digestion.

One useful expression vector for generating maltose binding protein fusion proteins is pMAL (New England Biolabs), which encodes the *malE* gene. In the pMal protein fusion system, the cloned gene is inserted into a pMal vector downstream from the *malE* gene. This results in the expression of an MBP-fusion protein. The fusion protein is purified by affinity chromatography. These techniques as described are well known to those skilled in the art of molecular biology.

EXAMPLE 7

Production of an Antibody to an isolated *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa ,Enterococcus faecalis,Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori*, or *Salmonella typhi* Protein

Substantially pure protein or polypeptide (including one of the polypeptides of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110) is isolated from the transformed cells as described in Example 6. The concentration of protein in the final preparation is adjusted, for example, by concentration on a 10,000 molecular weight cut off AMICON filter device (Millipore, Bedford, MA), to the level of a few micrograms/ml. Monoclonal or polyclonal antibody to the protein can then be prepared as follows:

Monoclonal Antibody Production by Hybridoma Fusion

Monoclonal antibody to epitopes of any of the peptides identified and isolated as described can be prepared from murine hybridomas according to the classical method of Kohler, G. and Milstein, C., **Nature 256**:495 (1975) or any of the well-known derivative methods thereof. Briefly, a mouse is repetitively inoculated with a few micrograms of the selected protein or peptides derived therefrom over a period of a few weeks. The mouse is then sacrificed, and the antibody-producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells are destroyed by growth of the system on selective medium comprising aminopterin (HAT medium). The successfully-fused cells are diluted and aliquots of the dilution placed in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as ELISA, as described by Engvall, E., "Enzyme immunoassay ELISA and EMIT," **Meth. Enzymol.** 70:419 (1980), and derivative methods thereof. Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Davis, L. et al. **Basic Methods in Molecular Biology** Elsevier, New York. Section 21-2.

Polyclonal Antibody Production by Immunization

Polyclonal antiserum containing antibodies to heterogeneous epitopes of a single protein or a peptide can be prepared by immunizing suitable animals with the expressed protein or peptides derived therefrom described above, which can be unmodified or modified to enhance immunogenicity. Effective polyclonal antibody production is affected by many factors related both to the antigen and the host species. For example, small molecules tend to be less immunogenic than larger molecules and can require the use of carriers and adjuvant. Also, host animals vary in response to site of inoculations and dose, with both inadequate or excessive doses of antigen resulting in low titer antisera. Small doses (ng level) of antigen administered at multiple intradermal sites appears to be most reliable. An effective immunization protocol for rabbits can be found in Vaitukaitis, J. et al. **J. Clin. Endocrinol. Metab. 33**:988-991 (1971).

Booster injections can be given at regular intervals, and antiserum harvested when antibody titer thereof, as determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen, begins to fall. See, for example, Ouchterlony, O. et al., Chap. 19 in: **Handbook of Experimental Immunology** D. Wier (ed) Blackwell (1973). Plateau concentration of antibody is usually in the range of 0.1 to 0.2 mg/ml of serum (about 12 μM). Affinity of the antisera for the antigen is determined by preparing competitive binding curves, as described, for example, by Fisher, D., Chap. 42 in: **Manual of Clinical Immunology**, 2d Ed. (Rose and Friedman, Eds.) Amer. Soc. For Microbiol., Washington, D.C. (1980).

Antibody preparations prepared according to either protocol are useful in quantitative immunoassays which determine concentrations of antigen-bearing substances in biological samples; they are also used semi-quantitatively or qualitatively to identify the presence of antigen in a biological sample. The antibodies can also be used in therapeutic compositions for killing bacterial cells expressing the protein.

EXAMPLE 8

Screening Chemical Libraries

A. Protein-Based Assays

Having isolated and expressed bacterial proteins shown to be required for bacterial proliferation, the present invention further contemplates the use of these expressed target proteins in assays to screen libraries of compounds for potential drug candidates. The generation of chemical libraries is well known in the art. For example, combinatorial chemistry can be used to generate a library of compounds to be screened in the assays described herein. A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building block" reagents. For example, a linear combinatorial chemical library such as a polypeptide library is formed by combining amino acids in every possible combination to yield peptides of a given length. Millions of chemical compounds theoretically can be synthesized through such combinatorial mixings of chemical building blocks. For example, one commentator observed that the systematic, combinatorial mixing of 100 interchangeable chemical building blocks results in the theoretical synthesis of 100 million tetrameric compounds or 10 billion pentameric compounds. (Gallop et al., "Applications of Combinatorial Technologies to Drug Discovery, Background and Peptide Combinatorial Libraries," **Journal of Medicinal Chemistry**, Vol. 37, No. 9, 1233-1250 (1994). Other chemical libraries known to those in the art may also be used, including natural product libraries.

Once generated, combinatorial libraries can be screened for compounds that possess desirable biological properties. For example, compounds which may be useful as drugs or to develop drugs would likely have the ability to bind to the target protein identified, expressed and purified as discussed above. Further, if the identified target protein is an enzyme, candidate compounds would likely interfere with the enzymatic properties of the target protein. For example, the enzymatic function of a

target protein may be to serve as a protease, nuclease, phosphatase, dehydrogenase, transporter protein, transcriptional enzyme, and any other type of enzyme known or unknown. Thus, the present invention contemplates using the protein products described above to screen combinatorial chemical libraries.

In one example, the target protein is a serine protease and the substrate of the enzyme is known. The present example is directed towards the analysis of libraries of compounds to identify compounds that function as inhibitors of the target enzyme. First, a library of small molecules is generated using methods of combinatorial library formation well known in the art. U.S. Patent Nos. 5,463,564 and 5,574, 656, to Agrafiotis, et al., entitled "System and Method of Automatically Generating Chemical Compounds with Desired Properties," are two such teachings. Then the library compounds are screened to identify those compounds that possess desired structural and functional properties. U.S. Patent No. 5,684,711, also discusses a method for screening libraries.

To illustrate the screening process, the target polypeptide and chemical compounds of the library are combined with one another and permitted to interact with one another. A labeled substrate is added to the incubation. The label on the substrate is such that a detectable signal is emitted from the products of the substrate molecules that result from the activity of the target polypeptide. The emission of this signal permits one to measure the effect of the combinatorial library compounds on the enzymatic activity of target enzymes by comparing it to the signal emitted in the absence of combinatorial library compounds. The characteristics of each library compound are encoded so that compounds demonstrating activity against the enzyme can be analyzed and features common to the various compounds identified can be isolated and combined into future iterations of libraries.

Once a library of compounds is screened, subsequent libraries are generated using those chemical building blocks that possess the features shown in the first round of screen to have activity against the target enzyme. Using this method, subsequent iterations of candidate compounds will possess more and more of those structural and functional features required to inhibit the function of the target enzyme, until a group of enzyme inhibitors with high specificity for the enzyme can be found. These compounds can then be further tested for their safety and efficacy as antibiotics for use in mammals.

It will be readily appreciated that this particular screening methodology is exemplary only. Other methods are well known to those skilled in the art. For example, a wide variety of screening techniques are known for a large number of naturally-occurring targets when the biochemical function of the target protein is known. For example, some techniques involve the generation and use of small peptides to probe and analyze target proteins both biochemically and genetically in order to identify and develop drug leads. Such techniques include the methods described in PCT publications No. WO9935494, WO9819162, WO9954728. Other techniques utilize natural product libraries or libraries of larger molecules such as proteins.

It will be appreciated that the above protein-based assays may be performed with any of the proliferation-required polypeptides from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* (including the polypeptides of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110) or portions thereof. In addition, the above protein-based assays may be performed with homologous polypeptides or portions thereof.

B. Cell-Based Assays

Current cell-based assays used to identify or to characterize compounds for drug discovery and development frequently depend on detecting the ability of a test compound to modulate the activity of a target molecule located within a cell or located on the surface of a cell. An advantage of cell-based assays is that they allow the effect of a compound on a target molecule's activity to be detected within the physiologically relevant environment of the cell as opposed to an *in vitro* environment. Most often such target molecules are proteins such as enzymes, receptors and the like. However, target molecules may also include other molecules such as DNAs, lipids, carbohydrates and RNAs including messenger RNAs, ribosomal RNAs, tRNAs, regulatory RNAs and the like. A number of highly sensitive cell-based assay methods are available to those of skill in the art to detect binding and interaction of test compounds with specific target molecules. However, these methods are generally not highly effective when the test compound binds to or otherwise interacts with its target molecule with moderate or low affinity. In addition, the target molecule may not be readily accessible to a test compound in solution, such as when the target molecule is located inside the cell or within a cellular compartment. Thus, current cell-based assay methods are limited in that they are not effective in identifying or characterizing compounds that interact with their targets with moderate to low affinity or compounds that interact with targets that are not readily accessible.

The cell-based assay methods of the present invention have substantial advantages over current cell-based assays. These advantages derive from the use of sensitized cells in which the level or activity of at least one proliferation-required gene product (the target molecule) has been specifically reduced to the point where the presence or absence of its function becomes a rate-determining step for cellular proliferation. Bacterial, fungal, plant, or animal cells can all be used with the present method. Such sensitized cells become much more sensitive to compounds that are active against the affected target molecule. Thus, cell-based assays of the present invention are capable of detecting compounds exhibiting low or moderate potency against the target molecule of interest because such compounds are substantially more potent on sensitized cells than on non-sensitized cells. The effect may be such that a test compound may be two to several times more potent, at least 10 times more potent, at least 20 times more potent, at least 50 times more potent, at least 100 times more potent, at least 1000 times more potent, or even more than 1000 times more potent when tested on the sensitized cells as compared to the non-sensitized cells. The

proliferation-required nucleic acids or polypeptides from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi,* or portions thereof, may be employed in any of the cell-based assays described herein. Similarly, homologous coding nucleic acids, homologous antisense nucleic acids, or homologous polypeptides or portions of the homologous nucleic acids or homologous polypeptides, may be employed in any of the cell-based assays described herein.

Due in part to the increased appearance of antibiotic resistance in pathogenic microorganisms and to the significant side-effects associated with some currently used antibiotics, novel antibiotics acting at new targets are highly sought after in the art. Yet, another limitation in the current art related to cell-based assays is the problem of repeatedly identifying hits against the same kinds of target molecules in the same limited set of biological pathways. This may occur when compounds acting at such new targets are discarded, ignored or fail to be detected because compounds acting at the "old" targets are encountered more frequently and are more potent than compounds acting at the new targets. As a result, the majority of antibiotics in use currently interact with a relatively small number of target molecules within an even more limited set of biological pathways.

The use of sensitized cells of the current invention provides a solution to the above problem in two ways. First, desired compounds acting at a target of interest, whether a new target or a previously known but poorly exploited target, can now be detected above the "noise" of compounds acting at the "old" targets due to the specific and substantial increase in potency of such desired compounds when tested on the sensitized cells of the current invention. Second, the methods used to sensitize cells to compounds acting at a target of interest may also sensitize these cells to compounds acting at other target molecules within the same biological pathway. For example, expression of an antisense molecule to a gene encoding a ribosomal protein is expected to sensitize the cell to compounds acting at that ribosomal protein and may also sensitize the cells to compounds acting at any of the ribosomal components (proteins or rRNA) or even to compounds acting at any target which is part of the protein synthesis pathway. Thus an important advantage of the present invention is the ability to reveal new targets and pathways that were previously not readily accessible to drug discovery methods.

Sensitized cells of the present invention are prepared by reducing the activity or level of a target molecule. The target molecule may be a gene product, such as an RNA or polypeptide produced from the proliferation-required nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* (including a gene product produced from the nucleic acids of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, such as the polypeptides of SEQ ID NOs.: 3801-3805, 4861-

5915, 10013-14110) or from homologous nucleic acids. For example, the target molecule may be one of the polypeptides of SEQ ID NOs. 3801-3805, 4861-5915, 10013-14110 or a homologous polypeptide. Alternatively, the target may be a gene product such as an RNA or polypeptide which is produced from a sequence within the same operon as the proliferation-required nucleic acids from*Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* or from homologous nucleic acids. In addition, the target may be an RNA or polypeptide in the same biological pathway as the proliferation-required nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* or from homologous nucleic acids. Such biological pathways include, but are not limited to, enzymatic, biochemical and metabolic pathways as well as pathways involved in the production of cellular structures such the cell wall.

Current methods employed in the arts of medicinal and combinatorial chemistries are able to make use of structure-activity relationship information derived from testing compounds in various biological assays including direct binding assays and cell-based assays. Occasionally compounds are directly identified in such assays that are sufficiently potent to be developed as drugs. More often, initial hit compounds exhibit moderate or low potency. Once a hit compound is identified with low or moderate potency, directed libraries of compounds are synthesized and tested in order to identify more potent leads. Generally these directed libraries are combinatorial chemical libraries consisting of compounds with structures related to the hit compound but containing systematic variations including additions, subtractions and substitutions of various structural features. When tested for activity against the target molecule, structural features are identified that either alone or in combination with other features enhance or reduce activity. This information is used to design subsequent directed libraries containing compounds with enhanced activity against the target molecule. After one or several iterations of this process, compounds with substantially increased activity against the target molecule are identified and may be further developed as drugs. This process is facilitated by use of the sensitized cells of the present invention since compounds acting at the selected targets exhibit increased potency in such cell-based assays, thus; more compounds can now be characterized providing more useful information than would be obtained otherwise.

Thus, it is now possible using cell-based assays of the present invention to identify or characterize compounds that previously would not have been readily identified or characterized including compounds that act at targets that previously were not readily exploited using cell-based assays. The process of evolving potent drug leads from initial hit compounds is also substantially

improved by the cell-based assays of the present invention because, for the same number of test compounds, more structure-function relationship information is likely to be revealed.

The method of sensitizing a cell entails selecting a suitable gene or operon. A suitable gene or operon is one whose transcription and/or expression is required for the proliferation of the cell to be sensitized. The next step is to introduce into the cells to be sensitized, an antisense RNA capable of hybridizing to the suitable gene or operon or to the RNA encoded by the suitable gene or operon. Introduction of the antisense RNA can be in the form of a vector in which antisense RNA is produced under the control of an inducible promoter. The amount of antisense RNA produced is modulated by varying an inducer concentration to which the cell is exposed and thereby varying the activity of the promoter driving transcription of the antisense RNA. Thus, cells are sensitized by exposing them to an inducer concentration that results in a sub-lethal level of antisense RNA expression. The requisite maount of inducer may be derived empiracally by one of skill in the art.

In one embodiment of the cell-based assays, antisense nucleic acids complementary to the identified *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* nucleotide sequences or portions thereof (including antisense nucleic acids comprising a nucleotide sequence complementary to one of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, and the antisense nucleic acids of SEQ ID NOs.: 8-3795 or antisense nucleic acids comprising a nucleotide sequence complementary to portions of the foregoing nucleic acids thereof), antisense nucleic complementary to homologous coding nucleic acids or portions thereof or homologous antisense nucleic acids are used to inhibit the production of a proliferation-required protein. Vectors producing antisense RNA complementary to identified genes required for proliferation, or portions thereof, are used to limit the concentration of a proliferation-required protein without severely inhibiting growth. The proliferation-required protein may be one of the proteins of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 or a homologous polypeptide. To achieve that goal, a growth inhibition dose curve of inducer is calculated by plotting various doses of inducer against the corresponding growth inhibition caused by the antisense expression. From this curve, the concentration of inducer needed to achieve various percentages of antisense induced growth inhibition, from 1 to 100% can be determined.

A variety of different regulatable promoters may be used to produce the antisense nucleic acid. Transcription from the regulatable promoters may be modulated by controlling the activity of a transcription factor repressor which acts at the regulatable promoter. For example, if transcription is modulated by affecting the activity of a repressor, the choice of inducer to be used depends on the repressor/operator responsible for regulating transcription of the antisense nucleic acid. If the regulatable promoter comprises a T5 promoter fused to a *xylO* (xylose operator; e.g. derived from *Staphylococcus xylosis* (Schnappinger, D. et al., FEMS Microbiol. Let. 129: 121-128 (1995)) then transcription of the antisense nucleic acid may be regulated by a xylose repressor. The xylose

repressor may be provided by ectoptic expression within an *S. aureus* cell of an exogenous xylose repressor gene, e.g. derived from *S. xylosis* DNA. In such cases transcription of antisense RNA from the promoter is inducible by adding xylose to the medium and the promoter is thus "xylose inducible." Similarly, IPTG inducible promoters may be used. For example, the highest concentration of the inducer that does not reduce the growth rate significantly can be estimated from the curve. Cellular proliferation can be monitored by growth medium turbidity via OD measurements. In another example, the concentration of inducer that reduces growth by 25% can be predicted from the curve. In still another example, a concentration of inducer that reduces growth by 50% can be calculated. Additional parameters such as colony forming units (cfu) can be used to measure cellular viability.

Cells to be assayed are exposed to the above-determined concentrations of inducer. The presence of the inducer at this sub-lethal concentration reduces the amount of the proliferation required gene product to a sub-optimal amount in the cell that will still support growth. Cells grown in the presence of this concentration of inducer are therefore specifically more sensitive to inhibitors of the proliferation-required protein or RNA of interest or to inhibitors of proteins or RNAs in the same biological pathway as the proliferation-required protein or RNA of interest but not to inhibitors of unrelated proteins or RNAs.

Cells pretreated with sub-inhibitory concentrations of inducer and thus containing a reduced amount of proliferation-required target gene product are then used to screen for compounds that reduce cell growth. The sub-lethal concentration of inducer may be any concentration consistent with the intended use of the assay to identify candidate compounds to which the cells are more sensitive. For example, the sub-lethal concentration of the inducer may be such that growth inhibition is at least about 5%, at least about 8%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60% at least about 75%, or more. Cells which are pre-sensitized using the preceding method are more sensitive to inhibitors of the target protein because these cells contain less target protein to inhibit than do wild-type cells.

It will be appreciated that the above cell-based assays may be performed using antisense nucleic acids comprising a nucleotide sequence complementary to any of the proliferation-required nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi*, or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids or portions thereof or homologous antisense nucleic acids. In this way, the level or activity of a target, such as any of the proliferation-required polypeptides from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi*, or homologous polypeptides.

In another embodiment of the cell-based assays of the present invention, the level or activity of a proliferation required gene product is reduced using a mutation, such as a temperature sensitive mutation, in the gene encoding a gene product required for proliferation and an antisense nucleic acid comprising a nucleotide sequence complementary to the gene encoding the gene product required for proliferation or a portion thereof. Growing the cells at an intermediate temperature between the permissive and restrictive temperatures of the temperature sensitive mutant where the mutation is in a proliferation-required gene produces cells with reduced activity of the proliferation-required gene product. The antisense RNA complementary to the proliferation-required sequence further reduces the activity of the proliferation required gene product. Drugs that may not have been found using either the temperature sensitive mutation or the antisense nucleic acid alone may be identified by determining whether cells in which transcription of the antisense nucleic acid has been induced and which are grown at a temperature between the permissive temperature and the restrictive temperature are substantially more sensitive to a test compound than cells in which expression of the antisense nucleic acid has not been induced and which are grown at a permissive temperature. Also drugs found previously from either the antisense nucleic acid alone or the temperature sensitive mutation alone may have a different sensitivity profile when used in cells combining the two approaches, and that sensitivity profile may indicate a more specific action of the drug in inhibiting one or more activities of the gene product.

Temperature sensitive mutations may be located at different sites within the gene and correspond to different domains of the protein. For example, the *dnaB* gene of *Escherichia coli* encodes the replication fork DNA helicase. DnaB has several domains, including domains for oligomerization, ATP hydrolysis, DNA binding, interaction with primase, interaction with DnaC, and interaction with DnaA [(Biswas, E.E. and Biswas, S.B. 1999. Mechanism and DnaB helicase of *Escherichia coli*: structural domains involved in ATP hydrolysis, DNA binding, and oligomerization. Biochem. **38**:10919-10928; Hiasa, H. and Marians, K.J. 1999. Initiation of bidirectional replication at the chromosomal origin is directed by the interaction between helicase and primase. J. Biol. Chem. **274**:27244-27248; San Martin, C., Radermacher, M., Wolpensinger, B., Engel, A., Miles, C.S., Dixon, N.E., and Carazo, J.M. 1998. Three-dimensional reconstructions from cryoelectron microscopy images reveal an intimate complex between helicase DnaB and its loading partner DnaC. Structure **6**:501-9; Sutton, M.D., Carr, K.M., Vicente, M., and Kaguni, J.M. 1998. *Escherichia coli* DnaA protein. The N-terminal domain and loading of DnaB helicase at the *E. coli* chromosomal origin. J. Biol. Chem. **273**:34255-62.)]. Temperature sensitive mutations in different domains of DnaB confer different phenotypes at the restrictive temperature, which include either an abrupt stop or slow stop in DNA replication with or without DNA breakdown (Wechsler, J.A. and Gross, J.D. 1971. *Escherichia coli* mutants temperature-sensitive for DNA synthesis. Mol. Gen. Genetics **113**:273-284) and termination of growth or cell death. Combining the use of temperature sensitive mutations in the *dnaB* gene that cause cell death at the restrictive temperature

with an antisense to the *dnaB* gene could lead to the discovery of very specific and effective inhibitors of one or a subset of activities exhibited by DnaB.

It will be appreciated that the above method may be performed with any mutation which reduces but does not eliminate the activity or level of the gene product which is required for proliferation.

It will be appreciated that the above cell-based assays may be performed using mutations in, such as temperature sensitive mutations, and antisense nucleic acids comprising a nucleotide sequence complementary to any of the genes encoding proliferation-required gene products from from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi*, or portions thereof (including the nucleic acids of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012), mutations in and antisense nucleic acids complementary to homologous coding nucleic acids or portions thereof or homologous antisense nucleic acids. In this way, the level or activity of a target, such as any of the proliferation-required polypeptides from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* (including the polypeptides of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110), or homologous polypeptides may be reduced.

When screening for antimicrobial agents against a gene product required for proliferation, growth inhibition of cells containing a limiting amount of that proliferation-required gene product can be assayed. Growth inhibition can be measured by directly comparing the amount of growth, measured by the optical density of the growth medium, between an experimental sample and a control sample. Alternative methods for assaying cell proliferation include measuring green fluorescent protein (GFP) reporter construct emissions, various enzymatic activity assays, and other methods well known in the art.

It will be appreciated that the above method may be performed in solid phase, liquid phase or a combination of the two. For example, cells grown on nutrient agar containing the inducer of the antisense construct may be exposed to compounds spotted onto the agar surface. If desired, the cells may be grown on agar containing varying concentrations of the inducer. A compound's effect may be judged from the diameter of the resulting killing zone, the area around the compound application point in which cells do not grow. Multiple compounds may be transferred to agar plates and simultaneously tested using automated and semi-automated equipment including but not restricted to multi-channel pipettes (for example the Beckman Multimek) and multi-channel spotters (for example the Genomic Solutions Flexys). In this way multiple plates and thousands to millions of compounds may be tested per day.

The compounds may also be tested entirely in liquid phase using microtiter plates as described below. Liquid phase screening may be performed in microtiter plates containing 96, 384, 1536 or more wells per microtiter plate to screen multiple plates and thousands to millions of compounds per day. Automated and semi-automated equipment may be used for addition of reagents (for example cells and compounds) and determination of cell density.

EXAMPLE 9

Cell-Based Assay Using Antisense Complementary to Genes Encoding Ribosomal Proteins

The effectiveness of the above cell-based assay was validated using constructs transribing antisense RNA to the proliferation required *E. coli* genes *rplL*, *rplJ*, and *rplW* encoding ribosomal proteins L7/L12, L10 and L23 respectively. These proteins are essential components of the protein synthesis apparatus of the cell and as such are required for proliferation. These constructs were used to test the effect of antisense transcription on cell sensitivity to antibiotics known to bind to the ribosome and thereby inhibit protein synthesis. Constructs transcribing antisense RNA to several other genes (*elaD*, *visC*, *yohH*, and *atpE/B*), the products of which are not involved in protein synthesis were used for comparison.

First, pLex5BA (Krause et al., J. Mol. Biol. 274: 365 (1997)) vectors containing antisense constructs to either *rplW* or to *elaD* were introduced into separate *E. coli* cell populations. Vector introduction is a technique well known to those of ordinary skill in the art. The vectors of this example contain IPTG inducible promoters that drive the transcription of the antisense RNA in the presence of the inducer. However, those skilled in the art will appreciate that other inducible promoters may also be used. Suitable vectors are also well known in the art. Antisense clones to genes encoding different ribosomal proteins or to genes encoding proteins that are not involved in protein synthesis were utilized to test the effect of antisense transcription on cell sensitivity to the antibiotics known to bind to ribosomal proteins and inhibit protein synthesis. Antisense nucleic acids comprising a nucleotide sequence complementarty to the *elaD*, *atpB&atpE*, *visC* and *yohH* genes are referred to as AS-*elaD*, AS-*atpB/E*, AS-*visC*, AS-*yohH* respectively. These genes are not known to be involved in protein synthesis. Antisense nucleic acids to the *rplL*, *rplL&rplJ* and *rplW* genes are referred to as AS-*rplL*, AS-*rplL/J*, and AS-*rplW* respectively. These genes encode ribosomal proteins L7/L12 (*rplL*) L10 (*rplJ*) and L23 (*rplW*). Vectors containing these antisense nucleic acids were introduced into separate *E. coli* cell populations.

The cell populations containing vectors producing AS-*elaD* or AS-*rplW* were exposed to a range of IPTG concentrations in liquid medium to obtain the growth inhibitory dose curve for each clone (Fig. 1). First, seed cultures were grown to a particular turbidity measured by the optical density (OD) of the growth solution. The OD of the solution is directly related to the number of bacterial cells contained therein. Subsequently, sixteen 200 μl liquid medium cultures were grown in a 96 well microtiter plate at 37° C with a range of IPTG concentrations in duplicate two-fold

serial dilutions from 1600 uM to 12.5 μM (final concentration). Additionally, control cells were grown in duplicate without IPTG. These cultures were started from an inoculum of equal amounts of cells derived from the same initial seed culture of a clone of interest. The cells were grown for up to 15 hours and the extent of growth was determined by measuring the optical density of the cultures at 600 nm. When the control culture reached mid-log phase the percent growth (relative to the control culture) for each of the IPTG containing cultures was plotted against the log concentrations of IPTG to produce a growth inhibitory dose response curve for the IPTG. The concentration of IPTG that inhibits cell growth to 50% (IC_{50}) as compared to the 0 mM IPTG control (0% growth inhibition) was then calculated from the curve. Under these conditions, an amount of antisense RNA was produced that reduced the expression levels of *rplW* or *elaD* to a degree such that growth of cells containing their respective antisense vectors was inhibited by 50%.

Alternative methods of measuring growth are also contemplated. Examples of these methods include measurements of proteins, the expression of which is engineered into the cells being tested and can readily be measured. Examples of such proteins include green fluorescent protein (GFP), luciferase, and various enzymes.

Cells were pretreated with the selected concentration of IPTG and then used to test the sensitivity of cell populations to tetracycline, erythromycin and other known protein synthesis inhibitors. Figure 1 is an IPTG dose response curve in *E. coli* transformed with an IPTG-inducible plasmid containing either an antisense clone to the *E. coli* *rpl*W gene (AS-*rplW*) which encodes ribosomal protein L23 which is required for protein synthesis and essential for cell proliferation, or an antisense clone to the *elaD* (AS-*elaD*) gene which is not known to be involved in protein synthesis.

An example of a tetracycline dose response curve is shown in Figures 2A and 2B for the *rplW* and *elaD* genes, respectively. Cells were grown to log phase and then diluted into medium alone or medium containing IPTG at concentrations which give 20% and 50% growth inhibition as determined by IPTG dose response curves. After 2.5 hours, the cells were diluted to a final OD_{600} of 0.002 into 96 well plates containing (1) +/- IPTG at the same concentrations used for the 2.5 hour pre-incubation; and (2) serial two-fold dilutions of tetracycline such that the final concentrations of tetracycline range from 1 μg/ml to 15.6 ng/ml and 0 μg/ml. The 96 well plates were incubated at 37°C and the OD_{600} was read by a plate reader every 5 minutes for up to 15 hours. For each IPTG concentration and the no IPTG control, tetracycline dose response curves were determined when the control (absence of tetracycline) reached 0.1 OD_{600}.

To compare tetracycline sensitivity with and without IPTG, tetracycline IC_{50s} were determined from the dose response curves (Figs. 3A-B). Cells transcribing antisense nucleic acids AS-*rplL* or AS-*rplW* to genes encoding ribosomal proteins L7/L12 and L23 respectively showed increased sensitivity to tetracycline (Fig. 2A) as compared to cells with reduced levels of the *elaD*

gene product (AS-*elaD)* (Fig. 2B). Figure 3 shows a summary bar chart in which the ratios of tetracycline IC_{50s} determined in the presence of IPTG which gives 50% growth inhibition versus tetracycline IC_{50s} determined without IPTG (fold increase in tetracycline sensitivity) were plotted. Cells with reduced levels of either L7/L12 (encoded by genes *rplL, rplJ*) or L23 (encoded by the *rplW* gene) showed increased sensitivity to tetracycline (Fig. 3). Cells expressing antisense to genes not known to be involved in protein synthesis (AS-*atpB/E*, AS-*visC*, AS-*elaD*, AS-*yohH*) did not show the same increased sensitivity to tetracycline, validating the specificity of this assay (Fig. 3).

In addition to the above, it has been observed in initial experiments that clones transcribing antisense RNA to genes involved in protein synthesis (including genes encoding ribosomal proteins L7/L12 & L10, L7/L12 alone, L22, and L18, as well as genes encoding rRNA and Elongation Factor G) have increased sensitivity to the macrolide, erythromycin, whereas clones transcribing antisense to the non-protein synthesis genes *elaD*, *atpB/E* and *visC* do not. Furthermore, the clone transcribing antisense to *rplL* and *rplJ* (AS-*rplL/J*) does not show increased sensitivity to nalidixic acid and ofloxacin, antibiotics which do not inhibit protein synthesis.

The results with the ribosomal protein genes *rplL, rplJ*, and *rplW* as well as the initial results using various other antisense clones and antibiotics show that limiting the concentration of an antibiotic target makes cells more sensitive to the antimicrobial agents that specifically interact with that protein. The results also show that these cells are sensitized to antimicrobial agents that inhibit the overall function in which the protein target is involved but are not sensitized to antimicrobial agents that inhibit other functions. It will be appreciated that the cell-based assays described above may be implemented using the *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* antisense nucleotide sequences which inhibit the activity of genes required for proliferation described herein (including the antisense nucleic acids of SEQ ID NOs.: 8-3795) or antisense nucleic acids comprising nucleotide sequences which are complementary to the sequences of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012 or portions thereof.

It will be appreciated that the above cell-based assays may be performed using antisense nucleic acids complementary to any of the proliferation-required nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi*, or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids or portions thereof, or homologous antisense nucleic acids. In this way, the level or activity of a target, such as any of the proliferation-required polypeptides from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa,*

Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, or *Salmonella typhi,* or homologous polypeptides may be reduced.

The cell-based assay described above may also be used to identify the biological pathway in which a proliferation-required nucleic acid or its gene product lies. In such methods, cells transcribing a sub-lethal level of antisense to a target proliferation-required nucleic acid and control cells in which transcription of the antisense has not been induced are contacted with a panel of antibiotics known to act in various pathways. If the antibiotic acts in the pathway in which the target proliferation-required nucleic acid or its gene product lies, cells in which transcription of the antisense has been induced will be more sensitive to the antibiotic than cells in which expression of the antisense has not been induced.

As a control, the results of the assay may be confirmed by contacting a panel of cells transcribing antisense nucleic acids to many different proliferation-required genes including the target proliferation-required gene. If the antibiotic is acting specifically, heightened sensitivity to the antibiotic will be observed only in the cells transcribing antisense to a target proliferation-required gene (or cells expressing antisense to other proliferation-required genes in the same pathway as the target proliferation-required gene) but will not be observed generally in all cells expressing antisense to proliferation-required genes.

It will be appreciated that the above cell-based assays may be performed using antisense nucleic acids complementary to any of the proliferation-required nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* ,(including antisense nucleic acids complementary to SEQ ID NOs: 3796-3800, 3806-4860, 5916-10012, or the antisense nucleic acids of SEQ ID NOs.: 8-3795) or portions thereof, antisense nucleic acids comprising nucleotide sequences complementary to homologous coding nucleic acids or portions thereof, or homologous antisense nucleic acids In this way, the level or activity of a target, such as any of the proliferation-required polypeptides from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* (including the polypeptides of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110), or homologous polypeptides may be reduced.

Similarly, the above method may be used to determine the pathway on which a test compound, such as a test antibiotic acts. A panel of cells, each of which transcribes an antisense to a proliferation-required nucleic acid in a known pathway, is contacted with a compound for which it is desired to determine the pathway on which it acts. The sensitivity of the panel of cells to the test compound is determined in cells in which transcription of the antisense has been induced and in control cells in which expression of the antisense has not been induced. If the test compound acts on the pathway on which an antisense nucleic acid acts, cells in which expression of the antisense

has been induced will be more sensitive to the compound than cells in which expression of the antisense has not been induced. In addition, control cells in which expression of antisense to proliferation-required genes in other pathways has been induced will not exhibit heightened sensitivity to the compound. In this way, the pathway on which the test compound acts may be determined.

It will be appreciated that the above cell-based assays may be performed using antisense nucleic acids comprising nucleotide sequences complementary to any of the proliferation-required nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* (including antisense nucleic acids complementary to SEQ ID NOs: 3796-3800, 3806-4860, 5916-10012, such as the antisense nucleic acids of SEQ ID NOs.: 8-3795) or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids or portions thereof, or homologous antisense nucleic acids In this way, the level or activity of a target, such as any of the proliferation-required polypeptides from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* (including the polypeptides of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110) or homologous polypeptides may be reduced.

The Example below provides one method for performing such assays.

EXAMPLE 10

Identification of the Pathway in which a Proliferation-Required Gene Lies or the Pathway on which an Antibiotic Acts

A. Preparation of Bacterial Stocks for Assay

To provide a consistent source of cells to screen, frozen stocks of host bacteria containing the desired antisense construct are prepared using standard microbiological techniques. For example, a single clone of the microorganism can be isolated by streaking out a sample of the original stock onto an agar plate containing nutrients for cell growth and an antibiotic for which the antisense construct contains a selectable marker which confers resistance. After overnight growth an isolated colony is picked from the plate with a sterile needle and transferred to an appropriate liquid growth medium containing the antibiotic required for maintenance of the plasmid. The cells are incubated at 30°C to 37°C with vigorous shaking for 4 to 6 hours to yield a culture in exponential growth. Sterile glycerol is added to 15% (volume to volume) and 100μL to 500 μL aliquots are distributed into sterile cryotubes, snap frozen in liquid nitrogen, and stored at -80°C for future assays.

B. Growth of Bacteria for Use in the Assay

A day prior to an assay, a stock vial is removed from the freezer, rapidly thawed (37°C water bath) and a loop of culture is streaked out on an agar plate containing nutrients for cell growth and an antibiotic to which the selectable marker of the antisense construct confers resistance. After overnight growth at 37°C, ten randomly chosen, isolated colonies are transferred from the plate (sterile inoculum loop) to a sterile tube containing 5 mL of LB medium containing the antibiotic to which the antisense vector confers resistance. After vigorous mixing to form a homogeneous cell suspension, the optical density of the suspension is measured at 600 nm (OD_{600}) and if necessary an aliquot of the suspension is diluted into a second tube of 5 mL, sterile, LB medium plus antibiotic to achieve an $OD_{600} \leq 0.02$ absorbance units. The culture is then incubated at 37° C for 1-2 hrs with shaking until the OD_{600} reaches OD 0.2 – 0.3. At this point the cells are ready to be used in the assay.

C. Selection of Media to be Used in Assay

Two-fold dilution series of the inducer are generated in culture media containing the appropriate antibiotic for maintenance of the antisense construct. Several media are tested side by side and three to four wells are used to evaluate the effects of the inducer at each concentration in each media. For example, LB broth, TBD broth and Muller-Hinton media may be tested with the inducer xylose at the following concentrations, 5 mM, 10 mM, 20 mM, 40 mM, 80 mM, 120 mM and 160 mM. Equal volumes of test media-inducer and cells are added to the wells of a 384 well microtiter plate and mixed. The cells are prepared as described above and diluted 1:100 in the appropriate media containing the test antibiotic immediately prior to addition to the microtiter plate wells. For a control, cells are also added to several wells of each media that do not contain inducer, for example 0 mM xylose. Cell growth is monitored continuously by incubation at 37°C in a microtiter plate reader monitoring the OD_{600} of the wells over an 18-hour period. The percent inhibition of growth produced by each concentration of inducer is calculated by comparing the rates of logarithmic growth against that exhibited by cells growing in medium without inducer. The medium yielding greatest sensitivity to inducer is selected for use in the assays described below.

D. Measurement of Test Antibiotic Sensitivity in the Absence of Antisense Construct Induction

Two-fold dilution series of antibiotics of known mechanism of action are generated in the culture medium selected for further assay development that has been supplemented with the antibiotic used to maintain the construct. A panel of test antibiotics known to act on different pathways is tested side by side with three to four wells being used to evaluate the effect of a test antibiotic on cell growth at each concentration. Equal volumes of test antibiotic and cells are added to the wells of a 384 well microtiter plate and mixed. Cells are prepared as described above using the medium selected for assay development supplemented with the antibiotic required to maintain the antisense construct and are diluted 1:100 in identical medium immediately prior to addition to the microtiter plate wells. For a control, cells are also added to several wells that lack antibiotic,

but contain the solvent used to dissolve the antibiotics. Cell growth is monitored continuously by incubation at 37°C in a microtiter plate reader monitoring the OD_{600} of the wells over an 18-hour period. The percent inhibition of growth produced by each concentration of antibiotic is calculated by comparing the rates of logarithmic growth against that exhibited by cells growing in medium without antibiotic. A plot of percent inhibition against log[antibiotic concentration] allows extrapolation of an IC_{50} value for each antibiotic.

E. Measurement of Test Antibiotic Sensitivity in the Presence of Antisense Construct Inducer

The culture medium selected for use in the assay is supplemented with inducer at concentrations shown to inhibit cell growth by 50% and 80% as described above, as well as the antibiotic used to maintain the construct. Two-fold dilution series of the panel of test antibiotics used above are generated in each of these media. Several antibiotics are tested side by side in each medium with three to four wells being used to evaluate the effects of an antibiotic on cell growth at each concentration. Equal volumes of test antibiotic and cells are added to the wells of a 384 well microtiter plate and mixed. Cells are prepared as described above using the medium selected for use in the assay supplemented with the antibiotic required to maintain the antisense construct. The cells are diluted 1:100 into two 50 mL aliquots of identical medium containing concentrations of inducer that have been shown to inhibit cell growth by 50% and 80 % respectively and incubated at 37°C with shaking for 2.5 hours. Immediately prior to addition to the microtiter plate wells, the cultures are adjusted to an appropriate OD_{600} (typically 0.002) by dilution into warm (37°C) sterile medium supplemented with identical concentrations of the inducer and antibiotic used to maintain the antisense construct. For a control, cells are also added to several wells that contain solvent used to dissolve test antibiotics but which contain no antibiotic. Cell growth is monitored continuously by incubation at 37°C in a microtiter plate reader monitoring the OD_{600} of the wells over an 18-hour period. The percent inhibition of growth produced by each concentration of antibiotic is calculated by comparing the rates of logarithmic growth against that exhibited by cells growing in medium without antibiotic. A plot of percent inhibition against log[antibiotic concentration] allows extrapolation of an IC_{50} value for each antibiotic.

F. Determining the Specificity of the Test Antibiotics

A comparison of the IC_{50}s generated by antibiotics of known mechanism of action under antisense induced and non-induced conditions allows the pathway in which a proliferation-required nucleic acid lies to be identified. If cells expressing an antisense nucleic acid comprising a nucleotide sequence complementary to a proliferation-required gene are selectively sensitive to an antibiotic acting via a particular pathway, then the gene against which the antisense acts is involved in the pathway on which the antibiotic acts.

G. Identification of Pathway in which a Test Antibiotic Acts

As discussed above, the cell-based assay may also be used to determine the pathway against which a test antibiotic acts. In such an analysis, the pathways against which each member of a panel of antisense nucleic acids acts are identified as described above. A panel of cells, each containing an inducible vector which transcribes an antisense nucleic acid comprising a nucleotide sequence complementary to a gene in a known proliferation-required pathway, is contacted with a test antibiotic for which it is desired to determine the pathway on which it acts under inducing and non-inducing conditions. If heightened sensitivity is observed in induced cells transcribing antisense complementary to a gene in a particular pathway but not in induced cells transcribing antisense nucleic acids comprising nucleotide sequences complementary to genes in other pathways, then the test antibiotic acts against the pathway for which heightened sensitivity was observed.

One skilled in the art will appreciate that further optimization of the assay conditions, such as the concentration of inducer used to induce antisense transcription and/or the growth conditions used for the assay (for example incubation temperature and medium components) may further increase the selectivity and/or magnitude of the antibiotic sensitization exhibited.

It will be appreciated that the above cell-based assays may be performed using antisense nucleic acids comprising nucleotide sequences complementary to any of the proliferation-required nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi*, (including antisense nucleic acids comprising nucleotide sequences complemenatary to SEQ ID NOs: 3796-3800, 3806-4860, 5916-10012, such as the antisense nucleic acids of SEQ ID NOs.: 8-3795) or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids or portions thereof, or homologous antisense nucleic acids In this way, the level or activity of a target, such as any of the proliferation-required polypeptides from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* (including the polypeptides of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110), or homologous polypeptides may be reduced.

The following example confirms the effectiveness of the methods described above.

EXAMPLE 11

Identification of the Biological Pathway in which a Proliferation-Required Gene Lies

The effectiveness of the above assays was validated using proliferation-required genes from *E. coli* which were identified using procedures similar to those described above. Antibiotics of various chemical classes and modes of action were purchased from Sigma Chemicals (St. Louis, MO). Stock solutions were prepared by dissolving each antibiotic in an appropriate aqueous solution based on information provided by the manufacturer. The final working solution of each

antibiotic contained no more than 0.2% (w/v) of any organic solvent. To determine their potency against a bacterial strain engineered for transcription of an antisense comprising a nucleotide sequence complementary to a proliferation-required 50S ribosomal protein, each antibiotic was serially diluted two- or three- fold in growth medium supplemented with the appropriate antibiotic for maintenance of the antisense construct. At least ten dilutions were prepared for each antibiotic. 25 μL aliquots of each dilution were transferred to discrete wells of a 384-well microplate (the assay plate) using a multi-channel pipette. Quadruplicate wells were used for each dilution of an antibiotic under each treatment condition (plus and minus inducer). Each assay plate contained twenty wells for cell growth controls (growth medium replacing antibiotic), ten wells for each treatment (plus and minus inducer, in this example IPTG). Assay plates were usually divided into the two treatments: half the plate containing induced cells and an appropriate concentrations of inducer (in this example IPTG) to maintain the state of induction, the other half containing non-induced cells in the absence of IPTG.

Cells for the assay were prepared as follows. Bacterial cells containing a construct, from which transcription of antisense nucleic acid comprising a nucleotide sequence complementary to *rplL* and *rplJ* (AS-*rplL/J*), which encode proliferation-required 50S ribosomal subunit proteins, is inducible in the presence of IPTG, were grown into exponential growth (OD_{600} 0.2 to 0.3) and then diluted 1:100 into fresh medium containing either 400 μM or 0 μM inducer (IPTG). These cultures were incubated at 37° C for 2.5 hr. After a 2.5 hr incubation, induced and non-induced cells were respectively diluted into an assay medium at a final OD_{600} value of 0.0004. The medium contained an appropriate concentration of the antibiotic for the maintenance of the antisense construct. In addition, the medium used to dilute induced cells was supplemented with 800 μM IPTG so that addition to the assay plate would result in a final IPTG concentration of 400 μM. Induced and non-induced cell suspensions were dispensed (25 μl/well) into the appropriate wells of the assay plate as discussed previously. The plate was then loaded into a plate reader, incubated at constant temperature, and cell growth was monitored in each well by the measurement of light scattering at 595 nm. Growth was monitored every 5 minutes until the cell culture attained a stationary growth phase. For each concentration of antibiotic, a percentage inhibition of growth was calculated at the time point corresponding to mid-exponential growth for the associated control wells (no antibiotic, plus or minus IPTG). For each antibiotic and condition (plus or minus IPTG), a plot of percent inhibition versus log of antibiotic concentration was generated and the IC_{50} determined. A comparison of the IC_{50} for each antibiotic in the presence and absence of IPTG revealed whether induction of the antisense construct sensitized the cell to the mechanism of action exhibited by the antibiotic. Cells which exhibited a statistically significant decrease in the IC_{50} value in the presence of inducer were considered to have an increased sensitivity to the test antibiotic.

The results are provided in the table below, which lists the classes and names of the antibiotics used in the analysis, the targets of the antibiotics, the IC_{50} in the absence of IPTG, the IC_{50} in the presence of IPTG, the concentration units for the IC_{50s}, the fold increase in IC_{50} in the presence of IPTG, and whether increased sensitivity was observed in the presence of IPTG.

TABLE III

Effect of Expression of Antisense RNA to *rplL* and *rplJ* on Antibiotic Sensitivity

ANTIBIOTIC CLASS /Names	TARGET	IC_{50} (-IPTG)	IC_{50} (+IPTG)	Conc. Unit	Fold Increase in Sensitivity	Sensitivity Increased?
PROTEIN SYNTHESIS INHIBITOR						
AMINOGLYCOSIDES						
Gentamicin	30S ribosome function	2715	19.19	ng/ml	141	Yes
Streptomycin	30S ribosome function	11280	161	ng/ml	70	Yes
Spectinomycin	30S ribosome function	18050	<156	ng/ml		Yes
Tobramycin	30S ribosome function	3594	70.58	ng/ml	51	Yes
MACROLIDES						
Erythromycin	50S ribosome function	7467	187	ng/ml	40	Yes
AROMATIC POYKETIDES						
Tetracycline	30S ribosome function	199.7	1.83	ng/ml	109	Yes
Minocycline	30S ribosome function	668.4	3.897	ng/ml	172	Yes
Doxycycline	30S ribosome function	413.1	27.81	ng/ml	15	Yes
OTHER PROTEIN SYNTHESIS INHIBITORS						
Fusidic acid	Elongation Factor G function	59990	641	ng/ml	94	Yes
Chloramphenicol	30S ribosome function	465.4	1.516	ng/ml	307	Yes
Lincomycin	50S ribosome function	47150	324.2	ng/ml	145	Yes
OTHER ANTIBIOTIC MECHANISMS						
B-LACTAMS						
Cefoxitin	Cell wall biosynthesis	2782	2484	ng/ml	1	No
Cefotaxime	Cell wall biosynthesis	24.3	24.16	ng/ml	1	No
DNA SYNTHESIS INHIBITORS						
Nalidixic acid	DNA Gyrase activity	6973	6025	ng/ml	1	No
Ofloxacin	DNA Gyrase activity	49.61	45.89	ng/ml	1	No
OTHER						
Bacitracin	Cell membrane function	4077	4677	mg/ml	1	No
Trimethoprim	Dihydrofolate Reductase activity	128.9	181.97	ng/ml	1	No
Vancomycin	Cell wall biosynthesis	145400	72550	ng/ml	2	No

The above results demonstrate that induction of an antisense RNA complementary to genes encoding 50S ribosomal subunit proteins results in a selective and highly significant sensitization of cells to antibiotics that inhibit ribosomal function and protein synthesis. The above results further demonstrate that induction of an antisense to an essential gene sensitizes a cell or microorganism to compounds that interfere with that gene product's biological role. This sensitization is restricted to compounds that interfere with pathways associated with the targeted gene and its product.

It will be appreciated that the above cell-based assays may be performed using antisense nucleic acids complementary to any of the proliferation-required nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* (including antisense nucleic acids complementary to SEQ ID NOs. 3796-3800, 3806-4860, 5916-10012, such as the antisense nucleic acids of SEQ ID NOs.: 8-3795) or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids or portions thereof or homologous antisense nucleic acids. In this way, the level or activity of a target, such as any of the proliferation-required polypeptides from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi i* (including the polypeptides of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110), or homologous polypeptides may be reduced.

Example 11A below describes an analysis performed in *Staphylococcus aureus.*

EXAMPLE 11A

Identification of the Biological Pathway in which a Gene Required for Proliferation of *Staphylococcus aureus* Lies

Antibiotics of various chemical classes and modes of action were purchased from chemical suppliers, for example Sigma Chemicals (St. Louis, MO). Stock solutions were prepared by dissolving each antibiotic in an appropriate aqueous solution based on information provided by the manufacturer. The final working solution of each antibiotic contained no more than 0.2% (w/v) of any organic solvent.

To determine its potency against a bacterial strain containing an antisense nucleic acid comprising a nucleotide sequence complementary to the nucleotide sequence encoding the Beta subunit of DNA gyrase (which is required for proliferation) under the control of a xylose inducible promoter, each antibiotic was serially diluted two- or three- fold in growth medium supplemented with the appropriate antibiotic for maintenance of the antisense construct. At least ten dilutions were prepared for each antibiotic.

Aliquots (25 μL) of each dilution were transferred to discrete wells of a 384-well microplate (the assay plate) using a multi-channel pipette. Quadruplicate wells were used for each dilution of an antibiotic under each treatment condition (plus and minus inducer). Each assay plate

contained twenty wells for cell growth controls (growth medium, no antibiotic), ten wells for each treatment (plus and minus inducer, xylose, in this example). Half the assay plate contained induced cells (in this example *Staphylococcus aureus* cells) and appropriate concentrations of inducer (xylose, in this example) to maintain the state of induction while the other half of the assay plate contained non-induced cells maintained in the absence of inducer.

Preparation of Bacterial Cells

Cells of a bacterial clone containing a construct in which transcription of antisense comprising a nucleotide sequence complementary to the sequence encoding the Beta subunit of DNA gyrase under the control of the xylose inducible promoter (S1M10000001F08) were grown into exponential growth (OD_{600} 0.2 to 0.3) and then diluted 1:100 into fresh medium containing either 12 mM or 0 mM inducer (xylose). These cultures were incubated at 37° C for 2.5 hr. The presence of inducer (xylose) in the medium initiates and maintains production of antisense RNA from the antisense construct. After a 2.5 hr incubation, induced and non-induced cells were respectively diluted into an assay medium containing an appropriate concentration of the antibiotic for the maintenance of the antisense construct. In addition, medium used to dilute induced cells was supplemented with 24 mM xylose so that addition to the assay plate would result in a final xylose concentration of 12 mM. The cells were diluted to a final OD_{600} value of 0.0004.

Induced and non-induced cell suspensions were dispensed (25 µl/well) into the appropriate wells of the assay plate as discussed previously. The plate was then loaded into a plate reader and incubated at constant temperature while cell growth was monitored in each well by the measurement of light scattering at 595 nm. Growth was monitored every 5 minutes until the cell culture attained a stationary growth phase. For each concentration of antibiotic, a percentage inhibition of growth was calculated at the time point corresponding to mid-exponential growth for the associated control wells (no antibiotic, plus or minus xylose). For each antibiotic and condition (plus or minus xylose), plots of percent inhibition versus Log of antibiotic concentration were generated and IC_{50s} determined.

A comparison of each antibiotic's IC_{50} in the presence and absence of inducer (xylose, in this example) reveals whether induction of the antisense construct sensitized the cell to the antibiotic's mechanism of action. If the antibiotic acts against the β subunit of DNA gyrase, the IC_{50} of induced cells will be significantly lower than the IC_{50} of uninduced cells.

Figure 4 lists the antibiotics tested, their targets, and their fold increase in potency between induced cells and uninduced cells. As illustrated in Figure 4, the potency of cefotaxime, cefoxitin, fusidic acid, lincomycin, tobramycin, trimethoprim and vancomycin, each of which act on targets other than the β subunit of gyrase, was not significantly different in induced cells as compared to uninduced cells. However, the potency of novobiocin, which is known to act against the Beta subunit of DNA gyrase, was significantly different between induced cells and uninduced cells.

Thus, induction of an antisense nucleic acid comprising a nucleotide sequence complementary to the sequence encoding the β subunit of gyrase results in a selective and significant sensitization of *Staphylococcus aureus* cells to an antibiotic which inhibits the activity of this protein. Furthermore, the results demonstrate that induction of an antisense construct to an essential gene sensitizes a cell or microorganism to compounds that interfere with that gene product's biological role. This sensitization is apparently restricted to compounds that interfere with the targeted gene and its product.

It will be appreciated that the above cell-based assays may be performed using antisense nucleic acids complementary to any of the proliferation-required nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* (including antisense nucleic acids complementary to SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, such as the antisense nucleic acids of SEQ ID NOs. 8-3795), or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids or portions thereof, or homologous antisense nucleic acids. In this way, the level or activity of a target, such as any of the proliferation-required polypeptides from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa,Enterococcus faecalis Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi,* or homologous polypeptides may be reduced.

Assays utilizing antisense constructs to essential genes or portions thereof can be used to identify compounds that interfere with the activity of those gene products. Such assays could be used to identify drug leads, for example antibiotics.

Panels of cells transcribing different antisense nucleic acids can be used to characterize the point of intervention of a compound affecting an essential biochemical pathway including antibiotics with no known mechanism of action.

Assays utilizing antisense constructs to essential genes can be used to identify compounds that specifically interfere with the activity of multiple targets in a pathway. Such constructs can be used to simultaneously screen a sample against multiple targets in one pathway in one reaction (Combinatorial HTS).

Furthermore, as discussed above, panels of antisense construct-containing cells may be used to characterize the point of intervention of any compound affecting an essential biological pathway including antibiotics with no known mechanism of action.

It will be appreciated that the above cell-based assays may be performed using antisense nucleic acids complementary to any of the proliferation-required nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* (including antisense nucleic acids comprising nucleotide sequences

complementary to SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, such as the antisense nucleic acids of SEQ ID NOs. 8-3795), or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids or portions thereof, or homologous antisense nucleic acids. In this way, the level or activity of a target, such as any of the proliferation-required polypeptides from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* or homologous polypeptides may be reduced.

Another embodiment of the present invention is a method for determining the pathway against which a test antibiotic compound is active, in which the activity of target proteins or nucleic acids involved in proliferation-required pathways is reduced by contacting cells with a sub-lethal concentration of a known antibiotic which acts against the target protein or nucleic acid. In one embodiment, the target protein or nucleic acid corresponds to a proliferation-required nucleic acid identified using the methods described above, such as the polypeptides of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110, or homologous polypeptides. The method is similar to those described above for determining which pathway a test antibiotic acts against, except that rather than reducing the activity or level of a proliferation-required gene product using a sub-lethal level of antisense to a proliferation-required nucleic acid, the sensitized cell is generated by reducing the activity or level of the proliferation-required gene product using a sub-lethal level of a known antibiotic which acts against the proliferation required gene product. Heightened sensitivity determines the pathway on which the test compound is active.

Interactions between drugs which affect the same biological pathway have been described in the literature. For example, Mecillinam (Amdinocillin) binds to and inactivates the penicillin binding protein 2 (PBP2, product of the *mrdA* in *E. coli*). This antibiotic interacts with other antibiotics that inhibit PBP2 as well as antibiotics that inhibit other penicillin binding proteins such as PBP3 [(Gutmann, L., Vincent, S., Billot-Klein, D., Acar, J.F., Mrena, E., and Williamson, R. (1986) Involvement of penicillin-binding protein 2 with other penicillin-binding proteins in lysis of *Escherichia coli* by some beta-lactam antibiotics alone and in synergistic lytic effect of amdinocillin (mecillinam). Antimicrobial Agents & Chemotherapy, 30:906-912)]. Interactions between drugs could, therefore, involve two drugs that inhibit the same target protein or nucleic acid or inhibit different proteins or nucleic acids in the same pathway [(Fukuoka, T., Domon, H., Kakuta, M., Ishii, C., Hirasawa, A., Utsui, Y., Ohya, S., and Yasuda, H. (1997) Combination effect between panipenem and vancomycin on highly methicillin-resistant *Staphylococcus aureus*. Japan. J. Antibio. 50:411-419; Smith, C.E., Foleno, B.E., Barrett, J.F., and Frosc, M.B. (1997) Assessment of the synergistic interactions of levofloxacin and ampicillin against *Enterococcus faecium* by the checkerboard agar dilution and time-kill methods. Diagnos. Microbiol. Infect. Disease 27:85-92; den Hollander, J.G., Horrevorts, A.M., van Goor, M.L., Verbrugh, H.A., and Mouton, J.W. (1997)

Synergism between tobramycin and ceftazidime against a resistant *Pseudomonas aeruginosa* strain, tested in an in vitro pharmacokinetic model. Antimicrobial Agents & Chemotherapy. 41:95-110)].

Two drugs may interact even though they inhibit different targets. For example, the proton pump inhibitor, Omeprazole, and the antibiotic, Amoxycillin, two synergistic compounds acting together, can cure *Helicobacter pylori* infection [(Gabryelewicz, A., Laszewicz, W., Dzieniszewski, J., Ciok, J., Marlicz, K., Bielecki, D., Popiela, T., Legutko, J., Knapik, Z., Poniewierka, E. (1997) Multicenter evaluation of dual-therapy (omeprazol and amoxycillin) for *Helicobacter pylori*-associated duodenal and gastric ulcer (two years of the observation). J. Physiol. Pharmacol. 48 Suppl 4:93-105)].

The growth inhibition from the sub-lethal concentration of the known antibiotic may be at least about 5%, at least about 8%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, or at least about 75%, or more.

Alternatively, the sub-lethal concentration of the known antibiotic may be determined by measuring the activity of the target proliferation-required gene product rather than by measuring growth inhibition.

Cells are contacted with a combination of each member of a panel of known antibiotics at a sub-lethal level and varying concentrations of the test antibiotic. As a control, the cells are contacted with varying concentrations of the test antibiotic alone. The IC_{50} of the test antibiotic in the presence and absence of the known antibiotic is determined. If the IC_{50}s in the presence and absence of the known drug are substantially similar, then the test drug and the known drug act on different pathways. If the IC_{50}s are substantially different, then the test drug and the known drug act on the same pathway.

It will be appreciated that the above cell-based assays may be performed using a sub-lethal concentration of a known antibiotic which acts against the product of any of the proliferation-required nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* (including the products of SEQ ID NOs: 3796-3800, 3806-4860, 5916-10012, or portions thereof, or the products of homologous coding nucleic acids or portions thereof. In this way, the level or activity of a target, such as any of the proliferation-required polypeptides from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* (including the polypeptides of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110), or homologous polypeptides may be reduced.

Another embodiment of the present invention is a method for identifying a candidate compound for use as an antibiotic in which the activity of target proteins or nucleic acids involved in proliferation-required pathways is reduced by contacting cells with a sub-lethal concentration of

a known antibiotic which acts against the target protein or nucleic acid. In one embodiment, the target protein or nucleic acid is a target protein or nucleic acid corresponding to a proliferation-required nucleic acid identified using the methods described above. The method is similar to those described previously herein for identifying candidate compounds for use as antibiotics except that rather than reducing the activity or level of a proliferation-required gene product using a sub-lethal level of antisense to a proliferation-required nucleic acid, the activity or level of the proliferation-required gene product is reduced using a sub-lethal level of a known antibiotic which acts against the proliferation required gene product.

The growth inhibition from the sub-lethal concentration of the known antibiotic may be at least about 5%, at least about 8%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, or at least about 75%, or more.

Alternatively, the sub-lethal concentration of the known antibiotic may be determined by measuring the activity of the target proliferation-required gene product rather than by measuring growth inhibition.

In order to characterize test compounds of interest, cells are contacted with a panel of known antibiotics at a sub-lethal level and one or more concentrations of the test compound. As a control, the cells are contacted with the same concentrations of the test compound alone. The IC_{50} of the test compound in the presence and absence of the known antibiotic is determined. If the IC_{50} of the test compound is substantially different in the presence and absence of the known drug then the test compound is a good candidate for use as an antibiotic. As discussed above, once a candidate compound is identified using the above methods its structure may be optimized using standard techniques such as combinatorial chemistry.

Representative known antibiotics which may be used in each of the above methods are provided in Table IV below. However, it will be appreciated that other antibiotics may also be used.

TABLE IV

Antibiotics and Their Targets

ANTIBIOTIC	INHIBITS/TARGET	RESISTANT MUTANTS
Inhibitors of Transcription		
Rifamycin, Rifampicin Rifabutin Rifaximin	Inhibits initiation of transcription/ß-subunit RNA polymerase, *rpoB*	*rpoB, crp, cyaA*
Streptolydigin	Accelerates transcription chain termination/ß-subunit RNA polymerase	*rpoB*
Streptovaricin	an acyclic ansamycin, inhibits RNA polymerase	*rpoB*
Actinomycin D+EDTA	Intercalates between 2 successive G-C pairs, *rpoB*, inhibits RNA synthesis	*pldA*

ANTIBIOTIC	INHIBITS/TARGET	RESISTANT MUTANTS
Inhibitors of Nucleic Acid Metabolism		
Quinolones, Nalidixic acid Oxolinic acid	subunit gyrase and/or topoisomerase IV, *gyrA*	*gyrAorB, icd, sloB*
Fluoroquinolones Ciprofloxacin, Norfloxacin	subunit gyrase,*gyrA* and/or topoisomerase IV (probable target in Staph)	*gyrA* *norA* (efflux in Staph) *hipQ*
Coumerins Novobiocin	Inhibits ATPase activity of ß-subunit gyrase, *gyrB*	*gyrB, cysB, cysE, nov, ompA*
Coumermycin	Inhibits ATPase activity of ß-subunit gyrase, *gyrB*	*gyrB, hisW*
Albicidin	DNA synthesis	*tsx* (nucleoside channel)
Metronidazole	Causes single-strand breaks in DNA	*nar*
Inhibitors of Metabolic Pathways		
Sulfonamides, Sulfanilamide	blocks synthesis of dihydrofolate,dihydro-pteroate synthesis,*folP*	*folP, gpt, pabA, pabB, pabC*
Trimethoprim,	Inhibits dihydrofolate reductase,*folA*	*folA, thyA*
Showdomycin	Nucleoside analogue capable of alkylating sulfhydryl groups, inhibitor of thymidylate synthetase	*nupC, pnp*
Thiolactomycin	type II fatty acid synthase inhibitor	*emrB* *fadB, emrB* due to gene dosage
Psicofuranine	Adenosine glycoside antibiotic, target is GMP synthetase	*guaA,B*
Triclosan	Inhibits fatty acid synthesis	*fabI (envM)*
Diazoborines Isoniazid, Ethionamide	heterocyclic, contain boron, inhibit fatty acid synthesis, enoyl-ACP reductase, *fabI*	*fabI (envM)*
Inhibitors of Translation		
Phenylpropanoids Chloramphenicol,	Binds to ribosomal peptidyl transfer center preventing peptide translocation/ binds to S6, L3, L6, L14, L16, L25, L26, L27, but preferentially to L16	*rrn, cmlA, marA, ompF, ompR*
Tetracyclines, type II polyketides Minocycline Doxycycline	Binding to 30S ribosomal subunit, "A" si on 30S subunit, blocks peptide elongation, strongest binding to S7	*clmA (cmr), mar, ompF*
Macrolides (type I polyketides) Erythromycin, Carbomycin,	Binding to 50 S ribosomal subunit, 23S rRNA, blocks peptide translocation, L15, L4, L12	*rrn, rplC, rplD, rplV, mac*
Spiramycin etc		

ANTIBIOTIC	INHIBITS/TARGET	RESISTANT MUTANTS
Aminoglycosides	Irreversible binding to 30S ribosomal	
Streptomycin,	subunit, prevents translation or causes mistranslation of mRNA/16S rRNA	*rpsL, strC,M, ubiF*
Neomycin		*atpA-E, ecfB, hemAC,D,E,G, topA,*
Spectinomycin		*rpsC,D,E, rrn, spcB*
Kanamycin		*atpA-atpE, cpxA, ecfB, hemA,B,L, topA*
Kasugamycin		*ksgA,B,C,D, rplB,K, rpsI,N,M,R*
Gentamicin, Amikacin		*rplF, ubiF* *cpxA*
Paromycin		*rpsL*
Lincosamides	Binding to 50 S ribosomal subunit,	
Lincomycin, Clindamycin	blocks peptide translocation	*linB, rplN,O, rpsG*
Streptogramins Virginiamycin, Pristinamycin Synercid: quinupristin /dalfopristin	2 components, Streptogramins A&B, bind to the 50S ribosomal subunit blocking peptide translocation and peptide bond formation	
Fusidanes Fusidic Acid	Inhibition of elongation factor G (EF-G) prevents peptide translocation	*fusA*
Kirromycin (Mocimycin)	Inhibition of elongation factor TU (EF-Tu), prevents peptide bond formation	*tufA,B*
Pulvomycin	Binds to and inhibits EF-TU	
Thiopeptin	Sulfur-containing antibiotic, inhibits protein synthesis,EF-G	*rplE*
Tiamulin	Inhibits protein synthesis	*rplC, rplD*
Negamycin	Inhibits termination process of protein synthesis	*prfB*
Oxazolidinones Linezolid	23S rRNA	
Isoniazid		*pdx*
Nitrofurantoin	Inhibits protein synthesis, nitroreductases convert nitrofurantoin to highly reactive electrophilic intermediates which attack bacterial ribosomal proteins non-specifically	*nfnA,B*
Pseudomonic Acids Mupirocin (Bactroban)	Inhibition of isoleucyl tRNA synthetase-used for Staph, topical cream, nasal spray	*ileS*
Indolmycin	Inhibits tryptophanyl-tRNA synthetase	*trpS*
Viomycin		*rrmA* (23S rRNA methyltransferase; mutant has slow growth rate, slow chain elongation rate, and viomycin resistance)

ANTIBIOTIC	INHIBITS/TARGET	RESISTANT MUTANTS
Thiopeptides	Binds to L11-23S RNA complex	
Thiostrepton	Inhibits GTP hydrolysis by EF-G	
Micrococcin	Stimulates GTP hydrolysis by EF-G	
Inhibitors of Cell Walls/Membranes		
ß-lactams Penicillin, Ampicillin Methicillin,	Inhibition of one or more cell wall transpeptidases, endopeptidases, and glycosidases (PBPs), of the 12 PBPs only 2 are essential: *mrdA* (PBP2) and *ftsI* (*pbpB*, PBP3)	*ampC, ampD, ampE, envZ, galU, hipA, hipQ, ompC, ompF, ompR, ptsI, rfa, tolD, tolE*
Cephalosporins,		*tonB*
Mecillinam (amdinocillin)	Binds to and inactivates PBP2 (*mrdA*)	*alaS, argS, crp, cyaA, envB, mrdA,B, mreB,C,D*
Aztreonam (Furazlocillin)	Inactivates PBP3 (*ftsI*)	
Bacilysin, Tetaine	Dipeptide, inhib glucosamine synthase	*dppA*
Glycopeptides Vancomycin,	Inhib G+ cell wall syn, binds to terminal D-ala-D-ala of pentapeptide,	
Polypeptides Bacitracin	Prevents dephosphorylation and regeneration of lipid carrier	*rfa*
Cyclic lipopeptide Daptomycin,	Disrupts multiple aspects of membrane function, including peptidoglycan synthesis, lipoteichoic acid synthesis, and the bacterial membrane potential	
Cyclic polypeptides Polymixin,	Surfactant action disrupts cell membrane lipids, binds lipid A mioety of LPS	*pmrA*
Fosfomycin,	Analogue of P-enolpyruvate, inhibits 1st step in peptidoglycan synthesis - UDP-N-acetylglucosamine enolpyruvyl transferase, *murA*. Also acts as Immunosuppressant	*murA, crp, cyaA glpT, hipA, ptsI, uhpT*
Cycloserine	Prevents formation of D-ala dimer, inhibits D-ala ligase, *ddlA,B*	*hipA, cycA*
Alafosfalin	phosphonodipeptide, cell wall synthesis inhibitor, potentiator of ß-lactams	*pepA, tpp*
Inhibitors of Protein Processing/Transport		
Globomycin	Inhibits signal peptidase II (cleaves prolipoproteins subsequent to lipid modification, *lspA*	*lpp, dnaE*

It will be appreciated that the above cell-based assays may be performed using a sub-lethal concentration of a known antibiotic which acts against the product of any of the proliferation-required nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi*, or portions thereof, or homologous nucleic acids. In this way, the level or activity of a target, such as any of the proliferation-required polypeptides from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi*, or homologous polypeptides may be reduced.

EXAMPLE 12

Transfer of Exogenous Nucleic Acid Sequences to other Bacterial Species

The ability of an antisense molecule identified in a first organism to inhibit the proliferation of a second organism (thereby confirming that a gene in the second organism which is homologous to the gene from the first organism is required for proliferation of the second organism) was validated using antisense nucleic acids which inhibit the growth of *E. coli* which were identified using methods similar to those described above. Expression vectors which inhibited growth of *E. coli* upon induction of antisense RNA expression with IPTG were transformed directly into *Enterobacter cloacae, Klebsiella pneumonia* or *Salmonella typhimurium*. The transformed cells were then assayed for growth inhibition according to the method of Example 1. After growth in liquid culture, cells were plated at various serial dilutions and a score determined by calculating the log difference in growth for INDUCED vs. UNINDUCED antisense RNA expression as determined by the maximum 10 fold dilution at which a colony was observed. The results of these experiments are listed below in Table V. If there was no effect of antisense RNA expression in a microorganism, the clone is minus in Table V. In contrast, a positive in Table V means that at least 10 fold more cells were required to observe a colony on the induced plate than on the non-induced plate under the conditions used and in that microorganism.

TABLE V

Sensitivity of Other Microorganisms to Antisense Nucleic Acids That Inhibit Proliferation in *E. coli*

Mol. No.	*S. typhimurium*	*E. cloacae*	*K. pneumoniae*
EcXA001	+	+	-
EcXA004	+	-	-
EcXA005	+	+	+
EcXA006	-	-	-
EcXA007	-	+	-
EcXA008	+	-	+
EcXA009	-	-	-
EcXA010	+	+	+
EcXA011	-	+	-

Mol. No.	*S. typhimurium*	*E. cloacae*	*K. pneumoniae*
EcXA012	-	+	-
EcXA013	+	+	+
EcXA014	+	+	-
EcXA015	+	+	+
EcXA016	+	+	+
EcXA017	+	+	+
EcXA018	+	+	+
EcXA019	+	+	+
EcXA020	+	+	+
EcXA021	+	+	+
EcXA023	+	+	+
EcXA024	+	-	+
EcXA025	-	-	-
EcXA026	+	+	-
EcXA027	+	+	-
EcXA028	+	-	-
EcXA029	-	-	-
EcXA030	+	+	+
EcXA031	+	-	-
EcXA032	+	+	-
EcXA033	+	+	+
EcXA034	+	+	+
EcXA035	-	-	-
EcXA036	+	-	+
EcXA037	+	+	-
EcXA038	+	+	+
EcXA039	+	-	-
EcXA041	+	+	+
EcXA042	-	+	+
EcXA043	-	-	-
EcXA044	-	-	-
EcXA045	+	+	+
EcXA046	-	-	-
EcXA047	+	+	-
EcXA048	-	-	-
EcXA049	+	-	-
EcXA050	-	-	-
EcXA051	+	-	-
EcXA052	+	-	-
EcXA053	+	+	+
EcXA054	-	-	+
EcXA055	+	-	-
EcXA056	+	-	+
EcXA057	+	+	-
EcXA058	-	-	-
EcXA059	+	+	+
EcXA060	-	-	-
EcXA061	-	-	-
EcXA062	-	-	-
EcXA063	+	+	-
EcXA064	-	-	-
EcXA065	+	+	-
EcXA066	-	-	-
EcXA067	-	+	-

Mol. No.	*S. typhimurium*	*E. cloacae*	*K. pneumoniae*
EcXA068	-	-	-
EcXA069	-	+	-
EcXA070	-	-	-
EcXA071	+	-	-
EcXA072	+	-	+
EcXA073	+	+	+
EcXA074	+	+	+
EcXA075	+	-	-
EcXA076	-	+	-
EcXA077	+	+	-
EcXA079	+	+	+
EcXA080	+	-	-
EcXA082	-	+	-
EcXA083	-	-	-
EcXA084	-	+	-
EcXA086	-	-	-
EcXA087	-	-	-
EcXA088	-	-	-
EcXA089	-	-	-
EcXA090	-	-	-
EcXA091	-	-	-
EcXA092	-	-	-
EcXA093	-	-	-
EcXA094	+	+	+
EcXA095	+	+	-
EcXA096	-	-	-
EcXA097	+	-	-
EcXA098	+	-	-
EcXA099	-	-	-
EcXA100	-	-	-
EcXA101	-	-	-
EcXA102	-	-	-
EcXA103	-	+	-
EcXA104	+	+	+
EcXA106	+	+	-
EcXA107	-	-	-
EcXA108	-	-	-
EcXA109	-	-	-
EcXA110	+	+	-
EcXA111	-	-	-
EcXA112	-	+	-
EcXA113	+	+	+
EcXA114	-	+	-
EcXA115	-	+	-
EcXA116	+	+	-
EcXA117	+	-	-
EcXA118	-	-	-
EcXA119	+	+	-
EcXA120	-	-	-
EcXA121	-	-	-
EcXA122	+	-	+
EcXA123	+	-	-
EcXA124	-	-	-
EcXA125	-	-	-

Mol. No.	*S. typhimurium*	*E. cloacae*	*K. pneumoniae*
EcXA126	-	-	-
EcXA127	+	+	-
EcXA128	-	-	-
EcXA129	-	+	-
EcXA130	+	+	-
EcXA132	-	-	-
EcXA133	-	-	-
EcXA136	-	-	-
EcXA137	-	-	-
EcXA138	+	-	-
EcXA139	-	-	-
EcXA140	+	-	-
EcXA141	+	-	-
EcXA142	-	-	-
EcXA143	-	+	-
EcXA144	+	+	-
EcXA145	-	-	-
EcXA146	-	-	-
EcXA147	-	-	-
EcXA148	-	-	-
EcXA149	+	+	+
EcXA150	-	-	-
EcXA151	+	-	-
EcXA152	-	-	-
EcXA153	+	+	-
EcXA154	-	-	-
EcXA155	-	-	ND
EcXA156	-	+	-
EcXA157	-	-	-
EcXA158	-	-	-
EcXA159	+	-	-
EcXA160	+	-	-
EcXA162	-	-	-
EcXA163	-	-	-
EcXA164	-	-	-
EcXA165	-	-	-
EcXA166	-	-	-
EcXA167	-	-	-
EcXA168	-	-	-
EcXA169	-	+	-
EcXA171	-	-	-
EcXA172	-	-	-
EcXA173	-	-	-
EcXA174	-	-	-
EcXA175	-	-	-
EcXA176	-	-	-
EcXA178	-	-	-
EcXA179	-	-	-
EcXA180	+	-	-
EcXA181	-	-	-
EcXA182	-	-	-
EcXA183	-	-	-
EcXA184	-	-	-
EcXA185	-	-	-

Mol. No.	*S. typhimurium*	*E. cloacae*	*K. pneumoniae*
EcXA186	-	-	-
EcXA187	+	+	+
EcXA189	+	-	-
EcXA190	+	+	+
EcXA191	+	+	-
EcXA192	-	+	-

Thus, the ability of an antisense nucleic acid which inhibits the proliferation of *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* to inhibit the growth of other organims may be evaluated by transforming the antisense nucleic acid directly into species other than the organism from which they were obtained. In particular, the ability of the antisense nucleic acid to inhibit the growth of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* or any species falling within the genera of any of the above species. may be evaluated. In some embodiments of the present invention, the ability of the antisense nucleic acid to inhibit the growth of an organism other than *E. coli* may be evaluated. In such embodiments, the antisense nucleic acids are inserted into expression vectors functional in the organisms in which the antisense nucleic acids are evaluated.

It will be appreciated that the above methods for evaluating the ability of an antisense nucleic acid to inhibit the proliferation of a heterologous organism may be performed using antisense nucleic acids complementary to any of the proliferation-required nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae,*

Helicobacter pylori, or *Salmonella typhi* (including antisense nucleic acids complementary to SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, such as the antisense nucleic acids of SEQ ID NOs.: 8-3795) or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids or portions thereof, or homologous antisense nucleic acids.

Those skilled in the art will appreciate that a negative result in a heterologous cell or microorganism does not mean that that cell or microorganism is missing that gene nor does it mean that the gene is unessential. However, a positive result means that the heterologous cell or microorganism contains a homologous gene which is required for proliferation of that cell or microorganism. The homologous gene may be obtained using the methods described herein. Those cells that are inhibited by antisense may be used in cell-based assays as described herein for the identification and characterization of compounds in order to develop antibiotics effective in these cells or microorganisms. Those skilled in the art will appreciate that an antisense molecule which works in the microorganism from which it was obtained will not always work in a heterologous cell or microorganism.

EXAMPLE 12A

Transfer of Exogenous Nucleic Acid Sequences to other Bacterial Species Using the *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori*, or *Salmonella typhi* Expression Vectors or Expression Vectors Functional in Bacterial Species other than *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori*, or *Salmonella typhi*.

The antisense nucleic acids that inhibit the growth of *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori*, or *Salmonella typhi*, or portions thereof, may also be evaluated for their ability to inhibit the growth of cells or microorganisms other than *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori*, or *Salmonella typhi*. For example, the antisense nucleic acids that inhibit the growth of *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori*, or *Salmonella typhi* may be evaluated for their ability to inhibit the growth of other organisms. In particular, the ability of the antisense nucleic acid to inhibit the growth of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr*

(also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis or any species falling within the genera of any of the above species may be evaluated. In some embodiments of the present invention, the ability of the antisense nucleic acid to inhibit the growth of an organism other than *E. coli* may be evaluated.

In such methods, expression vectors in which the expression of an antisense nucleic acid that inhibits the growth of *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* is under the control of an inducible promoter are introduced into the cells or microorganisms in which they are to be evaluated. In some embodiments, the antisense nucleic acids may be evaluated in cells or microorganisms which are closely related to *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli; Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typh*. The ability of these antisense nucleic acids to inhibit the growth of the related cells or microorganisms in the presence of the inducer is then measured.

For example, thirty-nine antisense nucleic acids which inhibited the growth of *Staphylococcus aureus* were identified using methods such as those described herein and were inserted into an expression vector such that their expression was under the control of a xylose-inducible Xyl-T5 promoter. A vector with Green Fluorescent Protein (GFP) under control of the Xyl-T5 promoter was used to show that expression from the Xyl-T5 promoter in *Staphylococcus epidermidis* was comparable to that in *Staphylococcus aureus*.

The vectors were introduced into *Staphylococcus epidermidis* by electroporation as follows: *Staphylococcus epidermidis* was grown in liquid culture to mid-log phase and then harvested by centrifugation. The cell pellet was resuspended in 1/3 culture volume of ice-cold EP buffer (0.625 M sucrose, 1 mM $MgCl_2$, pH=4.0), and then harvested again by centrifugation. The cell pellet was then resuspended with 1/40 volume EP buffer and allowed to incubate on ice for 1 hour. The cells

were then frozen for storage at -80°C. For electroporation, 50 μl of thawed electrocompetent cells were combined with 0.5 μg plasmid DNA and then subjected to an electrical pulse of 10 kV/cm, 25 uFarads, 200 ohm using a biorad gene pulser electroporation device. The cells were immediately resuspended with 200 μl outgrowth medium and incubated for 2 hours prior to plating on solid growth medium with drug selection to maintain the plasmid vector. Colonies resulting from overnight growth of these platings were selected, cultured in liquid medium with drug selection, and then subjected to dilution plating analysis as described for *Staphylococcus aureus* in Example 10 above to test growth sensitivity in the presence of the inducer xylose.

The results are shown in Table VI below. The first column indicates the Molecule Number of the *Staphylococcus aureus* antisense nucleic acid which was introduced into *Staphylococcus epidermidis*. The second column indicates whether the antisense nucleic acid inhibited the growth of *Staphylococcus epidermidis*, with a "+" indicating that growth was inhibited. Of the 39 *Staphylococcus aureus* antisense nucleic acids evaluated, 20 inhibited the growth of *Staphylococcus epidermidis*.

TABLE VI
Sensitivity of Other Microorganisms to Antisense Nucleic Acids That Inhibit Proliferation of *Staphylococcus aureus*

Mol. No.	*S. epidermidis*
SaXA005	+
SaXA007	+
SaXA008	+
SaXA009	+
SaXA010	+
SaXA011	-
SaXA012	-
SaXA013	-
SaXA015	+
SaXA017	-
SaXA022	+
SaXA023	-
SaXA024	-
SaXA025	+
SaXA026	+
SaXA027	-
SaXA027b	-

SaXA02c	-
SaXA028	-
SaXA029	+
SaXA030	+
SaXA032	+
SaXA033	+
SaXA034	-
SaXA035	+
SaXA037	+
SaXA039	-
SaXA042	-
SaXA043	-
SaXA044	-
SaXA045	+
SaXA051	+
SaXA053	-
SaXA056b	-
SaXA059a	+
SaXA060	-
SaXA061	+
SaXA062	+
SaXA063	-
SaXA065	-

Although the results shown above were obtained using a subset of the nucleic acids of the present invention, it will be appreciated that similar analyses may be performed using the other nucleic acids of the present invention to determine whether they inhibit the proliferation of cells or microorganisms other than *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi*.

Thus, it will be appreciated that the above methods for evaluating the ability of an antisense nucleic acid to inhibit the proliferation of a heterologous organism may be performed using antisense nucleic acids complementary to any of the proliferation-required nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae,*

Helicobacter pylori, or *Salmonella typhi*, (including antisense nucleic acids complementary to SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, such as the antisense nucleic acids of SEQ ID NOs.: 8-3795) or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids or portions thereof, or homologous antisense nucleic acids.

EXAMPLE 12C

As a demonstration of the methodology required to find homologues to an essential gene, nine prokaryotic organisms were analyzed and compared in detail. First, the most reliable source of gene sequences for each organism was assessed by conducting a survey of the public and private data sources. The nine organisms studied are *Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus, Streptococcus pneumoniae* and *Salmonella typhi.* Full-length gene protein and nucleotide sequences for these organisms were assembled from various sources. For *Escherichia coli, Haemophilus influenzae* and *Helicobacter pylori,* gene sequences were adopted from the public sequencing projects, and derived from the GenPept 115 database (available from NCBI). For *Pseudomonas aeruginosa,* gene sequences were adopted from the Pseudomonas genome sequencing project (downloaded from http://www.pseudomonas.com). For *Klebsiella pneumoniae, Staphylococcus aureus, Streptococcus pneumoniae* and *Salmonella typhi,* genomic sequences from PathoSeq v 4.1 (Mar 2000 release) was reanalyzed for ORFs using the gene finding software GeneMark v 2.4a, which was purchased from GenePro Inc. 451 Bishop St., N.W., Suite B, Atlanta, GA, 30318, USA.

Subsequently, the essential genes found by the antisense methodology were compared to the derived proteomes of interest, in order to find all the homologous genes to a given gene. This comparison was done using the FASTA program v3.3. Genes were considered homologues if they were greater than 25% identical and the alignment between the two genes covered more than 70% of the length of one of the genes. The best homologue for each of the nine organisms, defined as the most significantly scoring match which also fulfilled the above criteria, was reported in Table VIIA. Table VIIA lists the best ORF identified as described above (column labelled LOCUSID), the SEQ ID, % identity, and the amount of the protein which aligns well with the query sequence (coverage) for the gene identified in each of the nine organisms evaluated as described above.

Table VIIB lists the PathoSeq cluster ID for genes identified as being required for proliferation in *Enterococcus faecalis, Escherichia coli, Pseudomonas aeruginosa,* and *Staphylococcus aureus* using the methods described herein. As indicated in the column labelled PathoSeq cluster ID, these sequences share homology to one another and were consequently grouped within the same PathoSeq cluster. Thus, the methods described herein identified genes required for proliferation in several species which share homology.

TABLE VIIA

LOCUSID	*Data*	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
EFA100001	SeqID	10430	10618	10998	11603	11739		12309	13524	14040
	IDENTITY	27%	100%	28%	28%	29%		52%	55%	28%
	COVERAGE	99%	100%	101%	79%	77%		98%	98%	98%
EFA100023	SeqID		10505					12860	13392	
	IDENTITY		100%					27%	39%	
	COVERAGE		100%					95%	101%	
EFA100065	SeqID	10322	10813	11177	11351		12018	12820	13186	13733
	IDENTITY	49%	100%	49%	44%		48%	59%	65%	48%
	COVERAGE	96%	100%	95%	96%		97%	97%	98%	96%
EFA100151	SeqID	10128	10516	11247	11340		11891	12529	13362	
	IDENTITY	50%	100%	37%	46%		49%	54%	51%	
	COVERAGE	99%	100%	100%	100%		100%	99%	100%	
EFA100157	SeqID		10673		11448			12352	13176	
	IDENTITY		100%		39%			64%	74%	
	COVERAGE		100%		98%			98%	99%	
EFA100165	SeqID	10031	10637	11189	11564		12009	12614	13399	14078
	IDENTITY	31%	100%	33%	28%		32%	29%	27%	29%
	COVERAGE	97%	100%	98%	100%		96%	90%	96%	97%
EFA100190	SeqID	10364	10480	11061	11408	11659	11996	12444	13232	13966
	IDENTITY	54%	100%	57%	55%	55%	54%	78%	80%	54%
	COVERAGE	100%	101%	100%	99%	90%	100%	101%	101%	101%
EFA100194	SeqID	10336	10540	11120	11426		11989	12230	13222	14096
	IDENTITY	60%	100%	62%	62%		60%	85%	86%	61%
	COVERAGE	100%	101%	100%	102%		100%	101%	92%	101%
EFA100200	SeqID	10323	10798	11193			12020	12527	13561	13731
	IDENTITY	39%	100%	38%			40%	50%	59%	39%
	COVERAGE	85%	100%	87%			85%	85%	88%	85%
EFA100210	SeqID	10352	10560	11104	11439		5171	12260	13204	13968
	IDENTITY	53%	100%	53%	53%		54%	74%	93%	53%
	COVERAGE	95%	101%	95%	94%		95%	101%	94%	95%
EFA100211	SeqID	10351	10523	11105	11438		11992	12214	13205	
	IDENTITY	46%	100%	46%	39%		43%	69%	63%	
	COVERAGE	87%	101%	87%	81%		87%	97%	81%	

TABLE VIIA

LOCUSID	*Data*	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
EFA100289	SeqID	10284	10810				11827		13245	
	IDENTITY	30%	100%				31%		25%	
	COVERAGE	85%	100%				90%		84%	
EFA100295	SeqID	10045	10517	11174	11601		11937	12390	13616	13911
	IDENTITY	43%	100%	41%	41%		45%	44%	45%	43%
	COVERAGE	92%	101%	95%	97%		97%	99%	94%	72%
EFA100312	SeqID		10641					12178		
	IDENTITY		100%					33%		
	COVERAGE		100%					88%		
EFA100329	SeqID		10782							
	IDENTITY		100%							
	COVERAGE		100%							
EFA100394	SeqID	10465	10675	11238	11563		11961	13003	13684	13853
	IDENTITY	43%	100%	43%	42%		44%	66%	72%	44%
	COVERAGE	108%	100%	109%	101%		108%	99%	100%	108%
EFA100397	SeqID	10027	10773	11185			12012	12396	13478	14074
	IDENTITY	31%	100%	29%			29%	43%	46%	31%
	COVERAGE	96%	100%	98%			93%	91%	97%	93%
EFA100399	SeqID	10295	10766	11196	11483		11791	12281	13413	13739
	IDENTITY	63%	100%	59%	59%		58%	72%	76%	63%
	COVERAGE	98%	100%	98%	99%		101%	99%	100%	98%
EFA100426	SeqID	10224	10702			11638		12139	13348	13957
	IDENTITY	28%	100%			29%		42%	41%	28%
	COVERAGE	99%	101%			99%		91%	109%	99%
EFA100478	SeqID		10486	11135	11338			12986	13184	
	IDENTITY		100%	29%	31%			44%	43%	
	COVERAGE		100%	72%	70%			99%	98%	
EFA100615	SeqID		10501	11139			12028	12641	13331	
	IDENTITY		100%	44%			47%	61%	78%	
	COVERAGE		100%	82%			81%	100%	100%	
EFA100617	SeqID	10314	10764	11216	11391		5198	12322	13381	13765
	IDENTITY	43%	100%	43%	44%		51%	63%	69%	44%
	COVERAGE	95%	100%	96%	78%		73%	84%	82%	93%
EFA100641	SeqID	10205	10793				11896	12862	13334	
	IDENTITY	28%	100%				31%	50%	32%	
	COVERAGE	79%	100%				74%	85%	82%	

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
EFA100642	SeqID		10792		11520		12023	12493	13367	
	IDENTITY		100%		46%		46%	73%	69%	
	COVERAGE		100%		100%		101%	100%	100%	
EFA100668	SeqID	10026	10679	11184	11613		12013	12891	13505	14073
	IDENTITY	28%	100%	28%	29%		28%	29%	50%	27%
	COVERAGE	83%	100%	76%	78%		92%	82%	99%	95%
EFA100689	SeqID		10717					12523	13698	
	IDENTITY		100%					33%	33%	
	COVERAGE		100%					100%	100%	
EFA100704	SeqID	10362	10482	11059	11415		11995	12442	13171	13964
	IDENTITY	78%	100%	78%	77%		75%	90%	78%	77%
	COVERAGE	100%	100%	100%	101%		101%	100%	101%	100%
EFA100739	SeqID	10111	10537	11052	11429	11651	11876	12228	13220	14010
	IDENTITY	71%	100%	69%	63%	70%	71%	84%	84%	70%
	COVERAGE	83%	101%	83%	86%	87%	83%	87%	87%	87%
EFA100740	SeqID	10075	10536	11008	11348	11633	11942	12227	13219	13717
	IDENTITY	45%	100%	47%	30%	45%	48%	64%	60%	44%
	COVERAGE	94%	100%	94%	93%	94%	82%	94%	93%	94%
EFA100741	SeqID	10339	10535	11118	11430		11991	12226	13218	14098
	IDENTITY	40%	100%	37%	34%		39%	48%	60%	40%
	COVERAGE	103%	100%	102%	101%		102%	101%	100%	103%
EFA100742	SeqID	10340	10534	11116	11431		5160	12225	13217	14099
	IDENTITY	52%	100%	52%	39%		46%	79%	88%	52%
	COVERAGE	99%	101%	99%	92%		99%	101%	101%	99%
EFA100748	SeqID	10287	10483	11004	11523	11690	11944	12595		13868
	IDENTITY	41%	100%	39%	29%	42%	44%	52%		41%
	COVERAGE	99%	100%	99%	94%	98%	100%	100%		100%
EFA100756	SeqID	10112	10575		11396		11875	12327	13343	14009
	IDENTITY	49%	100%		43%		45%	64%	62%	47%
	COVERAGE	75%	102%		75%		81%	94%	94%	75%
EFA100757	SeqID	10155	10897							
	IDENTITY	27%	100%							
	COVERAGE	85%	100%							
EFA100783	SeqID	10035	10811	10986	11543		11953	12738	13261	13914
	IDENTITY	32%	100%	34%	86%		37%	77%	75%	31%
	COVERAGE	104%	100%	83%	100%		78%	100%	99%	99%

TABLE VIIA

LOCUSID	Data	Escherichia coli	Enterococcus faecalis	Haemophilus influenzae	Helicobacter pylori	Klebsiella pneumoniae	Pseudomonas aeruginosa	Staphylococcus aureus	Streptococcus pneumoniae	Salmonella typhi
EFA100795	SeqID		10863						13416	
	IDENTITY		100%						50%	
	COVERAGE		101%						101%	
EFA100798	SeqID	10382	10818	11153	11550		11775		13641	
	IDENTITY	62%	100%	61%	56%		63%		85%	
	COVERAGE	95%	100%	95%	89%		92%		96%	
EFA100811	SeqID		10546					12236	13439	
	IDENTITY		100%					48%	58%	
	COVERAGE		101%					98%	99%	
EFA100870	SeqID	10439	10627	11036	11410		5179	12446	13646	14042
	IDENTITY	47%	100%	46%	52%		46%	72%	78%	46%
	COVERAGE	114%	100%	117%	79%		116%	99%	98%	114%
EFA100914	SeqID	10399	10579	11018	11617	11758	12111	12368	13230	14065
	IDENTITY	40%	100%	40%	34%	40%	40%	59%	63%	40%
	COVERAGE	102%	100%	102%	101%	102%	102%	101%	95%	102%
EFA100919	SeqID	10269	10491	11127	11419		11809	12556	13594	13874
	IDENTITY	44%	100%	45%	40%		46%	55%	63%	45%
	COVERAGE	101%	100%	101%	99%		101%	101%	100%	101%
EFA100955	SeqID	10333	10542	11123	11582	11627	5158	12232	13224	14093
	IDENTITY	48%	100%	48%	42%	49%	43%	65%	76%	48%
	COVERAGE	98%	101%	98%	98%	79%	98%	99%	101%	98%
EFA100970	SeqID		10906							
	IDENTITY		100%							
	COVERAGE		100%							
EFA100978	SeqID	10334	10541	11122	11583		11987	12231	13223	14094
	IDENTITY	46%	100%	46%	35%		45%	71%	70%	46%
	COVERAGE	100%	100%	99%	98%		102%	101%	100%	100%
EFA100991	SeqID	10221	10681	11210	11607	11668	11801	12289	13191	14027
	IDENTITY	42%	100%	40%	29%	42%	39%	49%	56%	30%
	COVERAGE	91%	100%	93%	98%	94%	91%	93%	92%	93%
EFA101022	SeqID	10260	10875	10982	11401		11945	12715	13251	14086
	IDENTITY	59%	100%	58%	50%		61%	76%	86%	56%
	COVERAGE	85%	101%	85%	88%		85%	85%	89%	89%
EFA101060	SeqID		10722		11575	11646	11957	12504	13554	
	IDENTITY		100%		35%	37%	34%	71%	67%	
	COVERAGE		101%		83%	77%	97%	100%	101%	

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
EFA101086	SeqID	10315	10763	11215	11454	11716	12052	12953	13662	13764
	IDENTITY	37%	100%	37%	27%	38%	35%	57%	55%	36%
	COVERAGE	91%	100%	89%	98%	91%	92%	98%	95%	93%
EFA101120	SeqID	10017	10687	11219	11331		12057	12505	13498	14012
	IDENTITY	30%	100%	31%	27%		29%	26%	64%	29%
	COVERAGE	102%	100%	102%	74%		103%	99%	98%	103%
EFA101121	SeqID		10686					12606	13600	
	IDENTITY		100%					38%	50%	
	COVERAGE		100%					98%	99%	
EFA101123	SeqID	10420	10748	11131	11478	11629	11820	12674	13265	13783
	IDENTITY	43%	100%	39%	33%	43%	40%	70%	70%	42%
	COVERAGE	98%	100%	97%	97%	94%	96%	99%	100%	98%
EFA101141	SeqID	10436	10614	11071	11573		5181	12450	13246	14045
	IDENTITY	35%	100%	40%	35%		40%	60%	70%	31%
	COVERAGE	94%	101%	96%	95%		95%	98%	101%	96%
EFA101150	SeqID	10174	10719	11221	11556		11880	12985	13385	13943
	IDENTITY	35%	100%	36%	26%		33%	45%	58%	36%
	COVERAGE	100%	100%	100%	102%		100%	100%	100%	73%
EFA101159	SeqID	10359	10543	11097	11442		5176	12235	13197	13974
	IDENTITY	55%	100%	52%	48%		49%	58%	89%	53%
	COVERAGE	100%	101%	100%	81%		101%	99%	99%	100%
EFA101160	SeqID	10358	10549	11098	11595		5175	12240	13198	13973
	IDENTITY	43%	100%	43%	33%		45%	62%	74%	43%
	COVERAGE	92%	100%	92%	96%		92%	100%	100%	93%
EFA101161	SeqID	10357	10551	11099			11994	12242	13199	13972
	IDENTITY	39%	100%	35%			37%	69%	66%	36%
	COVERAGE	86%	101%	99%			96%	93%	103%	100%
EFA101162	SeqID	10356	10555	11100	11441	11679	11993	12249	13200	13971
	IDENTITY	58%	100%	58%	59%	59%	57%	78%	84%	58%
	COVERAGE	100%	100%	100%	100%	100%	99%	100%	100%	100%
EFA101163	SeqID	10355	10557	11101	11594		5174	12255	13201	
	IDENTITY	66%	100%	68%	60%		70%	84%	90%	
	COVERAGE	100%	101%	99%	97%		100%	101%	100%	
EFA101164	SeqID	10354	10558	11102	11593		5173	12258	13202	13970
	IDENTITY	55%	100%	58%	47%		57%	66%	81%	55%
	COVERAGE	91%	101%	91%	91%		85%	91%	97%	91%

TABLE VIIA

LOCUSID	*Data*	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
EFA101165	SeqID	10353	10559	11103	11592		5172	12259	13203	13969
	IDENTITY	59%	100%	60%	52%		61%	78%	88%	59%
	COVERAGE	95%	100%	95%	99%		95%	100%	100%	95%
EFA101169	SeqID	10133	10574	11091			12025	12516		13849
	IDENTITY	27%	100%	28%			26%	41%		27%
	COVERAGE	93%	100%	97%			94%	100%		93%
EFA101253	SeqID	10389	10852	11065	11551		11838	13072	13457	
	IDENTITY	43%	100%	42%	31%		39%	54%	67%	
	COVERAGE	97%	100%	97%	96%		99%	97%	99%	
EFA101257	SeqID	10124	10917	10976	11484		11914	12528	13357	14037
	IDENTITY	40%	100%	39%	39%		37%	39%	58%	38%
	COVERAGE	99%	100%	99%	101%		97%	97%	100%	101%
EFA101258	SeqID	10127	10918	10973	11513		11892	12802	13358	13871
	IDENTITY	40%	100%	40%	39%		36%	41%	66%	29%
	COVERAGE	97%	101%	96%	95%		96%	92%	95%	92%
EFA101322	SeqID		10620					12534	13328	
	IDENTITY		100%					66%	65%	
	COVERAGE		100%					86%	86%	
EFA101339	SeqID		10743		11448			12326	13391	
	IDENTITY		100%		33%			46%	60%	
	COVERAGE		100%		97%			98%	98%	
EFA101340	SeqID		10745							
	IDENTITY		100%							
	COVERAGE		102%							
EFA101354	SeqID	10047	10648	11089	11608		11935	12617	13345	13913
	IDENTITY	33%	100%	33%	32%		34%	38%	36%	32%
	COVERAGE	101%	100%	104%	101%		104%	97%	100%	101%
EFA101370	SeqID		10738					13126		
	IDENTITY		100%					31%		
	COVERAGE		101%					98%		
EFA101403	SeqID		10662					12941		
	IDENTITY		100%					34%		
	COVERAGE		100%					100%		
EFA101404	SeqID	10210	10663	11214	11554		11921	12135	13418	13925
	IDENTITY	29%	100%	28%	39%		27%	59%	64%	30%
	COVERAGE	99%	100%	102%	98%		100%	99%	99%	99%

TABLE VIIA

LOCUSID	*Data*	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
EFA101409	SeqID IDENTITY COVERAGE	10350 54% 83%	10524 100% 101%	11106 58% 80%	11437 44% 86%		5170 53% 91%	12215 81% 91%	13207 87% 91%	
EFA101410	SeqID IDENTITY COVERAGE	10349 62% 101%	10525 100% 101%	11107 64% 101%	11436 63% 100%		5169 66% 100%	12216 90% 101%	13208 90% 101%	14108 62% 102%
EFA101411	SeqID IDENTITY COVERAGE	10348 50% 97%	10526 100% 101%	11108 43% 97%			5168 49% 93%	12217 66% 96%	13209 71% 99%	14107 46% 97%
EFA101412	SeqID IDENTITY COVERAGE	10347 60% 100%	10527 100% 101%	11109 59% 100%	11589 52% 98%	11654 61% 101%	5167 58% 99%	12218 85% 92%	13210 83% 100%	14106 60% 101%
EFA101414	SeqID IDENTITY COVERAGE	10345 49% 99%	10528 100% 101%	11111 47% 99%	11435 42% 99%		5165 46% 100%	12219 79% 101%	13212 81% 101%	14104 49% 101%
EFA101415	SeqID IDENTITY COVERAGE	10344 47% 98%	10529 100% 101%	11112 50% 98%	11434 39% 100%		5164 49% 98%	12220 63% 101%	13213 74% 101%	14103 47% 98%
EFA101416	SeqID IDENTITY COVERAGE	10343 50% 97%	10530 100% 101%	11113 48% 97%	11433 42% 91%		5163 52% 94%	12221 68% 99%	13214 82% 101%	14102 51% 98%
EFA101417	SeqID IDENTITY COVERAGE	10342 55% 100%	10531 100% 101%	11114 56% 95%	11432 61% 84%		5162 52% 92%	12222 72% 95%	13215 85% 94%	14101 55% 100%
EFA101424	SeqID IDENTITY COVERAGE	10220 44% 99%	10784 100% 101%	11276 38% 97%		11765 34% 73%	11950 36% 78%	12350 65% 101%	13280 79% 99%	13934 41% 99%
EFA101425	SeqID IDENTITY COVERAGE	10240 49% 99%	10785 100% 100%	11275 50% 99%			11925 39% 99%	12351 63% 100%	13281 78% 100%	13863 47% 84%
EFA101477	SeqID IDENTITY COVERAGE	10263 52% 91%	10861 100% 100%	10965 50% 95%	11562 41% 91%		11948 49% 95%	13066 59% 94%	13525 72% 91%	14089 50% 91%
EFA101536	SeqID IDENTITY COVERAGE	10281 30% 86%	10823 100% 100%							

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
EFA101540	SeqID	10041	10487	11149	11456		11941	12314	13438	13907
	IDENTITY	51%	100%	50%	50%		49%	73%	76%	51%
	COVERAGE	92%	100%	90%	86%		92%	92%	99%	92%
EFA101541	SeqID	10042	10488	11150	11620		11940	12742	13437	13908
	IDENTITY	41%	100%	45%	35%		44%	63%	44%	41%
	COVERAGE	100%	100%	98%	121%		101%	100%	116%	100%
EFA101583	SeqID		10593							
	IDENTITY		100%							
	COVERAGE		100%							
EFA101670	SeqID		10511							
	IDENTITY		100%							
	COVERAGE		100%							
EFA101682	SeqID	10238	10789	11178	11517		11829	12811	13673	13864
	IDENTITY	45%	100%	45%	40%		44%	57%	57%	45%
	COVERAGE	97%	100%	98%	95%		91%	96%	95%	97%
EFA101685	SeqID		10791		11369		12022	12492	13368	
	IDENTITY		100%		47%		51%	62%	69%	
	COVERAGE		100%		92%		98%	97%	99%	
EFA101686	SeqID	10237	10940	10999	11325		11901	12456	13455	13956
	IDENTITY	39%	100%	37%	37%		36%	64%	63%	38%
	COVERAGE	99%	100%	99%	99%		99%	99%	99%	99%
EFA101695	SeqID	10204	10629	11017	11479	11715	12106	12560	13284	13928
	IDENTITY	34%	100%	32%	34%	31%	35%	51%	75%	34%
	COVERAGE	104%	100%	106%	76%	93%	101%	100%	99%	105%
EFA101736	SeqID	10219	10775	11024			11924	12300	13340	13976
	IDENTITY	33%	100%	29%			27%	35%	32%	28%
	COVERAGE	100%	100%	100%			99%	98%	99%	100%
EFA101737	SeqID	10218	10778	11023			11923	12301	13341	13774
	IDENTITY	39%	100%	37%			42%	43%	43%	58%
	COVERAGE	98%	100%	98%			98%	100%	103%	96%
EFA101753	SeqID	10134	10552	11211			11895	12151	13693	13826
	IDENTITY	36%	100%	37%			36%	50%	50%	37%
	COVERAGE	91%	100%	89%			90%	94%	99%	91%
EFA101765	SeqID		10587					13010	13353	
	IDENTITY		100%					28%	35%	
	COVERAGE		100%					98%	97%	

TABLE VIIA

LOCUSID	*Data*	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
EFA101790	SeqID	10414	10803	11085			11915	12306		13747
	IDENTITY	42%	100%	41%			39%	46%		41%
	COVERAGE	101%	100%	101%			101%	101%		101%
EFA101791	SeqID		10804					12359		
	IDENTITY		100%					37%		
	COVERAGE		101%					77%		
EFA101792	SeqID	10030	10805	11188	11458		5187	12360	13333	14077
	IDENTITY	31%	100%	32%	27%		33%	34%	47%	31%
	COVERAGE	98%	100%	96%	98%		99%	101%	100%	98%
EFA101795	SeqID	10329	10922	11159	11322		12062	12581	13363	13886
	IDENTITY	34%	100%	36%	36%		37%	36%	47%	32%
	COVERAGE	98%	101%	98%	99%		98%	98%	99%	97%
EFA101797	SeqID	10330	10924	11160	11321		12063	13127	13364	13885
	IDENTITY	53%	100%	52%	49%		55%	59%	74%	53%
	COVERAGE	98%	100%	98%	98%		98%	98%	99%	98%
EFA101799	SeqID	10048	10926	11014	11339		11934	12908	13366	13897
	IDENTITY	53%	100%	55%	49%		55%	54%	66%	54%
	COVERAGE	97%	100%	97%	94%		97%	97%	97%	97%
EFA101833	SeqID	10429	10720		11335		12039	12340	13451	14072
	IDENTITY	31%	100%		36%		35%	51%	59%	31%
	COVERAGE	79%	100%		92%		89%	92%	91%	79%
EFA101868	SeqID		10829							
	IDENTITY		100%							
	COVERAGE		100%							
EFA101872	SeqID	10305	10815	11044	11343	11639	11797	12568	13288	13779
	IDENTITY	62%	100%	62%	38%	61%	60%	93%	92%	62%
	COVERAGE	86%	102%	86%	86%	79%	95%	97%	102%	86%
EFA101873	SeqID		10816				11796			
	IDENTITY		100%				36%			
	COVERAGE		101%				94%			
EFA101892	SeqID	10454	10506	11048	11281		12005	12142	13190	14021
	IDENTITY	47%	100%	47%	41%		53%	49%	46%	47%
	COVERAGE	100%	101%	100%	97%		100%	101%	100%	100%
EFA101924	SeqID		10891		11532			12331	13463	
	IDENTITY		100%		36%			65%	65%	
	COVERAGE		100%		101%			100%	94%	

TABLE VIIA

LOCUSID	*Data*	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
EFA101925	SeqID		10893					12332		
	IDENTITY		100%					59%		
	COVERAGE		100%					99%		
EFA101963	SeqID	10034	10848	11148	11536		12006	12552	13648	13901
	IDENTITY	48%	100%	47%	49%		47%	57%	69%	48%
	COVERAGE	105%	100%	105%	99%		108%	101%	100%	105%
EFA102006	SeqID		10580				11830	12804	13315	
	IDENTITY		100%				33%	42%	43%	
	COVERAGE		100%				84%	99%	95%	
EFA102022	SeqID	10313	10881	11224	11502	11754	12051	12324	13485	13767
	IDENTITY	53%	100%	53%	51%	54%	55%	78%	78%	52%
	COVERAGE	88%	101%	88%	87%	89%	88%	89%	89%	89%
EFA102023	SeqID	10312	10882	10989	11576	11755	12050	12325	13699	13768
	IDENTITY	51%	100%	50%	38%	50%	50%	63%	70%	50%
	COVERAGE	98%	100%	99%	99%	84%	97%	99%	99%	97%
EFA102091	SeqID	10363	10481	11060	11568		11858	12443	13233	13965
	IDENTITY	60%	100%	61%	63%		62%	75%	86%	59%
	COVERAGE	101%	100%	101%	100%		101%	100%	100%	101%
EFA102110	SeqID	10193	10841	11255			12082		13430	13752
	IDENTITY	32%	100%	34%			34%		62%	32%
	COVERAGE	103%	100%	94%			100%		100%	99%
EFA102183	SeqID	10393	10952	11057	11330		11774	12695	13420	13920
	IDENTITY	55%	100%	54%	50%		54%	67%	78%	55%
	COVERAGE	84%	100%	86%	85%		86%	98%	100%	84%
EFA102185	SeqID	10458	10950	11051	11421	11632	12075	12413	13501	13858
	IDENTITY	27%	100%	29%	29%	28%	29%	63%	73%	27%
	COVERAGE	93%	101%	90%	94%	93%	91%	91%	96%	93%
EFA102186	SeqID	10448	10949	10995	11579			12412	13543	13817
	IDENTITY	29%	100%	29%	27%			53%	60%	30%
	COVERAGE	92%	101%	90%	94%			101%	92%	90%
EFA102205	SeqID	10108	10769	10985	11375				13375	13997
	IDENTITY	46%	100%	38%	56%				55%	37%
	COVERAGE	71%	102%	82%	73%				96%	104%
EFA102253	SeqID	10275	10727	11175	11320		11933	12372	13376	13865
	IDENTITY	53%	100%	55%	48%		53%	67%	80%	54%
	COVERAGE	100%	100%	101%	101%		101%	100%	99%	96%

TABLE VIIA

LOCUSID	*Data*	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
EFA102282	SeqID		10729					12607	13424	
	IDENTITY		100%					40%	46%	
	COVERAGE		101%					81%	76%	
EFA102338	SeqID	10250	10651	11012	11488		11954	12940	13272	13705
	IDENTITY	39%	100%	38%	35%		39%	42%	50%	38%
	COVERAGE	95%	100%	92%	86%		98%	99%	99%	99%
EFA102350	SeqID		10632							
	IDENTITY		100%							
	COVERAGE		101%							
EFA102351	SeqID		10634					12795	13406	
	IDENTITY		100%					33%	38%	
	COVERAGE		100%					97%	101%	
EFA102352	SeqID	10028	10635	11186	11328	11691	12011	12347	13409	14075
	IDENTITY	40%	100%	39%	35%	40%	39%	51%	55%	40%
	COVERAGE	101%	100%	101%	101%	101%	101%	99%	100%	101%
EFA102353	SeqID	10029	10636	11187	11329		12010	12348	13398	14076
	IDENTITY	32%	100%	34%	28%		32%	50%	61%	31%
	COVERAGE	99%	100%	99%	83%		98%	98%	99%	99%
EFA102389	SeqID	10378	10904	11094			11781	12126	13263	
	IDENTITY	41%	100%	42%			40%	54%	52%	
	COVERAGE	97%	100%	83%			98%	82%	100%	
EFA102453	SeqID		10931	10995	11579	11762		12412	13502	13819
	IDENTITY		100%	29%	33%	33%		54%	54%	29%
	COVERAGE		101%	101%	88%	105%		101%	101%	96%
EFA102501	SeqID	10438	10626	11037	11410		11997	12447	13187	14043
	IDENTITY	45%	100%	44%	40%		44%	75%	76%	45%
	COVERAGE	112%	100%	111%	114%		113%	93%	96%	112%
EFA102502	SeqID	10439	10627	11036	11410		5179	12446	13646	14042
	IDENTITY	47%	100%	46%	52%		46%	72%	78%	46%
	COVERAGE	114%	100%	117%	79%		116%	99%	98%	114%
EFA102503	SeqID	10016	10643		11446		12027	12995	13481	13947
	IDENTITY	45%	100%		37%		43%	61%	65%	41%
	COVERAGE	99%	100%		101%		101%	98%	100%	85%
EFA102518	SeqID	10288	10647			11681		12248	13229	13881
	IDENTITY	33%	100%			50%		34%	54%	32%
	COVERAGE	105%	100%			71%		102%	100%	105%

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
EFA102541	SeqID	10327	10602	11241	11471		5188	12237	13356	13729
	IDENTITY	59%	100%	59%	49%		59%	69%	82%	56%
	COVERAGE	77%	101%	77%	73%		77%	77%	81%	77%
EFA102542	SeqID	10326	10603	11240	11288		12016	12238	13361	13732
	IDENTITY	75%	100%	70%	67%		75%	77%	100%	76%
	COVERAGE	95%	105%	95%	100%		95%	105%	100%	100%
EFA102549	SeqID	10338	10538	11117	11428		5159			
	IDENTITY	63%	100%	63%	71%		68%			
	COVERAGE	100%	103%	100%	100%		100%			
EFA102551	SeqID	10337	10539	11119	11427	11688	11990	12229	13221	14097
	IDENTITY	59%	100%	61%	58%	30%	62%	75%	81%	58%
	COVERAGE	96%	101%	91%	99%	74%	96%	101%	101%	96%
EFA102554	SeqID	10341	10532	11115			5161	12223	13216	
	IDENTITY	45%	100%	40%			42%	62%	63%	
	COVERAGE	93%	102%	93%			97%	102%	100%	
EFA102655	SeqID	10049	10733	11086	11305		11813	12952	13228	13898
	IDENTITY	47%	100%	47%	42%		48%	57%	60%	47%
	COVERAGE	97%	100%	99%	99%		99%	98%	108%	97%
EFA102656	SeqID		10734					12321	13668	
	IDENTITY		100%					55%	55%	
	COVERAGE		100%					100%	100%	
EFA102698	SeqID	10082	10909	10956			11807			14011
	IDENTITY	56%	100%	60%			31%			55%
	COVERAGE	96%	100%	96%			96%			96%
EFA102728	SeqID	10459	10948	11050	11420		12074	12411	13503	13859
	IDENTITY	51%	100%	53%	52%		54%	76%	81%	52%
	COVERAGE	89%	101%	89%	73%		82%	96%	100%	90%
EFA102736	SeqID	10285	10556	11205	11300		11943		13401	
	IDENTITY	53%	100%	52%	44%		51%		71%	
	COVERAGE	98%	100%	100%	98%		100%		99%	
EFA102764	SeqID	10201	10478	11054				12590	13425	13822
	IDENTITY	72%	100%	56%				68%	80%	71%
	COVERAGE	99%	100%	99%				99%	100%	99%
EFA102774	SeqID	10142	10896	11261	11362		12040	12150	13235	13978
	IDENTITY	50%	100%	52%	52%		51%	68%	74%	50%
	COVERAGE	96%	100%	96%	94%		95%	98%	97%	96%

TABLE VIIA

LOCUSID	*Data*	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
EFA102780	SeqID	10395	10908	11167	11616		11772	12701	13552	
	IDENTITY	49%	100%	46%	37%		51%	51%	46%	
	COVERAGE	77%	100%	76%	77%		75%	101%	98%	
EFA102788	SeqID	10176	10661	11223	11297		11882	12630	13303	13941
	IDENTITY	59%	100%	61%	54%		63%	70%	81%	59%
	COVERAGE	94%	101%	93%	97%		94%	93%	96%	94%
EFA102802	SeqID	10274	10854	11154	11298		11932	13128	13313	13866
	IDENTITY	66%	100%	64%	58%		64%	74%	83%	65%
	COVERAGE	99%	100%	100%	96%		100%	100%	100%	99%
EFA102813	SeqID	10191	10878	11005	11347		11815	12816	13492	13754
	IDENTITY	54%	100%	53%	51%		52%	64%	65%	53%
	COVERAGE	100%	100%	100%	99%		99%	99%	99%	100%
EFA102915	SeqID	10297	10640	10964	11323		11783	13090	13664	13737
	IDENTITY	27%	100%	32%	30%		31%	50%	52%	28%
	COVERAGE	100%	100%	100%	90%		100%	98%	99%	100%
EFA103021	SeqID	10434	10612	11039	11413		11999	12451	13517	
	IDENTITY	65%	100%	66%	60%		62%	86%	86%	
	COVERAGE	101%	101%	101%	99%		101%	101%	99%	
EFA103033	SeqID	10221	10681	11210	11607	11668	11801	12289	13191	14027
	IDENTITY	42%	100%	40%	29%	42%	39%	49%	56%	30%
	COVERAGE	91%	100%	93%	98%	94%	91%	93%	92%	93%
EFA103038	SeqID	10435	10613	11038	11412		11998	12784	13397	14046
	IDENTITY	54%	100%	52%	56%		51%	73%	73%	53%
	COVERAGE	99%	100%	100%	99%		100%	100%	100%	99%
EFA103039	SeqID	10293	10850	11041	11482	11728	11793	12541	13377	13741
	IDENTITY	45%	100%	46%	44%	40%	46%	73%	69%	45%
	COVERAGE	99%	100%	101%	98%	99%	99%	102%	101%	99%
EFA103062	SeqID	10437	10615	11072	11572		5180	12449	13247	14044
	IDENTITY	59%	100%	64%	54%		65%	64%	68%	59%
	COVERAGE	101%	101%	102%	102%		101%	99%	101%	102%
EFA103081	SeqID	10262	10862	10984	11403		11947		13415	14090
	IDENTITY	41%	100%	41%	40%		41%		74%	40%
	COVERAGE	85%	101%	83%	82%		80%		95%	85%
EFA103174	SeqID	10251	10689	10969	11370		11955	12600	13518	13703
	IDENTITY	32%	100%	32%	37%		33%	63%	77%	33%
	COVERAGE	93%	100%	94%	95%		96%	100%	100%	92%

TABLE VIIA

LOCUSID	*Data*	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
EFA103210	SeqID	10071	10688	11019	11371		11850	12601	13319	13945
	IDENTITY	56%	100%	63%	39%		57%	79%	76%	57%
	COVERAGE	97%	101%	98%	99%		97%	99%	101%	99%
EFA103268	SeqID	10365	10479	11062	11409		5178	12445	13231	13967
	IDENTITY	69%	100%	70%	68%		70%	83%	93%	70%
	COVERAGE	100%	101%	100%	100%		99%	101%	101%	101%
EFA103295	SeqID	10319	10633	11140	11493		12029	12640	13320	13771
	IDENTITY	66%	100%	58%	58%		70%	79%	86%	60%
	COVERAGE	77%	101%	85%	85%		77%	100%	96%	92%
EFA103348	SeqID		10873	10983	11402		11946			
	IDENTITY		100%	39%	59%		39%			
	COVERAGE		103%	82%	85%		82%			
EFA103365	SeqID	10360	10533	11096	11443	11643	5177	12224	13196	13975
	IDENTITY	57%	100%	58%	53%	58%	58%	82%	82%	58%
	COVERAGE	100%	101%	100%	97%	100%	100%	88%	101%	100%
EFA103375	SeqID	10177	10660	11222	11296		5120	12628	13302	
	IDENTITY	50%	100%	52%	36%		50%	66%	78%	
	COVERAGE	82%	102%	82%	97%		94%	102%	102%	
EFA103504	SeqID	10320	10671	11141	11492		12030	12638	13322	13766
	IDENTITY	42%	100%	45%	41%		48%	63%	81%	41%
	COVERAGE	97%	101%	97%	96%		97%	98%	100%	100%
EFA103508	SeqID		10672						13321	
	IDENTITY		100%						30%	
	COVERAGE		100%						80%	
EFA103571	SeqID	10335	10879	11121	11425		11988	12578	13240	14095
	IDENTITY	45%	100%	47%	48%		47%	67%	68%	45%
	COVERAGE	102%	100%	102%	103%		102%	99%	100%	102%
EFA103786	SeqID		10806					12361		
	IDENTITY		100%					59%		
	COVERAGE		100%					94%		

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU100040	SeqID IDENTITY COVERAGE							12533 100% 101%		
SAU100053	SeqID IDENTITY COVERAGE	10366 32% 97%	10504 46% 100%	11075 30% 99%	11376 32% 81%	11723 33% 84%	11855 33% 81%	12143 100% 100%	13318 48% 100%	13814 32% 97%
SAU100056	SeqID IDENTITY COVERAGE		10930 39% 98%					12577 100% 100%	13477 33% 100%	
SAU100059	SeqID IDENTITY COVERAGE	10213 28% 71%	10598 70% 97%	11161 26% 95%	11528 26% 95%	11750 27% 71%	12064 28% 96%	12652 100% 100%	13433 25% 95%	13929 28% 71%
SAU100062	SeqID IDENTITY COVERAGE	10430 27% 103%	10618 52% 96%	10998 29% 103%	11603 29% 77%	11739 31% 76%		12309 100% 100%	13294 53% 97%	14040 28% 102%
SAU100077	SeqID IDENTITY COVERAGE		10565 64% 102%					12520 100% 100%	13464 62% 102%	
SAU100112	SeqID IDENTITY COVERAGE	10059 49% 97%			11477 52% 100%	11702 53% 77%	12096 46% 100%	12634 100% 100%		13895 49% 97%
SAU100114	SeqID IDENTITY COVERAGE	10152 44% 98%	10515 51% 98%	11279 43% 98%	11302 45% 98%		11851 43% 98%	12535 100% 100%	13387 25% 102%	13824 43% 98%
SAU100118	SeqID IDENTITY COVERAGE		10903 41% 101%				11828 27% 100%	12125 100% 100%	13262 37% 101%	
SAU100123	SeqID IDENTITY COVERAGE	10258 52% 98%	10628 43% 100%	11134 53% 97%	11489 47% 96%		5192 52% 98%	12526 100% 100%	13421 45% 82%	14088 52% 98%
SAU100131	SeqID IDENTITY COVERAGE	10466 35% 71%		11274 33% 97%			11960 40% 70%	12517 100% 100%		13854 35% 71%

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU100133	SeqID	10311	10493	10990	11308	11703	11885	12574	13412	13769
	IDENTITY	34%	44%	34%	33%	30%	31%	100%	43%	34%
	COVERAGE	79%	99%	80%	78%	82%	79%	100%	99%	79%
SAU100139	SeqID	10355	10557	11101	11594		5174	12255	13201	
	IDENTITY	65%	84%	66%	64%		63%	100%	86%	
	COVERAGE	85%	86%	81%	83%		84%	101%	85%	
SAU100140	SeqID	10354	10558	11102	11440		5173	12258	13202	13970
	IDENTITY	54%	66%	54%	40%		48%	100%	63%	54%
	COVERAGE	93%	91%	93%	94%		93%	101%	91%	93%
SAU100141	SeqID	10353	10559	11103	11592		5172	12259	13203	13969
	IDENTITY	55%	78%	58%	54%		57%	100%	74%	55%
	COVERAGE	96%	101%	96%	96%		96%	100%	100%	96%
SAU100157	SeqID	10364	10480	11061	11408	11659	11996	12444	13232	13966
	IDENTITY	60%	78%	60%	55%	62%	57%	100%	77%	60%
	COVERAGE	100%	101%	100%	99%	88%	100%	101%	101%	101%
SAU100158	SeqID	10363	10481	11060	11568		11858	12443	13233	13965
	IDENTITY	60%	75%	59%	63%		59%	100%	77%	58%
	COVERAGE	98%	97%	98%	97%		98%	100%	97%	99%
SAU100162	SeqID	10069	10630	11239	11382		11971	12583	13597	14084
	IDENTITY	43%	49%	44%	37%		43%	100%	46%	43%
	COVERAGE	92%	89%	88%	80%		83%	100%	89%	93%
SAU100175	SeqID	10250	10651	11012			11954	12582	13272	13705
	IDENTITY	34%	42%	38%			34%	100%	42%	35%
	COVERAGE	98%	100%	93%			93%	100%	102%	99%
SAU100182	SeqID							12362		
	IDENTITY							100%		
	COVERAGE							101%		
SAU100186	SeqID	10043	10489	11124	11423		11939	12317	13355	13909
	IDENTITY	46%	61%	44%	46%		45%	100%	54%	45%
	COVERAGE	99%	99%	99%	98%		100%	101%	99%	101%
SAU100198	SeqID				11445			12120	13414	
	IDENTITY				29%			100%	29%	
	COVERAGE				78%			101%	79%	
SAU100227	SeqID		10765					12525		
	IDENTITY		36%					100%		
	COVERAGE		100%					100%		
SAU100242	SeqID	10097		11201			11836	12336		14056
	IDENTITY	65%		62%			65%	100%		65%
	COVERAGE	94%		96%			95%	100%		94%
SAU100246	SeqID		10821					12496	13490	

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
	IDENTITY COVERAGE		35% 101%					100% 101%	38% 93%	
SAU100251	SeqID IDENTITY COVERAGE							12363 100% 100%		
SAU100265	SeqID IDENTITY COVERAGE	10469 37% 88%						12122 100% 100%		
SAU100266	SeqID IDENTITY COVERAGE							12256 100% 101%		
SAU100272	SeqID IDENTITY COVERAGE		10617 26% 104%					12141 100% 100%		
SAU100275	SeqID IDENTITY COVERAGE	10041 52% 88%	10487 73% 94%	11149 47% 93%	11621 51% 98%		11941 51% 90%	12314 100% 100%	13438 65% 98%	13907 51% 88%
SAU100300	SeqID IDENTITY COVERAGE	10434 67% 99%	10612 86% 99%	11039 68% 99%	11413 63% 97%		11999 65% 99%	12451 100% 101%	13517 82% 97%	
SAU100301	SeqID IDENTITY COVERAGE	10433 41% 99%	10624 58% 98%	11083 41% 102%	11414 35% 96%		12000 42% 98%	12452 100% 101%	13168 51% 97%	
SAU100302	SeqID IDENTITY COVERAGE	10432 25% 92%		11082 34% 93%			12001 31% 103%	12453 100% 102%		
SAU100305	SeqID IDENTITY COVERAGE	10311 40% 94%	10774 50% 99%	10990 38% 94%			11885 40% 92%	12397 100% 100%	13491 49% 101%	13769 40% 94%
SAU100307	SeqID IDENTITY COVERAGE	10392 28% 99%	10725 32% 100%	10954 29% 99%		11685 28% 99%		12313 100% 100%	13252 29% 99%	13919 28% 99%
SAU100308	SeqID IDENTITY COVERAGE	10013 26% 90%	10814 44% 86%	10963 30% 86%				12312 100% 100%	13244 40% 92%	13711 27% 90%
SAU100313	SeqID IDENTITY COVERAGE		10757 46% 99%					12661 100% 100%	13293 43% 100%	
SAU100315	SeqID IDENTITY COVERAGE	10419 54% 96%	10802 73% 96%	11136 53% 96%	11326 53% 96%	11727 55% 82%	12087 53% 97%	12358 100% 100%	13521 74% 91%	13791 54% 96%

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU100323	SeqID	10216	10855					12575		13933
	IDENTITY	32%	71%					100%		34%
	COVERAGE	88%	99%					100%		88%
SAU100347	SeqID		10895	10961			12077	12334	13206	
	IDENTITY		44%	30%			30%	100%	42%	
	COVERAGE		106%	84%			100%	100%	100%	
SAU100355	SeqID		10683					12155	13300	
	IDENTITY		42%					100%	31%	
	COVERAGE		93%					100%	109%	
SAU100359	SeqID		10757					12239	13293	
	IDENTITY		52%					100%	43%	
	COVERAGE		97%					100%	99%	
SAU100381	SeqID	10411	10674				11903	12276		14031
	IDENTITY	28%	29%				33%	100%		28%
	COVERAGE	101%	99%				92%	100%		101%
SAU100389	SeqID	10473	10737		11374			12279	13344	
	IDENTITY	27%	50%		41%			100%	27%	
	COVERAGE	75%	95%		99%			100%	71%	
SAU100401	SeqID	10090	10706	10980		11641		12576		14053
	IDENTITY	31%	30%	27%		33%		100%		31%
	COVERAGE	95%	99%	95%		95%		101%		99%
SAU100412	SeqID	10102	10563	11194	11360		5150	12197	13468	
	IDENTITY	31%	42%	30%	33%		35%	100%	40%	
	COVERAGE	74%	100%	80%	74%		73%	100%	97%	
SAU100414	SeqID	10453	10556	11205	11300		11943	12148	13401	13872
	IDENTITY	60%	80%	61%	60%		67%	100%	76%	60%
	COVERAGE	96%	99%	98%	99%		91%	101%	96%	96%
SAU100432	SeqID	10436	10614	11071	11411		5181	12450	13246	14045
	IDENTITY	34%	60%	33%	31%		39%	100%	55%	31%
	COVERAGE	98%	98%	100%	95%		99%	101%	98%	98%
SAU100433	SeqID	10437	10615	11072	11572		5180	12449	13247	14044
	IDENTITY	58%	64%	63%	57%		58%	100%	69%	58%
	COVERAGE	97%	99%	98%	99%		98%	101%	99%	98%
SAU100436	SeqID		10569					12154	13393	
	IDENTITY		27%					100%	27%	
	COVERAGE		100%					100%	100%	
SAU100443	SeqID	10272	10894	11081			11930	12333	13515	13869
	IDENTITY	40%	52%	39%			38%	100%	45%	40%
	COVERAGE	92%	100%	96%			92%	100%	100%	92%
SAU100444	SeqID	10440	10583	11016	11540		11967	12392	13403	14041

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
	IDENTITY	29%	30%	41%	41%		28%	100%	52%	29%
	COVERAGE	75%	88%	94%	90%		81%	100%	91%	75%
SAU100475	SeqID		10927				11911	12337		
	IDENTITY		33%				30%	100%		
	COVERAGE		101%				101%	100%		
SAU100478	SeqID			11273				12605		
	IDENTITY			25%				100%		
	COVERAGE			96%				100%		
SAU100489	SeqID	10332	10685	11074	11580	11729	11778	12566	13298	14100
	IDENTITY	33%	33%	31%	34%	34%	29%	100%	34%	33%
	COVERAGE	101%	102%	99%	94%	101%	99%	100%	97%	94%
SAU100496	SeqID		10744					12484		
	IDENTITY		40%					100%		
	COVERAGE		80%					100%		
SAU100497	SeqID	10245	10709	11171	11395		11792	12140		13740
	IDENTITY	46%	59%	49%	44%		48%	100%		45%
	COVERAGE	99%	101%	99%	100%		99%	100%		100%
SAU100514	SeqID	10215			11388		12036	12626		13932
	IDENTITY	52%			34%		51%	100%		51%
	COVERAGE	93%			95%		98%	100%		95%
SAU100521	SeqID	10251		10969	11370		11955	12600		13703
	IDENTITY	43%		39%	34%		39%	100%		42%
	COVERAGE	104%		108%	103%		103%	100%		104%
SAU100522	SeqID	10114		11206		11680	11904	12599		14007
	IDENTITY	36%		34%		30%	36%	100%		35%
	COVERAGE	91%		89%		80%	90%	100%		91%
SAU100527	SeqID	10298	10721	10996			11782	12341	13452	13736
	IDENTITY	44%	48%	42%			41%	100%	43%	45%
	COVERAGE	98%	97%	99%			98%	101%	98%	97%
SAU100528	SeqID		10521					12507	13470	
	IDENTITY		30%					100%	33%	
	COVERAGE		83%					101%	71%	
SAU100532	SeqID	10235	10645	11128	11389			12580	13193	13744
	IDENTITY	39%	47%	29%	34%			100%	40%	31%
	COVERAGE	101%	100%	72%	90%			100%	97%	72%
SAU100542	SeqID	10371		11070	11422		12017	12532	13444	13806
	IDENTITY	52%		51%	46%		31%	100%	35%	52%
	COVERAGE	100%		98%	98%		102%	100%	102%	100%
SAU100546	SeqID	10359		11097	11596		5176	12235	13197	13974
	IDENTITY	43%		46%	34%		47%	100%	66%	46%
	COVERAGE	97%		97%	90%		99%	100%	99%	91%

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU100547	SeqID	10358	10549	11098	11595		5175	12240	13198	13973
	IDENTITY	41%	62%	39%	40%		46%	100%	63%	41%
	COVERAGE	92%	100%	97%	96%		97%	100%	100%	93%
SAU100557	SeqID		10928					12565	13651	
	IDENTITY		50%					100%	49%	
	COVERAGE		99%					100%	99%	
SAU100582	SeqID							12503		
	IDENTITY							100%		
	COVERAGE							100%		
SAU100590	SeqID							12121		
	IDENTITY							100%		
	COVERAGE							100%		
SAU100595	SeqID	10051	10832		11464		12109	12547	13174	13722
	IDENTITY	47%	66%		42%		50%	100%	46%	42%
	COVERAGE	88%	89%		89%		93%	100%	90%	91%
SAU100596	SeqID	10050	10833	11067	11624	11656	12110	12548	13173	13720
	IDENTITY	36%	50%	31%	41%	38%	42%	100%	30%	32%
	COVERAGE	99%	99%	100%	92%	89%	95%	100%	106%	95%
SAU100601	SeqID							12616		
	IDENTITY							100%		
	COVERAGE							100%		
SAU100608	SeqID	10032	10870	11190	11349		12008	12293	13507	14079
	IDENTITY	30%	61%	29%	29%		34%	100%	50%	28%
	COVERAGE	102%	96%	100%	98%		87%	100%	96%	104%
SAU100610	SeqID							12294		
	IDENTITY							100%		
	COVERAGE							100%		
SAU100613	SeqID	10378	10904	11094			11781	12126	13589	
	IDENTITY	44%	54%	43%			46%	100%	49%	
	COVERAGE	91%	88%	93%			73%	100%	89%	
SAU100617	SeqID		10502					12295	13314	
	IDENTITY		26%					100%	25%	
	COVERAGE		91%					100%	91%	
SAU100633	SeqID	10079	10589			11698	5107	12515	13644	13724
	IDENTITY	27%	42%			25%	29%	100%	35%	26%
	COVERAGE	92%	103%			89%	101%	100%	105%	103%
SAU100646	SeqID	10051	10570		11464		12109	12168	13174	14109
	IDENTITY	50%	48%		46%		49%	100%	42%	50%
	COVERAGE	95%	94%		97%		95%	100%	95%	96%
SAU100658	SeqID	10322	10813	11177	11351		12018	12388	13186	13733

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
	IDENTITY	49%	59%	49%	46%		48%	100%	58%	49%
	COVERAGE	100%	100%	100%	100%		100%	100%	100%	100%
SAU100659	SeqID	10045	10923	11174	11601		11937	12390	13616	13911
	IDENTITY	47%	54%	45%	40%		46%	100%	56%	44%
	COVERAGE	92%	92%	95%	103%		97%	101%	95%	81%
SAU100679	SeqID	10303		10997	11453	11713	11799	12137	13329	13757
	IDENTITY	32%		31%	32%	33%	35%	100%	42%	35%
	COVERAGE	96%		99%	106%	96%	97%	100%	104%	96%
SAU100684	SeqID	10412			11486		12097	12632		13749
	IDENTITY	46%			40%		46%	100%		46%
	COVERAGE	97%			99%		99%	100%		97%
SAU100685	SeqID							12633		
	IDENTITY							100%		
	COVERAGE							100%		
SAU100689	SeqID		10694					12323	13311	
	IDENTITY		55%					100%	46%	
	COVERAGE		98%					100%	96%	
SAU100702	SeqID		10655					12196	13671	
	IDENTITY		46%					100%	41%	
	COVERAGE		97%					100%	91%	
SAU100710	SeqID						11908	12546		
	IDENTITY						27%	100%		
	COVERAGE						73%	101%		
SAU100714	SeqID	10465	10675	11238	11563		11961	12635	13382	13853
	IDENTITY	48%	66%	41%	41%		44%	100%	60%	48%
	COVERAGE	108%	100%	110%	102%		108%	103%	101%	108%
SAU100731	SeqID	10071	10688	11019	11371		11850	12601	13319	13945
	IDENTITY	62%	79%	67%	40%		63%	100%	76%	60%
	COVERAGE	99%	100%	100%	101%		99%	101%	100%	101%
SAU100733	SeqID	10415			11611	11636	12084	12602		13746
	IDENTITY	41%			33%	42%	42%	100%		39%
	COVERAGE	95%			92%	74%	95%	100%		95%
SAU100734	SeqID	10321	10573	11142	11306		12031	12603	13273	13734
	IDENTITY	28%	36%	29%	27%		28%	100%	31%	29%
	COVERAGE	98%	95%	97%	90%		93%	100%	72%	101%
SAU100736	SeqID		10585					12391	13404	
	IDENTITY		27%					100%	26%	
	COVERAGE		97%					100%	97%	
SAU100738	SeqID	10188	10847	10953	11600	11634	11907	12624	13169	13981
	IDENTITY	48%	45%	46%	42%	48%	51%	100%	45%	49%
	COVERAGE	97%	98%	98%	97%	94%	97%	100%	97%	97%

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU100741	SeqID	10081	10591		11459		11776	12409		13714
	IDENTITY	65%	50%		35%		54%	100%		66%
	COVERAGE	100%	101%		82%		100%	101%		101%
SAU100745	SeqID	10442	10484	11202	11607	11733	11906	12596	13453	13847
	IDENTITY	34%	53%	35%	31%	35%	34%	100%	49%	35%
	COVERAGE	98%	97%	100%	99%	101%	98%	100%	98%	101%
SAU100747	SeqID		10749					12597	13266	
	IDENTITY		32%					100%	31%	
	COVERAGE		74%					100%	73%	
SAU100751	SeqID	10425	10866	11080		11747	11927	12335	13431	13788
	IDENTITY	62%	64%	59%		62%	62%	100%	63%	61%
	COVERAGE	99%	99%	98%		87%	99%	100%	99%	99%
SAU100752	SeqID	10140					11976	12524		14022
	IDENTITY	31%					35%	100%		38%
	COVERAGE	71%					82%	100%		72%
SAU100767	SeqID	10290					12094	12579		13875
	IDENTITY	43%					42%	100%		42%
	COVERAGE	100%					90%	100%		100%
SAU100771	SeqID	10084					11821	12545	13306	13710
	IDENTITY	30%					29%	100%	28%	26%
	COVERAGE	88%					80%	101%	90%	94%
SAU100773	SeqID	10055	10758	11093	11336	11763	11928	12377	13250	
	IDENTITY	47%	70%	41%	41%	46%	51%	100%	70%	
	COVERAGE	94%	100%	98%	96%	94%	93%	101%	96%	
SAU100776	SeqID							12482		
	IDENTITY							100%		
	COVERAGE							100%		
SAU100778	SeqID	10083		10957			11970	12514		14062
	IDENTITY	52%		52%			45%	100%		47%
	COVERAGE	89%		89%			88%	100%		89%
SAU100793	SeqID							12188	13392	
	IDENTITY							100%	27%	
	COVERAGE							100%	103%	
SAU100794	SeqID	10203						12189		
	IDENTITY	25%						100%		
	COVERAGE	101%						100%		
SAU100799	SeqID							12682		
	IDENTITY							100%		
	COVERAGE							100%		
SAU100808	SeqID							12345		14081

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
	IDENTITY							100%		35%
	COVERAGE							100%		70%
SAU100810	SeqID	10070					11824	12343		14080
	IDENTITY	51%					49%	100%		50%
	COVERAGE	94%					96%	100%		96%
SAU100813	SeqID	10314	10764	11216	11501		5198	12322	13381	13765
	IDENTITY	47%	63%	47%	45%		48%	100%	58%	50%
	COVERAGE	98%	94%	100%	91%		92%	100%	95%	92%
SAU100831	SeqID	10376	10741	11058			12093	12403	13349	13811
	IDENTITY	42%	58%	42%			42%	100%	51%	42%
	COVERAGE	97%	98%	102%			98%	100%	98%	101%
SAU100836	SeqID							12212		
	IDENTITY							100%		
	COVERAGE							100%		
SAU100838	SeqID							12211		
	IDENTITY							100%		
	COVERAGE							100%		
SAU100839	SeqID		10794					12210	13183	
	IDENTITY		42%					100%	44%	
	COVERAGE		100%					100%	100%	
SAU100843	SeqID	10126	10921	10974	11342			12328	13601	14092
	IDENTITY	26%	28%	28%	28%			100%	26%	26%
	COVERAGE	101%	73%	101%	102%			100%	100%	104%
SAU100845	SeqID							12329		
	IDENTITY							100%		
	COVERAGE							100%		
SAU100858	SeqID	10256	10776		11367	11719		12401	13472	13796
	IDENTITY	37%	48%		35%	37%		100%	39%	39%
	COVERAGE	106%	98%		103%	106%		101%	100%	106%
SAU100859	SeqID	10446	10777	11254	11548		12071	12402	13473	14026
	IDENTITY	33%	38%	33%	35%		34%	100%	38%	32%
	COVERAGE	94%	94%	95%	96%		94%	100%	92%	95%
SAU100865	SeqID	10252	10877	11010	11406		11956	12648	13506	13704
	IDENTITY	39%	49%	41%	28%		44%	100%	48%	38%
	COVERAGE	100%	99%	100%	101%		99%	100%	99%	100%
SAU100866	SeqID	10191	10878	11005	11347		11815	12553	13492	13754
	IDENTITY	54%	64%	51%	51%		53%	100%	57%	55%
	COVERAGE	100%	100%	100%	100%		100%	100%	99%	100%
SAU100879	SeqID							12483		
	IDENTITY							100%		

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
	COVERAGE							100%		
SAU100880	SeqID	10429	10720		11335		12039	12340	13451	14072
	IDENTITY	31%	51%		35%		36%	100%	45%	32%
	COVERAGE	81%	95%		97%		81%	100%	99%	85%
SAU100882	SeqID	10322	10750	11177	11351		12018	12374	13330	13733
	IDENTITY	43%	54%	42%	40%		45%	100%	52%	43%
	COVERAGE	98%	98%	98%	99%		98%	100%	98%	98%
SAU100885	SeqID	10410	10754	11001	11509		12095	12376		14032
	IDENTITY	52%	67%	53%	52%		53%	100%		52%
	COVERAGE	93%	74%	94%	96%		92%	100%		93%
SAU100886	SeqID	10224	10701	11213	11357		11905	12139	13348	13957
	IDENTITY	38%	60%	38%	36%		36%	100%	52%	38%
	COVERAGE	97%	83%	93%	99%		104%	100%	102%	98%
SAU100887	SeqID	10393	10952	11057	11330		11774	12138	13342	13920
	IDENTITY	50%	51%	50%	49%		48%	100%	70%	50%
	COVERAGE	85%	96%	82%	83%		83%	100%	96%	85%
SAU100899	SeqID							12277		
	IDENTITY							100%		
	COVERAGE							100%		
SAU100901	SeqID							12278		
	IDENTITY							100%		
	COVERAGE							100%		
SAU100916	SeqID	10209	10887					12394		13876
	IDENTITY	32%	34%					100%		32%
	COVERAGE	75%	72%					101%		75%
SAU100920	SeqID	10060	10772	11191	11530	11756	11983	12395		13896
	IDENTITY	43%	48%	31%	28%	40%	30%	100%		43%
	COVERAGE	91%	86%	87%	91%	86%	90%	100%		91%
SAU100921	SeqID	10027	10773	11185			12012	12396	13478	14074
	IDENTITY	32%	43%	33%			33%	100%	34%	32%
	COVERAGE	101%	96%	96%			96%	100%	98%	101%
SAU100932	SeqID	10095		11271			11834	12615		14055
	IDENTITY	39%		36%			39%	100%		39%
	COVERAGE	101%		101%			102%	100%		101%
SAU100944	SeqID	10017	10687	11219	11506		12057	12505	13498	14012
	IDENTITY	37%	26%	36%	36%		39%	100%	27%	39%
	COVERAGE	80%	108%	79%	79%		83%	100%	83%	80%

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU100952	SeqID		10717					12523	13312	
	IDENTITY		33%					100%	31%	
	COVERAGE		104%					100%	102%	
SAU100959	SeqID		10704					12485	13504	
	IDENTITY		58%					100%	49%	
	COVERAGE		99%					100%	101%	
SAU100961	SeqID	10320	10671	11141	11312		12030	12638	13322	13766
	IDENTITY	42%	63%	47%	40%		50%	100%	57%	42%
	COVERAGE	98%	99%	98%	97%		98%	101%	101%	99%
SAU100962	SeqID				11299			12639	13577	
	IDENTITY				28%			100%	26%	
	COVERAGE				80%			101%	92%	
SAU100963	SeqID	10319	10633	11140	11493		12029	12640	13320	13771
	IDENTITY	60%	79%	59%	61%		63%	100%	81%	60%
	COVERAGE	84%	96%	81%	81%		84%	101%	92%	88%
SAU100964	SeqID		10501	11139			12028	12641	13331	
	IDENTITY		61%	45%			47%	100%	60%	
	COVERAGE		101%	76%			77%	100%	101%	
SAU100965	SeqID							12642		
	IDENTITY							100%		
	COVERAGE							101%		
SAU100970	SeqID	10128	10516	11247	11512		11891	12529	13362	
	IDENTITY	52%	54%	39%	47%		52%	100%	46%	
	COVERAGE	99%	99%	100%	100%		99%	100%	99%	
SAU100996	SeqID		10686		11350			12606	13600	
	IDENTITY		38%		34%			100%	39%	
	COVERAGE		97%		73%			100%	96%	
SAU101006	SeqID	10185	10572	11022	11473		5122	12190		13820
	IDENTITY	29%	40%	31%	26%		26%	100%		30%
	COVERAGE	84%	98%	87%	94%		79%	100%		91%
SAU101020	SeqID							12710		
	IDENTITY							100%		
	COVERAGE							100%		
SAU101024	SeqID							12711		
	IDENTITY							100%		
	COVERAGE							101%		
SAU101028	SeqID	10034	10848	11148	11364		12006	12552	13471	13901
	IDENTITY	46%	57%	43%	46%		46%	100%	55%	45%
	COVERAGE	106%	101%	107%	100%		108%	100%	100%	106%
SAU101034	SeqID		10578					12608	13654	

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
	IDENTITY		36%					100%	37%	
	COVERAGE		80%					100%	71%	
SAU101038	SeqID		10716				11822	12521	13428	
	IDENTITY		42%				35%	100%	36%	
	COVERAGE		96%				78%	101%	103%	
SAU101039	SeqID							12522		
	IDENTITY							100%		
	COVERAGE							100%		
SAU101065	SeqID	10221	10681	11210	11607	11668	11801	12289	13191	14027
	IDENTITY	37%	49%	40%	28%	38%	36%	100%	46%	31%
	COVERAGE	98%	103%	100%	108%	97%	98%	100%	102%	98%
SAU101067	SeqID		10682					12290	13394	
	IDENTITY		41%					100%	40%	
	COVERAGE		100%					100%	99%	
SAU101070	SeqID		10770					12291	13380	
	IDENTITY		40%					100%	32%	
	COVERAGE		89%					100%	82%	
SAU101084	SeqID	10066		11156			11974	12283		
	IDENTITY	36%		34%			35%	100%		
	COVERAGE	90%		102%			92%	100%		
SAU101085	SeqID	10170		11263	11462		11973	12284	13225	13993
	IDENTITY	37%		34%	37%		38%	100%	47%	32%
	COVERAGE	89%		88%	94%		94%	100%	101%	88%
SAU101086	SeqID				11366		11972	12285	13666	
	IDENTITY				42%		34%	100%	49%	
	COVERAGE				74%		94%	100%	101%	
SAU101090	SeqID		10755					12191	13188	
	IDENTITY		36%					100%	31%	
	COVERAGE		97%					100%	97%	
SAU101092	SeqID	10450	10567				11847	12192		
	IDENTITY	35%	33%				30%	100%		
	COVERAGE	71%	96%				72%	100%		
SAU101104	SeqID	10135	10768	11248	11404	11732	11869	12195	13482	13827
	IDENTITY	38%	45%	39%	37%	37%	42%	100%	38%	37%
	COVERAGE	98%	100%	100%	92%	99%	99%	100%	96%	99%
SAU101143	SeqID	10040		11157	11315		11968	12502		13906
	IDENTITY	47%		27%	43%		44%	100%		47%
	COVERAGE	99%		82%	98%		100%	100%		99%
SAU101145	SeqID		10548				12070	12299		
	IDENTITY		42%				43%	100%		
	COVERAGE		98%				96%	101%		

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU101155	SeqID	10287	10697	11077	11352	11690	11944	12310	13549	13868
	IDENTITY	43%	49%	40%	30%	42%	42%	100%	37%	43%
	COVERAGE	95%	95%	95%	86%	95%	94%	100%	76%	95%
SAU101156	SeqID	10426	10698	11032	11333		12083	12311		13790
	IDENTITY	56%	63%	60%	52%		58%	100%		55%
	COVERAGE	96%	101%	96%	97%		96%	101%		96%
SAU101159	SeqID		10891		11532			12331	13463	
	IDENTITY		65%		36%			100%	54%	
	COVERAGE		100%		100%			100%	104%	
SAU101175	SeqID							12213		
	IDENTITY							100%		
	COVERAGE							101%		
SAU101180	SeqID	10061	10888				11910	12656		
	IDENTITY	38%	50%				37%	100%		
	COVERAGE	72%	89%				70%	100%		
SAU101183	SeqID		10843					12304		
	IDENTITY		42%					100%		
	COVERAGE		102%					100%		
SAU101184	SeqID	10477	10711	11218	11376	11735	12033	12305	13499	13709
	IDENTITY	37%	46%	36%	30%	38%	35%	100%	44%	38%
	COVERAGE	86%	100%	102%	85%	82%	85%	100%	98%	82%
SAU101189	SeqID							12264		
	IDENTITY							100%		
	COVERAGE							100%		
SAU101197	SeqID	10180	10787	11024			11924	12300	13340	13976
	IDENTITY	31%	44%	31%			27%	100%	46%	30%
	COVERAGE	98%	98%	101%			100%	100%	98%	98%
SAU101198	SeqID	10218	10786	11023			11923	12301	13341	
	IDENTITY	43%	50%	43%			41%	100%	46%	
	COVERAGE	74%	98%	73%			75%	100%	102%	
SAU101199	SeqID	10088	10742	10970			11949	12302	13178	14052
	IDENTITY	29%	40%	31%			36%	100%	37%	30%
	COVERAGE	97%	86%	94%			97%	100%	87%	98%
SAU101220	SeqID	10286	10864					12645	13390	13870
	IDENTITY	32%	37%					100%	39%	31%
	COVERAGE	74%	81%					100%	99%	74%
SAU101224	SeqID				11533			12647		
	IDENTITY				28%			100%		
	COVERAGE				77%			100%		
SAU101226	SeqID		10837			11658	11825	12298	13296	13721

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
	IDENTITY		52%			28%	37%	100%	27%	27%
	COVERAGE		96%			75%	90%	100%	77%	77%
SAU101231	SeqID	10301	10513				12079	12303		13759
	IDENTITY	32%	61%				32%	100%		31%
	COVERAGE	101%	100%				73%	101%		106%
SAU101235	SeqID		10616	11087				12561	13486	
	IDENTITY		37%	27%				100%	35%	
	COVERAGE		84%	90%				100%	97%	
SAU101236	SeqID	10089	10500			11673	11951	12564	13474	
	IDENTITY	42%	55%			29%	39%	100%	35%	
	COVERAGE	101%	77%			108%	100%	100%	103%	
SAU101239	SeqID				11361			12570		
	IDENTITY				33%			100%		
	COVERAGE				98%			100%		
SAU101240	SeqID							12573		
	IDENTITY							100%		
	COVERAGE							101%		
SAU101242	SeqID	10335	10879	11121	11425		11988	12578	13240	14095
	IDENTITY	48%	67%	47%	48%		47%	100%	55%	47%
	COVERAGE	104%	101%	104%	105%		104%	101%	101%	105%
SAU101247	SeqID		10919				11984	12512	13359	
	IDENTITY		32%				36%	100%	33%	
	COVERAGE		91%				90%	100%	85%	
SAU101262	SeqID	10137	10735		11399		11922	12488	13238	13837
	IDENTITY	28%	70%		47%		33%	100%	67%	28%
	COVERAGE	73%	100%		101%		97%	100%	100%	73%
SAU101266	SeqID	10238	10789	11178	11517		11829	12490	13317	13864
	IDENTITY	45%	57%	46%	41%		43%	100%	51%	44%
	COVERAGE	100%	99%	100%	98%		89%	100%	98%	100%
SAU101267	SeqID							12364		
	IDENTITY							100%		
	COVERAGE							100%		
SAU101270	SeqID	10175	10718	11220	11324		11881	12365	13383	13942
	IDENTITY	50%	62%	47%	45%		52%	100%	61%	50%
	COVERAGE	96%	99%	97%	93%		97%	100%	98%	96%
SAU101271	SeqID	10174	10719	11221	11556		11880	12366	13385	13943
	IDENTITY	37%	46%	36%	25%		35%	100%	46%	37%
	COVERAGE	100%	102%	100%	100%		100%	100%	101%	75%
SAU101275	SeqID	10232	10684	10981	11521	11708	11845	12604	13299	13954
	IDENTITY	35%	57%	38%	33%	34%	34%	100%	57%	35%
	COVERAGE	95%	101%	93%	98%	96%	94%	100%	101%	95%

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU101286	SeqID		10884					12292	13189	
	IDENTITY		47%					100%	40%	
	COVERAGE		100%					101%	99%	
SAU101293	SeqID							12631		
	IDENTITY							100%		
	COVERAGE							101%		
SAU101300	SeqID		10751					12557	13194	
	IDENTITY		57%					100%	54%	
	COVERAGE		93%					101%	90%	
SAU101301	SeqID		10752				11785	12558	13195	
	IDENTITY		57%				27%	100%	54%	
	COVERAGE		96%				94%	101%	99%	
SAU101302	SeqID		10753		11317			12559	13611	
	IDENTITY		49%		33%			100%	26%	
	COVERAGE		101%		86%			101%	72%	
SAU101310	SeqID	10330	10924	11160	11321		12063	12562	13364	13885
	IDENTITY	47%	52%	48%	43%		47%	100%	51%	47%
	COVERAGE	98%	98%	98%	98%		98%	100%	98%	98%
SAU101311	SeqID	10094		11278			11859	12563		13891
	IDENTITY	46%		46%			42%	100%		46%
	COVERAGE	98%		98%			96%	100%		95%
SAU101320	SeqID	10263	10861	10965	11562		11948	12128	13254	14089
	IDENTITY	50%	59%	49%	39%		51%	100%	56%	49%
	COVERAGE	100%	99%	99%	100%		99%	100%	97%	100%
SAU101327	SeqID	10018	10710	11147			11779	12612	13495	14014
	IDENTITY	35%	46%	43%			34%	100%	35%	35%
	COVERAGE	100%	97%	101%			92%	101%	99%	100%
SAU101339	SeqID	10093	10520		11365		11839	12399	13405	13888
	IDENTITY	55%	30%		26%		54%	100%	27%	45%
	COVERAGE	99%	74%		74%		97%	100%	76%	99%
SAU101340	SeqID	10092					11840	12400		13889
	IDENTITY	37%					35%	100%		39%
	COVERAGE	106%					101%	101%		104%
SAU101341	SeqID	10230	10925	11212	11385		11898	12618	13365	13952
	IDENTITY	47%	55%	48%	48%		45%	100%	48%	47%
	COVERAGE	93%	92%	92%	98%		92%	100%	100%	93%
SAU101343	SeqID	10422	10649	11162		11721		12619	13346	13785
	IDENTITY	50%	55%	49%		50%		100%	58%	51%
	COVERAGE	99%	100%	99%		99%		100%	92%	99%
SAU101344	SeqID	10171	10650	11252			11826	12620	13347	13755

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
	IDENTITY	48%	62%	40%			37%	100%	44%	38%
	COVERAGE	81%	88%	79%			82%	100%	79%	81%
SAU101346	SeqID	10058			11282		11803	12621		13894
	IDENTITY	36%			35%		43%	100%		36%
	COVERAGE	99%			103%		99%	100%		99%
SAU101347	SeqID	10139		11163	11283		11877	12622	13259	13839
	IDENTITY	63%		29%	62%		62%	100%	30%	62%
	COVERAGE	100%		96%	101%		100%	100%	91%	100%
SAU101350	SeqID	10184	10508		11318		12069	12487	13286	13982
	IDENTITY	61%	56%		32%		46%	100%	55%	60%
	COVERAGE	95%	98%		81%		100%	100%	97%	97%
SAU101351	SeqID		10507					12486	13285	
	IDENTITY		60%					100%	59%	
	COVERAGE		96%					100%	96%	
SAU101360	SeqID	10138	10571	10977	11598	11684	11878	12555	13175	13838
	IDENTITY	56%	70%	54%	35%	55%	58%	100%	71%	56%
	COVERAGE	98%	101%	98%	97%	88%	98%	100%	101%	98%
SAU101365	SeqID	10269	10491	11127	11577		11809	12556	13295	13874
	IDENTITY	45%	55%	44%	40%		45%	100%	50%	45%
	COVERAGE	101%	101%	101%	99%		101%	100%	100%	101%
SAU101366	SeqID	10147	10654					12266	13179	13843
	IDENTITY	49%	73%					100%	56%	48%
	COVERAGE	99%	98%					100%	99%	99%
SAU101369	SeqID							12274		
	IDENTITY							100%		
	COVERAGE							100%		
SAU101371	SeqID				11372		11902	12275	13243	
	IDENTITY				40%		32%	100%	34%	
	COVERAGE				86%		79%	100%	77%	
SAU101381	SeqID	10373						12145	13432	
	IDENTITY	26%						100%	41%	
	COVERAGE	98%						100%	99%	
SAU101382	SeqID	10239	10707	11179	11292	11635	11879	12146	13657	13862
	IDENTITY	53%	60%	50%	42%	39%	53%	100%	63%	52%
	COVERAGE	98%	99%	97%	97%	79%	98%	100%	96%	98%
SAU101383	SeqID	10317	10625	11226	11418		12055	12147	13422	13761
	IDENTITY	37%	39%	36%	26%		38%	100%	37%	39%
	COVERAGE	102%	90%	97%	98%		94%	100%	112%	94%
SAU101385	SeqID	10403	10830	11030	11368	11640	12115	12385	13508	14067
	IDENTITY	33%	52%	31%	27%	32%	29%	100%	38%	32%
	COVERAGE	99%	90%	92%	89%	96%	98%	100%	92%	99%

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU101387	SeqID	10402	10839		11549		12114	12386	13509	14068
	IDENTITY	27%	35%		27%		27%	100%	32%	27%
	COVERAGE	87%	88%		71%		87%	101%	90%	87%
SAU101389	SeqID	10401	10801	11029	11400		12113	12387	13510	14069
	IDENTITY	55%	72%	57%	60%		57%	100%	74%	55%
	COVERAGE	98%	99%	99%	100%		98%	100%	94%	98%
SAU101398	SeqID	10313	10881	11224	11502	11754	12051	12324	13485	13767
	IDENTITY	55%	78%	54%	51%	57%	56%	100%	68%	54%
	COVERAGE	100%	101%	100%	99%	101%	100%	101%	101%	101%
SAU101399	SeqID	10312	10882	10989	11416	11755	12050	12325	13699	13768
	IDENTITY	50%	63%	48%	38%	51%	51%	100%	58%	49%
	COVERAGE	99%	100%	98%	97%	85%	97%	100%	99%	99%
SAU101400	SeqID		10743		11448			12326	13391	
	IDENTITY		46%		32%			100%	41%	
	COVERAGE		96%		95%			100%	96%	
SAU101408	SeqID	10267	10509					12308	13278	14050
	IDENTITY	37%	43%					100%	42%	39%
	COVERAGE	100%	99%					100%	101%	100%
SAU101421	SeqID		10676					12498		
	IDENTITY		38%					100%		
	COVERAGE		93%					100%		
SAU101427	SeqID							12500	13234	
	IDENTITY							100%	48%	
	COVERAGE							100%	100%	
SAU101432	SeqID			11046	11286	11744	12065	12184	13538	
	IDENTITY			57%	60%	63%	68%	100%	26%	
	COVERAGE			99%	100%	101%	99%	101%	73%	
SAU101436	SeqID	10271		11045	11285		12067	12183		13873
	IDENTITY	27%		62%	61%		59%	100%		27%
	COVERAGE	90%		99%	97%		98%	100%		90%
SAU101438	SeqID	10146	10825	11042				12379	13337	13842
	IDENTITY	30%	29%	29%				100%	27%	30%
	COVERAGE	88%	94%	89%				100%	94%	88%
SAU101444	SeqID	10254	10827	11144	11301		12034	12381	13335	13792
	IDENTITY	60%	66%	57%	54%		60%	100%	61%	59%
	COVERAGE	100%	101%	100%	100%		100%	100%	99%	100%
SAU101445	SeqID	10248	10828	11207			12037	12382	13408	13949
	IDENTITY	52%	70%	52%			54%	100%	72%	51%
	COVERAGE	99%	100%	96%			99%	100%	100%	100%
SAU101446	SeqID	10411	10674				11903	12383		14031

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
	IDENTITY	50%	59%				33%	100%		50%
	COVERAGE	98%	100%				97%	100%		99%
SAU101447	SeqID							12683		
	IDENTITY							100%		
	COVERAGE							101%		
SAU101452	SeqID							12684		
	IDENTITY							100%		
	COVERAGE							100%		
SAU101455	SeqID							12686		
	IDENTITY							100%		
	COVERAGE							100%		
SAU101461	SeqID		10705				11790	12680		
	IDENTITY		54%				26%	100%		
	COVERAGE		93%				86%	101%		
SAU101463	SeqID	10268	10708				11919	12679	13584	14051
	IDENTITY	29%	45%				26%	100%	26%	29%
	COVERAGE	77%	98%				91%	101%	88%	77%
SAU101476	SeqID	10469	10905					12254	13454	13905
	IDENTITY	38%	29%					100%	25%	26%
	COVERAGE	84%	94%					100%	95%	73%
SAU101481	SeqID	10125	10920	10975	11290		11894	12130	13580	
	IDENTITY	40%	39%	40%	32%		39%	100%	41%	
	COVERAGE	93%	95%	96%	93%		96%	100%	96%	
SAU101482	SeqID	10126	10921	10974	11342	11738	11893	12123	13360	14092
	IDENTITY	55%	51%	52%	44%	36%	52%	100%	48%	37%
	COVERAGE	98%	100%	98%	98%	77%	98%	100%	99%	101%
SAU101483	SeqID	10127	10918	10973	11341		11892	12124	13674	13871
	IDENTITY	65%	41%	59%	58%		61%	100%	51%	31%
	COVERAGE	88%	90%	90%	90%		87%	101%	92%	94%
SAU101488	SeqID		10730				11868	12164	13450	13799
	IDENTITY		28%				25%	100%	33%	28%
	COVERAGE		95%				74%	100%	98%	73%
SAU101491	SeqID		10580					12165	13315	
	IDENTITY		42%					100%	42%	
	COVERAGE		104%					100%	95%	
SAU101492	SeqID	10073	10581	11020	11284		11831	12166	13323	13715
	IDENTITY	38%	52%	37%	29%		37%	100%	43%	38%
	COVERAGE	98%	101%	98%	78%		94%	101%	85%	98%
SAU101493	SeqID	10074		11021	11381		11832	12167	13564	13716
	IDENTITY	42%		41%	30%		43%	100%	64%	44%

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
	COVERAGE	96%		97%	94%		98%	101%	91%	96%
SAU101495	SeqID IDENTITY COVERAGE	10030 32% 92%	10805 34% 92%	11188 36% 90%	11458 29% 86%		5187 33% 90%	12360 100% 100%	13333 32% 94%	14077 32% 92%
SAU101497	SeqID IDENTITY COVERAGE		10806 59% 100%					12361 100% 100%		
SAU101509	SeqID IDENTITY COVERAGE	10121 34% 104%				11712 36% 104%		12418 100% 100%	13249 49% 83%	
SAU101526	SeqID IDENTITY COVERAGE		10901 38% 88%					12179 100% 100%	13465 34% 89%	
SAU101529	SeqID IDENTITY COVERAGE							12544 100% 100%		
SAU101541	SeqID IDENTITY COVERAGE	10024 41% 101%	10631 63% 100%	11182 42% 101%	11526 38% 98%		12014 42% 101%	12344 100% 100%	13647 59% 101%	14019 40% 100%
SAU101543	SeqID IDENTITY COVERAGE	10025 26% 78%	10634 33% 97%	11183 27% 78%			11867 27% 73%	12346 100% 100%	13406 32% 96%	14091 28% 76%
SAU101545	SeqID IDENTITY COVERAGE	10029 31% 98%	10636 50% 99%	11187 32% 97%	11329 27% 83%		12010 28% 97%	12348 100% 100%	13633 47% 97%	14076 30% 98%
SAU101546	SeqID IDENTITY COVERAGE		10638 27% 80%					12349 100% 100%		
SAU101549	SeqID IDENTITY COVERAGE	10443 40% 70%	10762 38% 95%	11228 30% 88%		11767 38% 70%	12049 29% 92%	12549 100% 102%	13460 39% 92%	14030 38% 70%
SAU101551	SeqID IDENTITY COVERAGE	10172 52% 97%	10490 77% 98%	11194 26% 98%	11360 27% 89%		12019 26% 96%	12550 100% 100%	13326 76% 98%	13939 52% 97%
SAU101554	SeqID IDENTITY COVERAGE		10485 48% 83%		11485 26% 81%			12551 100% 101%	13672 46% 91%	

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU101561	SeqID	10400	10937	11073	11355	11759	12112	12149	13307	14064
	IDENTITY	44%	57%	44%	38%	42%	44%	100%	49%	43%
	COVERAGE	99%	99%	99%	100%	99%	100%	100%	99%	99%
SAU101565	SeqID	10134	10552	11211			11895	12151	13448	13826
	IDENTITY	37%	50%	35%			36%	100%	44%	36%
	COVERAGE	93%	96%	94%			92%	100%	99%	92%
SAU101567	SeqID							12144		
	IDENTITY							100%		
	COVERAGE							100%		
SAU101570	SeqID	10037	10690	11208		11700	11835	12584	13563	13900
	IDENTITY	32%	48%	31%		34%	33%	100%	37%	30%
	COVERAGE	100%	100%	99%		95%	102%	100%	100%	100%
SAU101571	SeqID		10691				11917	12585	13308	
	IDENTITY		45%				33%	100%	31%	
	COVERAGE		98%				94%	100%	97%	
SAU101572	SeqID	10068	10692			11689	11864	12586	13309	14083
	IDENTITY	26%	56%			46%	43%	100%	45%	25%
	COVERAGE	75%	101%			89%	96%	100%	98%	75%
SAU101573	SeqID	10096	10693	11270			11865	12587		14054
	IDENTITY	31%	49%	35%			30%	100%		31%
	COVERAGE	98%	103%	98%			101%	100%		98%
SAU101574	SeqID							12588		
	IDENTITY							100%		
	COVERAGE							101%		
SAU101575	SeqID		10869					12589	13638	
	IDENTITY		31%					100%	27%	
	COVERAGE		98%					100%	96%	
SAU101576	SeqID		10762				12049	12554	13460	
	IDENTITY		32%				29%	100%	39%	
	COVERAGE		93%				98%	102%	98%	
SAU101586	SeqID							12598	13487	
	IDENTITY							100%	34%	
	COVERAGE							101%	78%	
SAU101592	SeqID	10249	10605	10987	11555	11741	11952	12406	13283	13950
	IDENTITY	51%	74%	53%	53%	51%	52%	100%	70%	51%
	COVERAGE	101%	100%	100%	100%	101%	101%	100%	100%	101%
SAU101599	SeqID							12478		
	IDENTITY							100%		
	COVERAGE							100%		
SAU101610	SeqID	10449			11390		12048	12629		13816

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
	IDENTITY	38%			38%		40%	100%		38%
	COVERAGE	105%			101%		99%	100%		105%
SAU101612	SeqID							12637		
	IDENTITY							100%		
	COVERAGE							100%		
SAU101614	SeqID	10167	10678	11262	11534		11978	12649	13462	13851
	IDENTITY	49%	55%	29%	29%		39%	100%	53%	48%
	COVERAGE	100%	98%	93%	94%		95%	100%	99%	100%
SAU101616	SeqID	10186	10667		11407	11695	11872	12432		13903
	IDENTITY	33%	28%		32%	29%	34%	100%		33%
	COVERAGE	102%	99%		88%	104%	96%	100%		100%
SAU101622	SeqID	10162			11619	11710	12104	12430		13832
	IDENTITY	69%			29%	67%	43%	100%		70%
	COVERAGE	100%			104%	78%	101%	100%		100%
SAU101624	SeqID	10193		11255	11316			12429	13430	13752
	IDENTITY	26%		27%	38%			100%	26%	26%
	COVERAGE	101%		106%	97%			100%	103%	107%
SAU101630	SeqID							12410		
	IDENTITY							100%		
	COVERAGE							100%		
SAU101632	SeqID							12407		
	IDENTITY							100%		
	COVERAGE							100%		
SAU101637	SeqID		10886					12201	13384	
	IDENTITY		44%					100%	38%	
	COVERAGE		99%					101%	98%	
SAU101641	SeqID	10223					11918	12193		
	IDENTITY	51%					53%	100%		
	COVERAGE	92%					95%	100%		
SAU101651	SeqID		10790		11552		12021	12491	13369	
	IDENTITY		38%		28%		34%	100%	42%	
	COVERAGE		97%		89%		90%	101%	100%	
SAU101652	SeqID		10791		11369		12022	12492	13368	
	IDENTITY		62%		49%		50%	100%	56%	
	COVERAGE		97%		91%		95%	100%	98%	
SAU101653	SeqID		10792		11520		12023	12493	13367	
	IDENTITY		73%		46%		49%	100%	63%	
	COVERAGE		100%		100%		100%	100%	100%	
SAU101655	SeqID	10205	10793				11896	12494	13334	
	IDENTITY	31%	50%				30%	100%	33%	
	COVERAGE	84%	97%				83%	100%	93%	

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU101663	SeqID							12261		
	IDENTITY							100%		
	COVERAGE							100%		
SAU101664	SeqID	10202	10512	11138			11863	12262	13685	13823
	IDENTITY	37%	41%	36%			38%	100%	38%	36%
	COVERAGE	98%	97%	108%			106%	101%	105%	98%
SAU101674	SeqID	10067					11846	12594		14082
	IDENTITY	27%					27%	100%		27%
	COVERAGE	103%					101%	100%		103%
SAU101679	SeqID	10190	10644	11055	11398		12105	12593	13264	13756
	IDENTITY	41%	53%	42%	36%		45%	100%	45%	40%
	COVERAGE	90%	100%	99%	86%		90%	100%	98%	90%
SAU101681	SeqID	10464	10746				11861	12592	13419	13987
	IDENTITY	39%	46%				31%	100%	44%	40%
	COVERAGE	100%	102%				95%	100%	102%	97%
SAU101682	SeqID	10156	10670	11265				12591	13488	13884
	IDENTITY	28%	30%	28%				100%	34%	26%
	COVERAGE	94%	96%	102%				100%	80%	94%
SAU101685	SeqID		10590				11920	12152	13396	
	IDENTITY		26%				37%	100%	56%	
	COVERAGE		88%				97%	100%	100%	
SAU101717	SeqID	10129	10586	11027	11610		11890	12131	13352	14070
	IDENTITY	33%	51%	35%	31%		38%	100%	49%	34%
	COVERAGE	101%	100%	93%	70%		99%	100%	93%	101%
SAU101724	SeqID	10309	10588	11268	11337		12015	12136	13678	13772
	IDENTITY	44%	44%	41%	36%		43%	100%	45%	43%
	COVERAGE	97%	99%	97%	87%		80%	100%	98%	97%
SAU101726	SeqID	10130	10664	11026	11461		11889	12134	13550	14071
	IDENTITY	37%	50%	42%	36%		40%	100%	48%	41%
	COVERAGE	101%	100%	101%	101%		100%	100%	100%	77%
SAU101727	SeqID		10665					12133	13551	
	IDENTITY		50%					100%	49%	
	COVERAGE		101%					101%	101%	
SAU101728	SeqID	10019	10666	11053		11734	11800	12132	13182	14015
	IDENTITY	34%	54%	35%		35%	34%	100%	53%	34%
	COVERAGE	86%	95%	88%		85%	90%	100%	94%	86%
SAU101736	SeqID	10225					11817	12519		13958
	IDENTITY	28%					38%	100%		29%
	COVERAGE	72%					99%	100%		72%
SAU101737	SeqID				11405		11817	12518		

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
	IDENTITY				32%		30%	100%		
	COVERAGE				78%		96%	101%		
SAU101744	SeqID		10562					12367		
	IDENTITY		44%					100%		
	COVERAGE		101%					100%		
SAU101751	SeqID	10474	10606			11671		12448	13165	13706
	IDENTITY	30%	46%			30%		100%	45%	31%
	COVERAGE	85%	100%			82%		100%	99%	79%
SAU101752	SeqID	10438	10626	11037	11410		11997	12447	13187	14043
	IDENTITY	46%	75%	47%	40%		45%	100%	69%	46%
	COVERAGE	115%	99%	114%	120%		116%	100%	99%	115%
SAU101754	SeqID	10439	10627	11036	11571		5179	12446	13646	14042
	IDENTITY	46%	72%	46%	53%		46%	100%	68%	46%
	COVERAGE	116%	100%	117%	80%		118%	100%	101%	116%
SAU101756	SeqID	10365	10479	11062	11409		5178	12445	13231	13967
	IDENTITY	65%	83%	66%	65%		68%	100%	82%	65%
	COVERAGE	91%	93%	91%	91%		91%	101%	93%	93%
SAU101771	SeqID	10220	10784	11276		11765	11950	12350	13280	13934
	IDENTITY	43%	65%	37%		35%	36%	100%	67%	41%
	COVERAGE	91%	101%	77%		82%	80%	101%	98%	91%
SAU101772	SeqID	10240	10785	11275	11294		11925	12351	13281	13863
	IDENTITY	50%	63%	51%	27%		38%	100%	61%	48%
	COVERAGE	100%	101%	100%	77%		100%	100%	101%	84%
SAU101777	SeqID		10673		11448			12352	13176	
	IDENTITY		64%		43%			100%	62%	
	COVERAGE		97%		88%			100%	98%	
SAU101781	SeqID		10495				11917	12353	13308	
	IDENTITY		67%				38%	100%	28%	
	COVERAGE		99%				93%	100%	85%	
SAU101782	SeqID		10496			11689	11916	12354	13309	
	IDENTITY		75%			44%	41%	100%	40%	
	COVERAGE		100%			89%	99%	100%	96%	
SAU101784	SeqID	10037	10498	11208		11700	11866	12355	13563	13900
	IDENTITY	44%	65%	45%		35%	42%	100%	37%	44%
	COVERAGE	97%	100%	97%		92%	99%	100%	99%	97%
SAU101790	SeqID	10350	10524	11106	11437		5170	12215	13207	
	IDENTITY	51%	81%	55%	48%		55%	100%	79%	
	COVERAGE	86%	99%	86%	86%		90%	101%	99%	
SAU101791	SeqID	10349	10525	11107	11436		5169	12216	13208	14108
	IDENTITY	67%	90%	69%	62%		66%	100%	89%	67%
	COVERAGE	101%	101%	101%	100%		100%	101%	101%	102%

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU101792	SeqID	10348	10526	11108			5168	12217	13209	14107
	IDENTITY	53%	66%	52%			49%	100%	68%	50%
	COVERAGE	96%	94%	95%			97%	101%	94%	96%
SAU101793	SeqID	10347	10527	11109	11589	11654	5167	12218	13210	14106
	IDENTITY	64%	85%	65%	51%	64%	63%	100%	79%	64%
	COVERAGE	100%	101%	99%	99%	101%	99%	101%	100%	101%
SAU101795	SeqID	10345	10528	11111	11435		5165	12219	13212	14104
	IDENTITY	51%	79%	47%	44%		44%	100%	76%	51%
	COVERAGE	99%	101%	99%	98%		100%	101%	101%	101%
SAU101797	SeqID	10343	10530	11113	11433		5163	12221	13214	14102
	IDENTITY	45%	68%	41%	41%		48%	100%	66%	46%
	COVERAGE	100%	101%	99%	93%		96%	101%	101%	101%
SAU101798	SeqID	10342	10531	11114	11432		5162	12222	13215	14101
	IDENTITY	55%	72%	55%	62%		52%	100%	66%	55%
	COVERAGE	99%	95%	99%	87%		99%	101%	96%	99%
SAU101799	SeqID	10341	10532	11115			5161	12223	13216	
	IDENTITY	51%	62%	42%			42%	100%	69%	
	COVERAGE	100%	102%	100%			97%	102%	98%	
SAU101800	SeqID	10340	10534	11116	11431		5160	12225	13217	14099
	IDENTITY	47%	79%	46%	40%		42%	100%	84%	47%
	COVERAGE	99%	101%	99%	90%		99%	101%	101%	99%
SAU101802	SeqID	10075	10536	11008	11348	11633	11942	12227	13219	13717
	IDENTITY	48%	64%	52%	31%	47%	53%	100%	56%	47%
	COVERAGE	97%	97%	97%	93%	97%	84%	100%	96%	97%
SAU101803	SeqID	10111	10537	11052	11429	11651	11876	12228	13220	14010
	IDENTITY	71%	84%	71%	60%	70%	71%	100%	82%	70%
	COVERAGE	97%	101%	97%	100%	101%	97%	101%	101%	101%
SAU101805	SeqID	10337	10539	11119	11427		11990	12229	13221	14097
	IDENTITY	53%	75%	52%	58%		60%	100%	74%	52%
	COVERAGE	96%	101%	99%	99%		96%	101%	101%	96%
SAU101806	SeqID	10336	10540	11120	11426		11989	12230	13222	14096
	IDENTITY	62%	85%	64%	60%		61%	100%	85%	63%
	COVERAGE	100%	101%	100%	102%		100%	101%	92%	101%
SAU101807	SeqID	10334	10541	11122	11583		11987	12231	13223	14094
	IDENTITY	42%	71%	42%	37%		42%	100%	58%	42%
	COVERAGE	99%	100%	99%	94%		99%	100%	99%	99%
SAU101808	SeqID	10333	10542	11123	11582	11627	5158	12232	13224	14093
	IDENTITY	48%	65%	49%	46%	48%	45%	100%	67%	48%
	COVERAGE	98%	103%	98%	99%	78%	98%	101%	106%	98%
SAU101810	SeqID	10053	10544	11229	11625	11666	11909	12233	13441	14110

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
	IDENTITY	35%	52%	34%	32%	36%	33%	100%	47%	36%
	COVERAGE	76%	88%	78%	77%	73%	72%	100%	88%	73%
SAU101811	SeqID	10196	10545	11068	11463	11666	11888	12234	13440	13721
	IDENTITY	38%	49%	33%	32%	33%	32%	100%	45%	34%
	COVERAGE	78%	87%	82%	82%	83%	82%	100%	87%	76%
SAU101814	SeqID	10327	10602	11241	11471	11655	5188	12237	13356	13729
	IDENTITY	58%	69%	57%	47%	56%	55%	100%	65%	56%
	COVERAGE	94%	96%	94%	92%	71%	97%	101%	99%	94%
SAU101815	SeqID	10326		11240	11288		12016	12238	13361	13732
	IDENTITY	49%		48%	46%		53%	100%	69%	51%
	COVERAGE	98%		98%	93%		93%	101%	99%	99%
SAU101818	SeqID			11231	11307		11814	12369	13494	
	IDENTITY			32%	33%		31%	100%	35%	
	COVERAGE			95%	90%		96%	101%	93%	
SAU101824	SeqID	10158					12004	12371		
	IDENTITY	33%					28%	100%		
	COVERAGE	71%					75%	100%		
SAU101833	SeqID	10207	10747	11040	11481		11794	12373	13388	13775
	IDENTITY	42%	49%	28%	44%		35%	100%	46%	44%
	COVERAGE	100%	102%	95%	107%		117%	100%	103%	89%
SAU101839	SeqID	10398	10849	11236			12100	12495	13291	13924
	IDENTITY	30%	33%	32%			25%	100%	32%	28%
	COVERAGE	94%	78%	90%			98%	100%	83%	94%
SAU101842	SeqID	10105	10942	11075	11376	11723	11855	12510	13445	13999
	IDENTITY	45%	70%	33%	48%	33%	47%	100%	65%	45%
	COVERAGE	98%	95%	95%	99%	94%	97%	100%	82%	99%
SAU101845	SeqID	10231	10739		11567		11899	12506	13544	13953
	IDENTITY	30%	47%		40%		26%	100%	43%	28%
	COVERAGE	101%	102%		102%		101%	100%	102%	101%
SAU101849	SeqID	10015	10740	11209	11472		12058	12567	13379	13713
	IDENTITY	56%	77%	54%	56%		56%	100%	75%	56%
	COVERAGE	103%	99%	103%	101%		103%	100%	98%	104%
SAU101857	SeqID							12569		
	IDENTITY							100%		
	COVERAGE							100%		
SAU101862	SeqID	10257	10817	10955	11334		11802	12571	13305	13797
	IDENTITY	40%	63%	40%	33%		39%	100%	62%	39%
	COVERAGE	98%	100%	98%	101%		98%	100%	99%	98%
SAU101864	SeqID							12572		
	IDENTITY							100%		
	COVERAGE							100%		

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU101865	SeqID	10044	10834	11151	11417		11938	12318	13227	13910
	IDENTITY	43%	58%	45%	40%		40%	100%	54%	41%
	COVERAGE	85%	88%	88%	87%		87%	100%	88%	88%
SAU101866	SeqID		10835				11873	12319	13586	
	IDENTITY		42%				29%	100%	40%	
	COVERAGE		102%				99%	100%	100%	
SAU101868	SeqID	10049	10733	11086	11305		11813	12320	13228	13898
	IDENTITY	45%	56%	45%	42%		48%	100%	49%	45%
	COVERAGE	101%	99%	101%	96%		100%	100%	108%	99%
SAU101869	SeqID		10734					12321	13668	
	IDENTITY		55%					100%	49%	
	COVERAGE		100%					100%	101%	
SAU101876	SeqID							12169		
	IDENTITY							100%		
	COVERAGE							101%		
SAU101881	SeqID	10325					12081	12162		13728
	IDENTITY	42%					41%	100%		42%
	COVERAGE	98%					97%	100%		98%
SAU101882	SeqID	10246	10824			11743	12080	12163		13727
	IDENTITY	33%	30%			31%	31%	100%		33%
	COVERAGE	96%	89%			73%	94%	100%		95%
SAU101890	SeqID	10374		11125			12091	12280		13809
	IDENTITY	53%		49%			47%	100%		53%
	COVERAGE	91%		92%			93%	100%		91%
SAU101891	SeqID	10295	10766	11196	11483		11791	12281	13413	13739
	IDENTITY	63%	72%	62%	60%		58%	100%	67%	64%
	COVERAGE	91%	91%	90%	90%		93%	100%	92%	91%
SAU101893	SeqID	10300	10724			11748	11981	12282	13290	13825
	IDENTITY	46%	47%			41%	35%	100%	40%	43%
	COVERAGE	87%	100%			78%	93%	100%	95%	96%
SAU101904	SeqID	10047	10648	11089	11451		11935	12617	13345	13913
	IDENTITY	34%	38%	33%	31%		31%	100%	34%	33%
	COVERAGE	98%	101%	102%	105%		104%	100%	93%	98%
SAU101907	SeqID	10362	10482	11059	11415		11995	12442	13171	13964
	IDENTITY	75%	90%	76%	74%		73%	100%	75%	74%
	COVERAGE	100%	101%	100%	101%		101%	100%	101%	100%
SAU101909	SeqID	10390		11249	11346		11789	12441		14063
	IDENTITY	41%		32%	29%		36%	100%		32%
	COVERAGE	99%		88%	90%		93%	100%		73%
SAU101910	SeqID	10199					11818	12440		

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
	IDENTITY COVERAGE	56% 97%					60% 97%	100% 100%		
SAU101915	SeqID IDENTITY COVERAGE		10838 26% 90%					12439 100% 100%		
SAU101922	SeqID IDENTITY COVERAGE							12438 100% 100%		
SAU101948	SeqID IDENTITY COVERAGE							12709 100% 100%		
SAU101966	SeqID IDENTITY COVERAGE	10101 45% 88%	10561 31% 91%	11007 32% 92%	11538 37% 86%	11705 43% 88%	11897 45% 88%	12186 100% 101%		14003 45% 88%
SAU101968	SeqID IDENTITY COVERAGE	10106 30% 90%	10568 31% 92%	11242 33% 90%	11480 27% 88%		11965 30% 83%	12187 100% 100%		13998 31% 76%
SAU101991	SeqID IDENTITY COVERAGE		10938 40% 101%					12454 100% 101%	13500 25% 80%	
SAU101995	SeqID IDENTITY COVERAGE	10388 46% 72%	10939 47% 78%	11066 49% 73%	11575 58% 72%	11646 46% 72%	11957 57% 76%	12455 100% 100%	13386 51% 74%	
SAU101996	SeqID IDENTITY COVERAGE	10237 38% 98%	10940 64% 99%	10999 36% 98%	11325 38% 98%		11901 35% 99%	12456 100% 100%	13455 58% 100%	13956 37% 98%
SAU101999	SeqID IDENTITY COVERAGE	10476 48% 97%	10941 61% 98%	11259 46% 98%	11304 49% 91%		12035 51% 96%	12423 100% 100%	13241 64% 97%	13708 48% 97%
SAU102001	SeqID IDENTITY COVERAGE	10258 47% 105%	10628 58% 98%	11134 47% 106%	11489 43% 105%		11787 49% 98%	12424 100% 100%	13636 46% 98%	14088 47% 105%
SAU102002	SeqID IDENTITY COVERAGE							12425 100% 100%		
SAU102003	SeqID IDENTITY COVERAGE							12426 100% 101%		
SAU102006	SeqID IDENTITY			11267 44%	11555 28%			12427 100%	13260 47%	

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
	COVERAGE			92%	74%			101%	105%	
SAU102007	SeqID			11266				12428	13258	
	IDENTITY			60%				100%	61%	
	COVERAGE			97%				100%	97%	
SAU102032	SeqID						12086	12198		13989
	IDENTITY						62%	100%		58%
	COVERAGE						99%	100%		75%
SAU102035	SeqID	10299	10933	10974	11514		11860	12199	13360	13763
	IDENTITY	60%	50%	26%	29%		41%	100%	31%	56%
	COVERAGE	98%	99%	85%	84%		97%	100%	86%	99%
SAU102044	SeqID	10141	10916	11011	11344		12041	12414	13447	13977
	IDENTITY	56%	67%	59%	50%		58%	100%	69%	56%
	COVERAGE	100%	102%	100%	101%		101%	100%	102%	100%
SAU102046	SeqID	10103	10723				12089	12415		14001
	IDENTITY	32%	28%				29%	100%		29%
	COVERAGE	74%	86%				90%	100%		89%
SAU102049	SeqID	10427	10518	10962	11291		11784	12416	13652	13781
	IDENTITY	36%	39%	49%	40%		41%	100%	46%	36%
	COVERAGE	101%	99%	97%	99%		100%	100%	98%	101%
SAU102054	SeqID	10280	10494	11095	11356	11676	11856	12417		13877
	IDENTITY	53%	50%	55%	51%	53%	55%	100%		53%
	COVERAGE	100%	79%	100%	100%	70%	100%	100%		100%
SAU102059	SeqID	10085	10771	11152	11622		11969	12286	13226	14059
	IDENTITY	43%	72%	43%	40%		41%	100%	72%	40%
	COVERAGE	107%	100%	107%	102%		109%	100%	71%	89%
SAU102067	SeqID	10380	10564	11155			11795	12287	13407	13798
	IDENTITY	32%	52%	31%			28%	100%	44%	31%
	COVERAGE	95%	98%	98%			97%	100%	98%	94%
SAU102068	SeqID		10680					12288		
	IDENTITY		29%					100%		
	COVERAGE		101%					100%		
SAU102102	SeqID							12696		
	IDENTITY							100%		
	COVERAGE							100%		
SAU102113	SeqID		10641					12178		
	IDENTITY		34%					100%		
	COVERAGE		110%					101%		

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU102116	SeqID		10642					12180	13480	
	IDENTITY		29%					100%	31%	
	COVERAGE		85%					100%	81%	
SAU102117	SeqID	10016	10643		11604		12027	12181	13481	13947
	IDENTITY	43%	61%		38%		42%	100%	55%	41%
	COVERAGE	101%	100%		102%		103%	100%	100%	85%
SAU102129	SeqID		10859					12176	13400	
	IDENTITY		60%					100%	56%	
	COVERAGE		98%					100%	99%	
SAU102132	SeqID		10760					12177	13304	
	IDENTITY		39%					100%	41%	
	COVERAGE		101%					100%	101%	
SAU102142	SeqID	10154						12457		
	IDENTITY	37%						100%		
	COVERAGE	99%						100%		
SAU102143	SeqID	10154						12458		
	IDENTITY	32%						100%		
	COVERAGE	100%						100%		
SAU102144	SeqID							12459		
	IDENTITY							100%		
	COVERAGE							100%		
SAU102162	SeqID							12462		
	IDENTITY							100%		
	COVERAGE							100%		
SAU102165	SeqID							12460		
	IDENTITY							100%		
	COVERAGE							100%		
SAU102200	SeqID							12665		
	IDENTITY							100%		
	COVERAGE							101%		
SAU102201	SeqID							12666		
	IDENTITY							100%		
	COVERAGE							101%		
SAU102222	SeqID	10447	10797	10994	11358		11986	12511	13192	13818
	IDENTITY	58%	68%	58%	52%		59%	100%	67%	58%
	COVERAGE	99%	99%	99%	99%		99%	100%	99%	99%
SAU102231	SeqID	10323	10798	11193			12020	12527	13561	13731
	IDENTITY	41%	50%	42%			38%	100%	46%	41%
	COVERAGE	94%	93%	89%			94%	100%	99%	94%
SAU102232	SeqID	10100	10799			11687		12530	13562	14004

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
	IDENTITY	36%	40%			35%		100%	42%	34%
	COVERAGE	75%	79%			74%		100%	79%	75%
SAU102233	SeqID		10800					12531	13496	
	IDENTITY		61%					100%	45%	
	COVERAGE		98%					100%	91%	
SAU102241	SeqID	10163	10845					12539		
	IDENTITY	28%	43%					100%		
	COVERAGE	74%	99%					100%		
SAU102242	SeqID	10188	10847	10953	11600	11634	11907	12540	13593	13981
	IDENTITY	47%	72%	44%	38%	47%	47%	100%	70%	47%
	COVERAGE	100%	99%	101%	100%	98%	100%	100%	100%	100%
SAU102246	SeqID	10274	10854	11154	11476		11932	12542	13313	13866
	IDENTITY	59%	74%	60%	54%		62%	100%	81%	58%
	COVERAGE	99%	100%	97%	96%		100%	100%	101%	99%
SAU102247	SeqID							12543	13180	
	IDENTITY							100%	28%	
	COVERAGE							101%	74%	
SAU102252	SeqID	10300	10677			11748	11981	12241	13290	13825
	IDENTITY	39%	48%			39%	37%	100%	43%	41%
	COVERAGE	79%	93%			73%	91%	100%	95%	98%
SAU102256	SeqID	10451			11515			12243	13531	
	IDENTITY	33%			32%			100%	75%	
	COVERAGE	97%			97%			101%	101%	
SAU102257	SeqID	10451			11515			12244	13274	
	IDENTITY	38%			29%			100%	85%	
	COVERAGE	81%			75%			101%	101%	
SAU102259	SeqID		10844					12245	13519	13782
	IDENTITY		65%					100%	72%	25%
	COVERAGE		97%					100%	97%	87%
SAU102260	SeqID	10182	10646			11682		12246	13275	13984
	IDENTITY	34%	37%			32%		100%	83%	32%
	COVERAGE	96%	87%			96%		101%	100%	87%
SAU102261	SeqID	10183	10731					12247	13276	13983
	IDENTITY	25%	30%					100%	74%	26%
	COVERAGE	79%	80%					100%	99%	79%
SAU102262	SeqID	10270	10759			11724		12248	13277	13881
	IDENTITY	35%	39%			31%		100%	82%	34%
	COVERAGE	104%	103%			84%		100%	100%	104%
SAU102264	SeqID	10160					5103	12250		13830
	IDENTITY	45%					44%	100%		43%
	COVERAGE	100%					100%	100%		101%

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU102265	SeqID						11926	12251		
	IDENTITY						37%	100%		
	COVERAGE						100%	100%		
SAU102268	SeqID							12252		
	IDENTITY							100%		
	COVERAGE							101%		
SAU102270	SeqID							12253		
	IDENTITY							100%		
	COVERAGE							100%		
SAU102280	SeqID							12378		
	IDENTITY							100%		
	COVERAGE							100%		
SAU102281	SeqID	10316		11227	11469		12054	12384	13497	13762
	IDENTITY	45%		48%	39%		45%	100%	61%	44%
	COVERAGE	99%		99%	100%		99%	100%	100%	99%
SAU102283	SeqID	10260	10875	10982	11560		11945	12119	13251	14086
	IDENTITY	41%	59%	43%	41%		41%	100%	54%	41%
	COVERAGE	88%	88%	88%	92%		95%	102%	88%	88%
SAU102284	SeqID							12389		
	IDENTITY							100%		
	COVERAGE							100%		
SAU102286	SeqID	10385	10595					12393	13688	
	IDENTITY	37%	42%					100%	39%	
	COVERAGE	104%	99%					100%	101%	
SAU102287	SeqID	10220	10594	11025		11663	11925	12398	13427	13934
	IDENTITY	42%	45%	40%		39%	41%	100%	41%	39%
	COVERAGE	81%	95%	88%		89%	84%	101%	94%	83%
SAU102292	SeqID	10399	10579	11018	11455	11758	12111	12368	13230	14065
	IDENTITY	41%	59%	40%	37%	41%	42%	100%	57%	41%
	COVERAGE	101%	100%	101%	100%	101%	101%	100%	94%	101%
SAU102294	SeqID							12610		
	IDENTITY							100%		
	COVERAGE							100%		
SAU102297	SeqID	10405	10912	11063	11303		12117	12704	13686	14066
	IDENTITY	52%	66%	51%	46%		50%	100%	64%	48%
	COVERAGE	99%	100%	100%	99%		98%	100%	100%	77%
SAU102298	SeqID	10404	10914	11031		11686	12116	12705	13255	
	IDENTITY	36%	62%	33%		35%	28%	100%	54%	
	COVERAGE	72%	99%	87%		89%	87%	100%	100%	
SAU102308	SeqID	10077	10577	11248	11625	11732	12032	12706	13350	13995

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
	IDENTITY	38%	46%	37%	33%	39%	38%	100%	45%	39%
	COVERAGE	88%	100%	86%	87%	88%	90%	100%	100%	95%
SAU102318	SeqID	10122	10795				11806	12707	13242	14039
	IDENTITY	32%	75%				37%	100%	63%	31%
	COVERAGE	90%	97%				72%	100%	97%	89%
SAU102333	SeqID	10057	10550				12102	12657	13316	13829
	IDENTITY	41%	43%				40%	100%	31%	38%
	COVERAGE	96%	97%				96%	100%	90%	95%
SAU102334	SeqID	10056					12101	12658		
	IDENTITY	50%					50%	100%		
	COVERAGE	91%					92%	100%		
SAU102336	SeqID							12659		
	IDENTITY							100%		
	COVERAGE							101%		
SAU102340	SeqID							12660		
	IDENTITY							100%		
	COVERAGE							100%		
SAU102345	SeqID						11843	12655		
	IDENTITY						37%	100%		
	COVERAGE						86%	101%		
SAU102350	SeqID							12433		
	IDENTITY							100%		
	COVERAGE							101%		
SAU102352	SeqID		10657					12434	13426	
	IDENTITY		55%					100%	39%	
	COVERAGE		100%					100%	91%	
SAU102355	SeqID		10726					12435		
	IDENTITY		39%					100%		
	COVERAGE		87%					100%		
SAU102356	SeqID	10227	10669	11203	11546		11805	12436	13324	13960
	IDENTITY	43%	60%	45%	48%		43%	100%	56%	43%
	COVERAGE	95%	100%	95%	98%		95%	100%	99%	95%
SAU102378	SeqID							12437		
	IDENTITY							100%		
	COVERAGE							100%		
SAU102380	SeqID						11870	12265		
	IDENTITY						32%	100%		
	COVERAGE						71%	100%		
SAU102388	SeqID	10367		11157	11386		11808	12267		13802
	IDENTITY	36%		33%	27%		39%	100%		36%
	COVERAGE	96%		90%	101%		99%	100%		96%

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU102389	SeqID IDENTITY COVERAGE	10063 33% 99%	10547 59% 97%	10988 31% 97%			11837 36% 95%	12268 100% 100%	13395 35% 98%	13917 33% 99%
SAU102390	SeqID IDENTITY COVERAGE	10192 41% 100%				11678 26% 97%		12269 100% 101%		13753 42% 100%
SAU102392	SeqID IDENTITY COVERAGE	10131 50% 73%	10500 42% 80%			11673 32% 80%	11951 42% 74%	12270 100% 100%	13474 42% 76%	
SAU102394	SeqID IDENTITY COVERAGE		10807 32% 102%					12271 100% 100%		
SAU102396	SeqID IDENTITY COVERAGE	10243 37% 101%	10809 62% 99%					12272 100% 100%	13467 27% 98%	13794 37% 98%
SAU102401	SeqID IDENTITY COVERAGE							12209 100% 100%		
SAU102417	SeqID IDENTITY COVERAGE		10934 31% 79%				12068 25% 72%	12204 100% 100%		
SAU102418	SeqID IDENTITY COVERAGE					11760 25% 89%		12205 100% 100%		
SAU102420	SeqID IDENTITY COVERAGE							12206 100% 100%		
SAU102422	SeqID IDENTITY COVERAGE	10308 30% 92%				11665 30% 72%	11977 27% 93%	12207 100% 100%		13776 31% 92%
SAU102423	SeqID IDENTITY COVERAGE			11084 27% 94%	11491 25% 92%		12099 27% 93%	12208 100% 100%		
SAU102433	SeqID IDENTITY COVERAGE	10395 42% 101%	10908 51% 100%	11167 39% 100%	11616 37% 73%		11772 52% 72%	12701 100% 100%	13552 44% 98%	
SAU102434	SeqID IDENTITY COVERAGE	10394 26% 99%	10907 44% 100%	11166 28% 99%			11773 26% 100%	12700 100% 100%	13446 40% 101%	13921 27% 99%
SAU102437	SeqID	10393	10952	11057	11330		11774	12695	13420	13920

TABLE VIIA

LOCUSID	Data IDENTITY COVERAGE	*Escherichia coli* 55% 86%	*Enterococcus faecalis* 67% 99%	*Haemophilus influenzae* 57% 88%	*Helicobacter pylori* 51% 86%	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa* 55% 87%	*Staphylococcus aureus* 100% 100%	*Streptococcus pneumoniae* 64% 99%	*Salmonella typhi* 56% 86%
SAU102440	SeqID IDENTITY COVERAGE						12085 41% 98%	12692 100% 100%		13990 39% 99%
SAU102447	SeqID IDENTITY COVERAGE		10947 38% 98%					12685 100% 100%	13436 32% 98%	
SAU102448	SeqID IDENTITY COVERAGE	10460 32% 101%	10946 55% 102%	11049 31% 101%	11332 35% 101%		12073 34% 101%	12681 100% 101%	13435 46% 102%	13860 32% 102%
SAU102449	SeqID IDENTITY COVERAGE	10445 45% 97%	10945 55% 98%	11253 43% 98%	11444 35% 99%	11731 43% 76%	12072 44% 97%	12677 100% 100%	13434 51% 100%	14028 45% 97%
SAU102450	SeqID IDENTITY COVERAGE	10456 47% 100%	10943 70% 100%	11264 46% 100%	11487 43% 99%		12076 47% 99%	12675 100% 100%	13237 68% 100%	13857 47% 100%
SAU102452	SeqID IDENTITY COVERAGE	10420 41% 97%	10748 70% 98%	11143 37% 97%	11478 32% 97%	11629 40% 94%	11820 40% 97%	12674 100% 100%	13265 62% 100%	13783 38% 99%
SAU102453	SeqID IDENTITY COVERAGE		10749 43% 101%				12107 29% 70%	12669 100% 100%	13266 41% 71%	
SAU102460	SeqID IDENTITY COVERAGE	10063 34% 98%	10547 35% 100%	10988 34% 100%			11837 34% 100%	12171 100% 100%	13395 34% 101%	13917 34% 98%
SAU102469	SeqID IDENTITY COVERAGE	10217 58% 98%						12172 100% 100%		
SAU102473	SeqID IDENTITY COVERAGE		10868 28% 88%					12173 100% 100%	13475 35% 83%	
SAU102474	SeqID IDENTITY COVERAGE		10713 26% 96%	10971 26% 105%				12174 100% 100%	13476 26% 89%	14025 27% 97%
SAU102476	SeqID IDENTITY COVERAGE							12175 100% 100%		
SAU102479	SeqID IDENTITY COVERAGE	10306 26% 84%						12405 100% 100%		

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU102480	SeqID	10310	10935				11871	12404		13770
	IDENTITY	28%	33%				30%	100%		27%
	COVERAGE	100%	88%				100%	100%		100%
SAU102481	SeqID	10289	10831					12422		13879
	IDENTITY	26%	29%					100%		26%
	COVERAGE	102%	94%					101%		102%
SAU102485	SeqID	10457	10890					12421	13512	13961
	IDENTITY	28%	53%					100%	56%	60%
	COVERAGE	86%	100%					100%	99%	93%
SAU102486	SeqID	10294	10889	11025				12420	13513	13962
	IDENTITY	36%	38%	27%				100%	42%	37%
	COVERAGE	95%	97%	95%				101%	93%	95%
SAU102487	SeqID							12419		
	IDENTITY							100%		
	COVERAGE							100%		
SAU102498	SeqID	10241	10597	10974	11342	11706	11842	12688	13387	14092
	IDENTITY	36%	35%	35%	33%	37%	38%	100%	35%	36%
	COVERAGE	93%	94%	93%	92%	94%	94%	100%	93%	93%
SAU102502	SeqID						12060	12689		
	IDENTITY						26%	100%		
	COVERAGE						85%	100%		
SAU102503	SeqID						12059	12690		
	IDENTITY						32%	100%		
	COVERAGE						92%	100%		
SAU102526	SeqID							12691		
	IDENTITY							100%		
	COVERAGE							100%		
SAU102527	SeqID	10352	10560	11104	11439		5171	12260	13204	13968
	IDENTITY	54%	74%	55%	56%		58%	100%	75%	54%
	COVERAGE	93%	101%	93%	94%		93%	101%	94%	93%
SAU102531	SeqID		10765					12667		
	IDENTITY		34%					100%		
	COVERAGE		102%					100%		
SAU102541	SeqID	10076	10520	11000	11498		11966	12668	13405	13718
	IDENTITY	41%	49%	38%	37%		44%	100%	45%	41%
	COVERAGE	93%	102%	91%	93%		100%	100%	81%	93%
SAU102551	SeqID			11013	11353		11816	12672	13271	
	IDENTITY			47%	38%		39%	100%	41%	
	COVERAGE			87%	84%		84%	101%	95%	
SAU102554	SeqID		10494					12673	13466	

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
	IDENTITY COVERAGE		47% 99%					100% 100%	44% 98%	
SAU102575	SeqID IDENTITY COVERAGE	10166 28% 98%		11232 29% 91%	11618 35% 99%		11777 30% 96%	12609 100% 100%		13836 27% 98%
SAU102578	SeqID IDENTITY COVERAGE	10459 59% 88%	10948 76% 95%	11050 60% 88%	11420 51% 89%		12074 65% 81%	12411 100% 101%	13503 73% 94%	13859 59% 89%
SAU102584	SeqID IDENTITY COVERAGE							12537 100% 100%		
SAU102585	SeqID IDENTITY COVERAGE							12611 100% 100%		
SAU102593	SeqID IDENTITY COVERAGE		10889 27% 87%					12463 100% 100%	13513 27% 88%	
SAU102598	SeqID IDENTITY COVERAGE	10187 30% 102%		10958 32% 85%		11710 27% 75%	11979 31% 92%	12464 100% 100%		13833 31% 86%
SAU102599	SeqID IDENTITY COVERAGE	10206 36% 89%	10944 26% 76%	10958 30% 93%	11619 30% 73%		11975 33% 79%	12466 100% 100%	13653 32% 77%	13773 32% 101%
SAU102601	SeqID IDENTITY COVERAGE	10273 27% 95%		11076 30% 93%		11722 28% 95%	11931 28% 93%	12467 100% 100%	13256 51% 97%	13867 27% 92%
SAU102602	SeqID IDENTITY COVERAGE	10356 58% 100%	10555 78% 100%	11100 61% 100%	11441 57% 100%	11679 59% 100%	11993 60% 99%	12249 100% 100%	13200 77% 100%	13971 58% 99%
SAU102603	SeqID IDENTITY COVERAGE							12469 100% 100%		
SAU102605	SeqID IDENTITY COVERAGE		10836 47% 96%					12470 100% 100%		
SAU102606	SeqID IDENTITY COVERAGE	10273 27% 95%		11076 30% 92%		11722 27% 95%	11931 25% 93%	12471 100% 100%	13256 50% 97%	13867 26% 94%
SAU102607	SeqID IDENTITY							12472 100%	13579 43%	

TABLE VIIA

LOCUSID	Data COVERAGE	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus* 100%	*Streptococcus pneumoniae* 98%	*Salmonella typhi*
SAU102609	SeqID IDENTITY COVERAGE							12473 100% 100%		
SAU102610	SeqID IDENTITY COVERAGE							12474 100% 100%		
SAU102613	SeqID IDENTITY COVERAGE	10461 26% 97%		11272 28% 95%				12475 100% 100%		13988 26% 97%
SAU102614	SeqID IDENTITY COVERAGE	10211 33% 89%	10600 55% 100%					12476 100% 100%		13927 32% 89%
SAU102615	SeqID IDENTITY COVERAGE	10234 32% 98%	10601 40% 100%			11720 32% 92%	12098 26% 87%	12477 100% 100%		13926 31% 100%
SAU102620	SeqID IDENTITY COVERAGE							12479 100% 100%		
SAU102621	SeqID IDENTITY COVERAGE	10288 61% 100%	10519 62% 101%			11724 58% 81%		12480 100% 100%	13370 59% 101%	13881 61% 100%
SAU102629	SeqID IDENTITY COVERAGE		10885 26% 108%					12481 100% 100%		
SAU102631	SeqID IDENTITY COVERAGE		10522 27% 83%			11657 44% 83%	11841 32% 81%	12712 100% 100%		
SAU102636	SeqID IDENTITY COVERAGE							12650 100% 100%	13696 29% 102%	
SAU102637	SeqID IDENTITY COVERAGE							12651 100% 100%	13697 39% 98%	
SAU102652	SeqID IDENTITY COVERAGE							12653 100% 101%		

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU102658	SeqID	10283	10910	11064			12090	12654	13514	13855
	IDENTITY	45%	54%	42%			39%	100%	49%	41%
	COVERAGE	97%	92%	97%			97%	100%	96%	100%
SAU102663	SeqID	10304	10840	11043	11626		11798	12158	13172	13780
	IDENTITY	43%	58%	44%	34%		45%	100%	56%	41%
	COVERAGE	99%	99%	96%	95%		91%	100%	97%	99%
SAU102669	SeqID	10022	10756	11257			12045	12160	13371	14035
	IDENTITY	42%	26%	43%			41%	100%	54%	41%
	COVERAGE	96%	91%	95%			94%	100%	95%	93%
SAU102671	SeqID	10409		11079	11319	11683	12043	12161	13373	14033
	IDENTITY	34%		32%	44%	35%	56%	100%	69%	33%
	COVERAGE	91%		91%	96%	74%	99%	100%	96%	91%
SAU102674	SeqID	10020		11164		11648	5127	12156		14016
	IDENTITY	55%		54%		46%	55%	100%		53%
	COVERAGE	102%		103%		101%	105%	101%		102%
SAU102693	SeqID	10178	10659		11474		11883	12627	13301	13940
	IDENTITY	53%	74%		38%		49%	100%	61%	49%
	COVERAGE	82%	87%		86%		86%	101%	90%	72%
SAU102694	SeqID	10177	10660	11222	11296		5120	12628	13302	
	IDENTITY	48%	66%	50%	44%		55%	100%	60%	
	COVERAGE	97%	102%	97%	94%		94%	102%	102%	
SAU102725	SeqID	10418	10514	11137	11507		12088	12338	13378	13789
	IDENTITY	40%	72%	39%	38%		37%	100%	66%	40%
	COVERAGE	96%	100%	96%	103%		104%	100%	100%	96%
SAU102764	SeqID	10179	10929	11234	11295		11884	12625	13484	13938
	IDENTITY	44%	67%	42%	41%		42%	100%	63%	43%
	COVERAGE	99%	99%	99%	90%		97%	100%	99%	99%
SAU102812	SeqID		10860					12127	13253	
	IDENTITY		48%					100%	49%	
	COVERAGE		100%					101%	96%	
SAU102870	SeqID	10113	10880					12170	13270	14008
	IDENTITY	29%	35%					100%	29%	28%
	COVERAGE	92%	83%					100%	93%	87%
SAU102880	SeqID	10360	10533	11096	11443	11643	5177	12224	13196	13975
	IDENTITY	60%	82%	61%	57%	61%	58%	100%	85%	61%
	COVERAGE	100%	101%	100%	97%	100%	100%	101%	101%	100%
SAU102881	SeqID	10357	10551	11099			11994	12242	13199	13972
	IDENTITY	38%	69%	37%			38%	100%	54%	38%
	COVERAGE	89%	98%	89%			89%	101%	102%	89%
SAU102883	SeqID	10396		11168	11449		12118	12702	13181	

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
	IDENTITY	63%		70%	60%		65%	100%	76%	
	COVERAGE	86%		88%	86%		86%	102%	90%	
SAU102905	SeqID		10732	11217	11373			12273		
	IDENTITY		31%	26%	38%			100%		
	COVERAGE		92%	80%	87%			100%		
SAU102909	SeqID	10042	10488	11150	11457	11637	11940	12315	13437	13908
	IDENTITY	59%	68%	60%	69%	59%	60%	100%	73%	59%
	COVERAGE	95%	95%	95%	130%	95%	98%	101%	124%	95%
SAU102933	SeqID	10448	10949	10995	11579	11762	11985	12412	13502	13817
	IDENTITY	33%	53%	35%	32%	31%	29%	100%	50%	31%
	COVERAGE	104%	113%	101%	108%	107%	101%	101%	101%	103%
SAU102936	SeqID	10236	10872				11804	12356		13955
	IDENTITY	33%	66%				60%	100%		33%
	COVERAGE	97%	100%				96%	101%		98%
SAU102942	SeqID	10136	10492	11230		11696		12296	13339	13834
	IDENTITY	52%	55%	43%		50%		100%	51%	51%
	COVERAGE	100%	100%	99%		99%		100%	99%	99%
SAU102944	SeqID							12468	13257	
	IDENTITY							100%	42%	
	COVERAGE							100%	99%	
SAU102979	SeqID	10014		10979	11384		11936	12536	13429	13712
	IDENTITY	33%		37%	32%		41%	100%	33%	33%
	COVERAGE	88%		87%	87%		87%	100%	87%	90%
SAU102983	SeqID		10883					12676	13269	
	IDENTITY		28%					100%	27%	
	COVERAGE		70%					100%	76%	
SAU102992	SeqID	10176	10661	11223	11297		11882	12630	13303	13941
	IDENTITY	62%	70%	62%	48%		59%	100%	63%	61%
	COVERAGE	99%	92%	99%	97%		99%	101%	99%	101%
SAU103010	SeqID							12194		
	IDENTITY							100%		
	COVERAGE							100%		
SAU103024	SeqID					11670	12042	12200		
	IDENTITY					44%	26%	100%		
	COVERAGE					89%	72%	101%		
SAU103025	SeqID							12202		
	IDENTITY							100%		
	COVERAGE							100%		
SAU103037	SeqID		10867					12613	13267	
	IDENTITY		27%					100%	26%	
	COVERAGE		99%					101%	86%	

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU103077	SeqID							12408		
	IDENTITY							100%		
	COVERAGE							100%		
SAU103115	SeqID							12508	13469	
	IDENTITY							100%	32%	
	COVERAGE							101%	101%	
SAU103144	SeqID		10936					12663		
	IDENTITY		42%					100%		
	COVERAGE		84%					100%		
SAU103159	SeqID	10110	10783	11134	11489		11787	12670	13411	13994
	IDENTITY	43%	48%	38%	48%		48%	100%	63%	43%
	COVERAGE	115%	100%	112%	117%		98%	100%	101%	116%
SAU103169	SeqID							12678	13239	
	IDENTITY							100%	34%	
	COVERAGE							100%	84%	
SAU103175	SeqID	10157						12687		
	IDENTITY	36%						100%		
	COVERAGE	96%						100%		
SAU103191	SeqID							12465	13332	
	IDENTITY							100%	42%	
	COVERAGE							102%	75%	
SAU103204	SeqID							12499		
	IDENTITY							100%		
	COVERAGE							101%		
SAU103226	SeqID							12713		
	IDENTITY							100%		
	COVERAGE							100%		
SAU103232	SeqID	10368				11704	11848	12697		13803
	IDENTITY	36%				35%	48%	100%		35%
	COVERAGE	102%				98%	101%	101%		102%
SAU200006	SeqID	10033	10639	11192	11553		12007	12723	13479	
	IDENTITY	53%	70%	47%	43%		50%	100%	65%	
	COVERAGE	78%	80%	84%	82%		89%	100%	77%	
SAU200028	SeqID							12694		
	IDENTITY							100%		
	COVERAGE							100%		
SAU200030	SeqID	10372	10553	11056	11447	11672	12092	12745	13449	13807
	IDENTITY	42%	74%	39%	43%	41%	35%	100%	73%	42%
	COVERAGE	84%	98%	84%	93%	86%	93%	102%	95%	84%
SAU200058	SeqID		10621					12719	13327	

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
	IDENTITY COVERAGE		39% 79%					100% 101%	37% 78%	
SAU200059	SeqID IDENTITY COVERAGE	10259 31% 73%	10622 33% 97%	10978 32% 73%			12026 36% 74%	12720 100% 100%	13325 40% 96%	14087 31% 73%
SAU200088	SeqID IDENTITY COVERAGE	10262 51% 82%		10984 56% 91%	11403 57% 93%		11947 45% 93%	12724 100% 102%	13415 68% 100%	14090 49% 82%
SAU200242	SeqID IDENTITY COVERAGE		10712 28% 99%					12734 100% 100%		
SAU200297	SeqID IDENTITY COVERAGE	10109 33% 95%	10756 64% 100%	11257 34% 98%			11982 33% 95%	12739 100% 100%	13371 33% 95%	13996 32% 95%
SAU200345	SeqID IDENTITY COVERAGE							12751 100% 100%		
SAU200392	SeqID IDENTITY COVERAGE	10164 26% 97%	10584 30% 80%	10968 25% 96%	11566 27% 98%		11912 33% 93%	12755 100% 100%		13892 26% 98%
SAU200468	SeqID IDENTITY COVERAGE	10201 78% 74%	10478 75% 75%	11054 62% 74%			12061 36% 81%	12937 100% 101%	13425 76% 75%	13822 78% 74%
SAU200558	SeqID IDENTITY COVERAGE	10039 28% 72%	10728 31% 102%	11277 26% 80%			12046 30% 75%	12777 100% 100%	13423 32% 99%	13904 29% 72%
SAU200561	SeqID IDENTITY COVERAGE							12693 100% 100%		
SAU200564	SeqID IDENTITY COVERAGE	10099 33% 87%		11170 31% 87%	11602 31% 82%	11645 34% 86%	11788 32% 93%	12780 100% 100%		13992 34% 87%
SAU200565	SeqID IDENTITY COVERAGE	10098 32% 97%		11250 34% 96%	11386 35% 98%		11786 39% 97%	12781 100% 100%		13991 33% 97%
SAU200593	SeqID IDENTITY COVERAGE	10435 53% 99%	10613 73% 100%	11038 50% 99%	11412 53% 98%		11998 52% 100%	12784 100% 100%	13397 64% 99%	14046 52% 99%
SAU200628	SeqID IDENTITY COVERAGE	10173 32% 92%	10856 31% 97%					12790 100% 100%	13297 29% 97%	13937 34% 94%

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU200685	SeqID							12801	13185	
	IDENTITY							100%	31%	
	COVERAGE							100%	94%	
SAU200721	SeqID	10208	10582	11015	11541			12797	13681	13922
	IDENTITY	40%	33%	41%	36%			100%	42%	41%
	COVERAGE	92%	79%	99%	94%			100%	100%	94%
SAU200725	SeqID	10118	10761	10966			11780	12933	13632	14020
	IDENTITY	30%	46%	30%			25%	100%	47%	29%
	COVERAGE	98%	100%	97%			98%	100%	100%	98%
SAU200731	SeqID	10283	10822	11064			12090	12342	13514	13855
	IDENTITY	55%	54%	44%			43%	100%	51%	46%
	COVERAGE	99%	100%	98%			98%	100%	100%	99%
SAU200740	SeqID	10318	10554	11225	11393		12056	12798	13695	13760
	IDENTITY	48%	56%	48%	49%		50%	100%	55%	48%
	COVERAGE	86%	102%	86%	73%		87%	100%	93%	86%
SAU200752	SeqID							12809		
	IDENTITY							100%		
	COVERAGE							100%		
SAU200914	SeqID	10383	10714			11747	11927	12837	13431	13788
	IDENTITY	26%	28%			27%	27%	100%	25%	25%
	COVERAGE	96%	98%			79%	90%	100%	91%	90%
SAU200916	SeqID							12838		
	IDENTITY							100%		
	COVERAGE							100%		
SAU200928	SeqID	10439	10627	11036	11571		5179	12815	13646	14042
	IDENTITY	54%	73%	55%	53%		49%	100%	69%	54%
	COVERAGE	86%	99%	87%	86%		102%	100%	100%	86%
SAU200934	SeqID	10212	10780				11964	12842		13835
	IDENTITY	44%	60%				42%	100%		42%
	COVERAGE	72%	93%				82%	100%		88%
SAU200949	SeqID							12846		
	IDENTITY							100%		
	COVERAGE							100%		
SAU200960	SeqID				11500		11886	12431		
	IDENTITY				42%		33%	100%		
	COVERAGE				70%		91%	102%		
SAU200994	SeqID	10036	10497	11270			11865	12935	13310	14054
	IDENTITY	36%	62%	32%			37%	100%	35%	33%
	COVERAGE	100%	101%	100%			102%	100%	73%	99%
SAU201167	SeqID		10779					12887		

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
	IDENTITY		37%					100%		
	COVERAGE		98%					100%		
SAU201168	SeqID		10819					12889	13626	
	IDENTITY		53%					100%	56%	
	COVERAGE		102%					100%	100%	
SAU201184	SeqID	10448	10715	10995	11579		11985	12807	13502	13819
	IDENTITY	40%	52%	35%	37%		37%	100%	53%	32%
	COVERAGE	70%	108%	97%	82%		70%	101%	111%	111%
SAU201197	SeqID	10330	10924	11160	11321		5215	12938	13364	13885
	IDENTITY	58%	66%	60%	53%		58%	100%	63%	58%
	COVERAGE	99%	99%	99%	98%		99%	101%	96%	99%
SAU201225	SeqID		10812	11090				12896	13170	
	IDENTITY		41%	33%				100%	38%	
	COVERAGE		93%	80%				100%	87%	
SAU201236	SeqID	10026	10679	11184	11613		12013	12891	13505	14073
	IDENTITY	32%	29%	33%	33%		34%	100%	30%	32%
	COVERAGE	92%	96%	93%	89%		95%	100%	95%	90%
SAU201301	SeqID							12899		
	IDENTITY							100%		
	COVERAGE							100%		
SAU201333	SeqID	10192				11678		12905		13753
	IDENTITY	41%				28%		100%		41%
	COVERAGE	100%				96%		101%		100%
SAU201375	SeqID						11929	12926		
	IDENTITY						36%	100%		
	COVERAGE						95%	100%		
SAU201380	SeqID	10379	10499		11313		12024	12922		13801
	IDENTITY	34%	25%		26%		25%	100%		25%
	COVERAGE	94%	93%		95%		89%	100%		101%
SAU201381	SeqID	10241	10597	10974	11387	11706	11833	12923	13387	13878
	IDENTITY	68%	59%	46%	44%	56%	57%	100%	52%	64%
	COVERAGE	89%	96%	90%	91%	89%	100%	104%	92%	89%
SAU201403	SeqID							12913		
	IDENTITY							100%		
	COVERAGE							100%		
SAU201469	SeqID							12967		
	IDENTITY							100%		
	COVERAGE							100%		
SAU201486	SeqID							13023		
	IDENTITY							100%		
	COVERAGE							100%		

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU201506	SeqID	10145					11963	12946		13841
	IDENTITY	49%					49%	100%		50%
	COVERAGE	101%					102%	100%		100%
SAU201508	SeqID	10370					11874	12947		13805
	IDENTITY	37%					42%	100%		36%
	COVERAGE	73%					72%	100%		73%
SAU201513	SeqID	10229						12944		
	IDENTITY	29%						100%		
	COVERAGE	71%						101%		
SAU201539	SeqID	10109		11257			5099	12943	13625	13996
	IDENTITY	33%		28%			34%	100%	32%	33%
	COVERAGE	95%		96%			96%	100%	97%	95%
SAU201541	SeqID	10131	10500			11673	11951	12942	13474	
	IDENTITY	50%	39%			33%	41%	100%	41%	
	COVERAGE	71%	74%			77%	73%	100%	73%	
SAU201558	SeqID	10112		11258	11396		11875	12954	13598	14009
	IDENTITY	51%		51%	43%		49%	100%	46%	51%
	COVERAGE	96%		94%	94%		99%	101%	96%	96%
SAU201571	SeqID	10224	10951	11213	11357		11905	12997	13268	13957
	IDENTITY	50%	61%	47%	50%		45%	100%	54%	49%
	COVERAGE	98%	94%	99%	92%		103%	100%	70%	98%
SAU201611	SeqID				11539		11902	12973	13243	
	IDENTITY				38%		48%	100%	58%	
	COVERAGE				73%		99%	100%	95%	
SAU201615	SeqID						11962	12972		
	IDENTITY						40%	100%		
	COVERAGE						72%	100%		
SAU201621	SeqID	10038	10842		11392	11707	12047	12662		13902
	IDENTITY	49%	53%		42%	49%	47%	100%		46%
	COVERAGE	91%	91%		91%	91%	91%	101%		91%
SAU201654	SeqID							12982		
	IDENTITY							100%		
	COVERAGE							101%		
SAU201666	SeqID	10291	10900	11028	11557	11761	11811	12981		13743
	IDENTITY	33%	29%	35%	31%	32%	34%	100%		33%
	COVERAGE	71%	80%	71%	76%	79%	73%	100%		71%
SAU201752	SeqID		10623					12963	13689	
	IDENTITY		45%					100%	40%	
	COVERAGE		89%					100%	92%	
SAU201765	SeqID							12770		

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
	IDENTITY COVERAGE							100% 100%		
SAU201773	SeqID IDENTITY COVERAGE							12996 100% 100%		
SAU201775	SeqID IDENTITY COVERAGE							12996 100% 100%		
SAU201810	SeqID IDENTITY COVERAGE							12769 100% 100%		
SAU201827	SeqID IDENTITY COVERAGE	10258 38% 108%	10783 46% 100%	11134 41% 100%	11310 41% 104%		11787 45% 88%	13002 100% 100%	13411 63% 101%	14088 39% 108%
SAU201929	SeqID IDENTITY COVERAGE							13008 100% 100%		
SAU201952	SeqID IDENTITY COVERAGE							13020 100% 100%		
SAU201971	SeqID IDENTITY COVERAGE							13015 100% 101%		
SAU202006	SeqID IDENTITY COVERAGE							13018 100% 100%		
SAU202039	SeqID IDENTITY COVERAGE				11359 44% 96%			13009 100% 101%	13374 48% 98%	
SAU202126	SeqID IDENTITY COVERAGE	10261 51% 94%	10874 50% 94%	10983 52% 91%	11561 33% 84%		11946 46% 93%	12714 100% 101%	13417 58% 94%	14085 52% 94%
SAU202174	SeqID IDENTITY COVERAGE							12895 100% 101%		
SAU202176	SeqID IDENTITY COVERAGE							12895 100% 101%		
SAU202186	SeqID IDENTITY	10062 28%						12731 100%		

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
	COVERAGE	73%						101%		
SAU202267	SeqID IDENTITY COVERAGE							12727 100% 100%		
SAU202708	SeqID IDENTITY COVERAGE	10428 25% 86%	10913 28% 84%					12855 100% 100%		13735 25% 86%
SAU202736	SeqID IDENTITY COVERAGE	10148 39% 95%	10902 40% 93%	11181 37% 98%	11494 40% 91%	11677 37% 80%	11857 38% 93%	12927 100% 100%	13248 38% 103%	13844 39% 95%
SAU202756	SeqID IDENTITY COVERAGE	10436 44% 97%	10614 63% 92%	11071 47% 86%			5181 44% 92%	13027 100% 100%	13246 53% 91%	14045 40% 97%
SAU202781	SeqID IDENTITY COVERAGE							12718 100% 100%		
SAU202872	SeqID IDENTITY COVERAGE		10656 45% 101%					12866 100% 100%	13670 28% 98%	
SAU202882	SeqID IDENTITY COVERAGE							12848 100% 101%		
SAU202930	SeqID IDENTITY COVERAGE							12871 100% 100%		
SAU202945	SeqID IDENTITY COVERAGE							12868 100% 100%		
SAU202968	SeqID IDENTITY COVERAGE							12886 100% 100%		
SAU203001	SeqID IDENTITY COVERAGE							12894 100% 100%		
SAU203007	SeqID IDENTITY COVERAGE							12893 100% 100%		

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU203196	SeqID							12945		
	IDENTITY							100%		
	COVERAGE							101%		
SAU203293	SeqID							12979		
	IDENTITY							100%		
	COVERAGE							101%		
SAU203296	SeqID				11330			12263		
	IDENTITY				29%			100%		
	COVERAGE				88%			101%		
SAU203524	SeqID							12957		
	IDENTITY							100%		
	COVERAGE							100%		
SAU300110	SeqID	10054	10544			11662		13031	13441	
	IDENTITY	33%	38%			33%		100%	30%	
	COVERAGE	82%	109%			73%		102%	109%	
SAU300131	SeqID	10344	10529	11112	11434		5164	13034	13213	14103
	IDENTITY	45%	71%	44%	52%		47%	100%	60%	44%
	COVERAGE	100%	99%	100%	99%		99%	101%	99%	100%
SAU300156	SeqID							13036		
	IDENTITY							100%		
	COVERAGE							100%		
SAU300191	SeqID		10562		11519		11844	12367	13522	
	IDENTITY		43%		39%		32%	100%	41%	
	COVERAGE		103%		91%		72%	101%	104%	
SAU300572	SeqID				11522			12717		
	IDENTITY				32%			100%		
	COVERAGE				108%			100%		
SAU300617	SeqID		10851					12513	13289	
	IDENTITY		50%					100%	49%	
	COVERAGE		97%					100%	97%	
SAU300713	SeqID		10767				11823	13058		
	IDENTITY		26%				30%	100%		
	COVERAGE		83%				93%	100%		
SAU300719	SeqID	10468	10611	11246	11380	11644	11887	12987	13456	13726
	IDENTITY	46%	34%	34%	30%	30%	40%	100%	33%	34%
	COVERAGE	100%	87%	101%	94%	101%	100%	101%	96%	100%
SAU300732	SeqID	10282	10682					13061	13394	
	IDENTITY	26%	51%					100%	49%	
	COVERAGE	71%	88%					100%	86%	
SAU300825	SeqID		10655					13068	13671	

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
	IDENTITY		52%					100%	41%	
	COVERAGE		97%					100%	97%	
SAU300975	SeqID		10604					12203		
	IDENTITY		30%					100%		
	COVERAGE		72%					102%		
SAU300998	SeqID		10820					13077	13489	
	IDENTITY		40%					100%	40%	
	COVERAGE		99%					102%	99%	
SAU301004	SeqID		10744					13079		
	IDENTITY		40%					100%		
	COVERAGE		101%					100%		
SAU301030	SeqID							13080		
	IDENTITY							100%		
	COVERAGE							100%		
SAU301080	SeqID							13083		
	IDENTITY							100%		
	COVERAGE							100%		
SAU301118	SeqID	10242	10808	11092		11653		12904		13795
	IDENTITY	47%	58%	48%		53%		100%		48%
	COVERAGE	98%	98%	91%		78%		100%		96%
SAU301133	SeqID		10898					13087	13443	
	IDENTITY		39%					100%	30%	
	COVERAGE		96%					100%	93%	
SAU301223	SeqID	10297	10640	10964	11323		11783	13090	13664	13737
	IDENTITY	31%	50%	31%	32%		34%	100%	48%	32%
	COVERAGE	104%	99%	102%	90%		102%	100%	98%	104%
SAU301230	SeqID	10252	10877	11010		11669	11956	13092	13506	13704
	IDENTITY	52%	52%	63%		52%	59%	100%	59%	52%
	COVERAGE	95%	92%	74%		95%	77%	100%	92%	95%
SAU301268	SeqID							13102		
	IDENTITY							100%		
	COVERAGE							100%		
SAU301275	SeqID	10048	10926	11014	11511		11934	13103	13366	13897
	IDENTITY	54%	47%	55%	50%		53%	100%	46%	54%
	COVERAGE	99%	84%	97%	97%		97%	101%	84%	99%
SAU301357	SeqID		10696	11063		11766		12859	13354	
	IDENTITY		74%	32%		33%		100%	76%	
	COVERAGE		98%	80%		93%		101%	100%	
SAU301433	SeqID							12845	13393	
	IDENTITY							100%	26%	
	COVERAGE							100%	91%	

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
SAU301465	SeqID	10210	10663	11214	11554		11921	13013	13418	13925
	IDENTITY	29%	54%	32%	37%		28%	100%	52%	29%
	COVERAGE	100%	104%	104%	100%		101%	100%	103%	102%
SAU301472	SeqID	10157						12925		
	IDENTITY	36%						100%		
	COVERAGE	85%						100%		
SAU301592	SeqID							13137		
	IDENTITY							100%		
	COVERAGE							100%		
SAU301620	SeqID							13140		
	IDENTITY							100%		
	COVERAGE							100%		
SAU301758	SeqID							13156		
	IDENTITY							100%		
	COVERAGE							100%		
SAU301773	SeqID							12729		
	IDENTITY							100%		
	COVERAGE							100%		
SAU301829	SeqID	10107			11309		11857	13162	13248	13935
	IDENTITY	45%			40%		42%	100%	38%	41%
	COVERAGE	98%			97%		96%	100%	106%	99%
SAU301869	SeqID		10732		11373			12903		
	IDENTITY		30%		36%			100%		
	COVERAGE		80%		95%			100%		
SAU301898	SeqID		10932					13057		
	IDENTITY		27%					100%		
	COVERAGE		71%					100%		
SAU302060	SeqID							13042		
	IDENTITY							100%		
	COVERAGE							100%		
SAU302513	SeqID							12851		
	IDENTITY							100%		
	COVERAGE							100%		
SAU302626	SeqID							13105		
	IDENTITY							100%		
	COVERAGE							100%		
SAU302685	SeqID							13113		
	IDENTITY							100%		
	COVERAGE							100%		
SAU302698	SeqID							12725		

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
	IDENTITY COVERAGE							100% 100%		
SAU302699	SeqID IDENTITY COVERAGE							13115 100% 100%		
SAU302805	SeqID IDENTITY COVERAGE				11345 33% 75%			13133 100% 101%		
SAU302901	SeqID IDENTITY COVERAGE							12872 100% 100%		
SAU302931	SeqID IDENTITY COVERAGE							13155 100% 100%		
SAU302950	SeqID IDENTITY COVERAGE							12664 100% 101%		
SAU302956	SeqID IDENTITY COVERAGE	10023 32% 88%		11256 28% 88%		11742 31% 88%	12044 26% 86%	12930 100% 101%	13372 31% 88%	14018 32% 88%

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
ECO100078	Seq ID	10023		11256		11742	12044		13595	14018
	IDENTITY	100%		66%		95%	65%		41%	97%
	COVERAGE	100%		98%		100%	99%		97%	100%
ECO100252	Seq ID	10052			11503		12078	12626		13932
	IDENTITY	100%			41%		48%	38%		40%
	COVERAGE	100%			99%		96%	93%		93%
ECO100397	Seq ID	10064	10781	10993	11499		11959	12884	13614	13915
	IDENTITY	100%	50%	71%	38%		71%	45%	47%	94%
	COVERAGE	100%	96%	100%	97%		97%	97%	97%	99%
ECO100398	Seq ID	10065	10653	10992	11311		11958	12883	13177	13916
	IDENTITY	100%	53%	81%	46%		71%	57%	50%	98%
	COVERAGE	100%	95%	101%	98%		99%	95%	95%	100%
ECO100990	Seq ID	10120				11768				
	IDENTITY	100%				72%				
	COVERAGE	100%				82%				
ECO102108	Seq ID	10214	10608	11129		11757	11852		13627	13931
	IDENTITY	100%	36%	74%		94%	36%		36%	96%
	COVERAGE	100%	96%	100%		100%	97%		97%	73%
ECO102262	Seq ID	10228		11204		11631	12038	13132		13963
	IDENTITY	100%		42%		86%	51%	35%		87%
	COVERAGE	100%		100%		81%	100%	100%		100%
ECO102447	Seq ID	10247					11812			13948
	IDENTITY	100%					47%			99%
	COVERAGE	100%					93%			96%
ECO102539	Seq ID	10258	10628	11134	11489		5192	12526	13636	14088
	IDENTITY	100%	46%	77%	48%		71%	52%	47%	97%
	COVERAGE	100%	101%	100%	100%		100%	100%	82%	100%
ECO102620	Seq ID	10266	10510	11269	11524		11819	12915	13279	14049
	IDENTITY	100%	51%	26%	30%		28%	42%	49%	89%
	COVERAGE	100%	93%	80%	94%		91%	96%	101%	99%

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
ECO103101	Seq ID	10315	10763	11215	11615	11716	12052		13662	13764
	IDENTITY	100%	37%	73%	26%	96%	64%		33%	94%
	COVERAGE	100%	74%	100%	76%	100%	100%		74%	101%
ECO104120	Seq ID	10462	10609	11034		11726	11853			13887
	IDENTITY	100%	29%	34%		87%	28%			37%
	COVERAGE	100%	79%	89%		100%	89%			92%
ECO104268	Seq ID	10475	10607					12370	13166	13707
	IDENTITY	100%	43%					43%	38%	95%
	COVERAGE	100%	92%					99%	92%	100%
KPN100432	Seq ID	10258	10736	11134	11310	11628	5192	12789	13636	14088
	IDENTITY	90%	37%	62%	37%	100%	62%	41%	47%	92%
	COVERAGE	100%	97%	100%	93%	101%	97%	86%	87%	101%
KPN100854	Seq ID	10086	10652	11197	11565	11630	11862		13389	14060
	IDENTITY	35%	29%	26%	27%	100%	42%		32%	35%
	COVERAGE	74%	72%	72%	85%	100%	77%		71%	74%
KPN101022	Seq ID	10475	10607			11642		12370	13166	13707
	IDENTITY	90%	29%			100%		27%	26%	91%
	COVERAGE	100%	77%			101%		101%	79%	101%
KPN101026	Seq ID	10228		11204		11631	12038	13132		13963
	IDENTITY	86%		44%		100%	54%	37%		85%
	COVERAGE	99%		97%		100%	98%	99%		99%
KPN101729	Seq ID			11045	11467	11647	12067	13032		
	IDENTITY			50%	50%	100%	63%	63%		
	COVERAGE			96%	96%	102%	96%	96%		
KPN101750	Seq ID	10052			11503	11652	12078	12626		13918
	IDENTITY	94%			38%	100%	47%	37%		34%
	COVERAGE	100%			103%	100%	100%	96%		100%
KPN102057	Seq ID	10406	10892	11035		11661	11854	13153		13883
	IDENTITY	29%	30%	30%		100%	27%	28%		29%
	COVERAGE	96%	96%	84%		100%	97%	85%		96%
KPN102638	Seq ID	10266	10510		11524	11667		12915	13557	14049
	IDENTITY	77%	51%		29%	100%		44%	50%	77%
	COVERAGE	79%	79%		83%	100%		80%	79%	79%
KPN103882	Seq ID	10315	10763	11215	11454	11716	12052		13662	13764
	IDENTITY	96%	38%	73%	26%	100%	65%		33%	93%
	COVERAGE	100%	74%	100%	77%	100%	100%		74%	101%

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
KPN104183	Seq ID	10065	10653	10992	11490	11650	11958	12883	13177	13916
	IDENTITY	97%	56%	80%	46%	100%	80%	60%	55%	98%
	COVERAGE	85%	74%	89%	86%	100%	85%	74%	74%	85%
KPN104281	Seq ID	10023		11256		11742	12044		13595	14018
	IDENTITY	95%		68%		100%	66%		41%	95%
	COVERAGE	94%		92%		101%	94%		91%	101%
KPN104538	Seq ID	10462	10609	11034		11726	11853			13887
	IDENTITY	87%	27%	35%		100%	29%			38%
	COVERAGE	100%	87%	89%		100%	89%			94%
KPN104716	Seq ID	10214	10608	11129		11757	11852		13627	13931
	IDENTITY	94%	36%	75%		100%	36%		35%	94%
	COVERAGE	100%	96%	100%		100%	97%		97%	73%
KPN105779	Seq ID					11770	12103			
	IDENTITY					100%	28%			
	COVERAGE					101%	99%			
KPN106659	Seq ID	10064	10781	10993		11649	11959	12884	13614	13915
	IDENTITY	90%	58%	72%		100%	74%	51%	58%	91%
	COVERAGE	80%	70%	75%		101%	74%	72%	70%	81%
KPN106840	Seq ID	10259	10857	10978		11664	12026	12182	13691	14087
	IDENTITY	91%	44%	74%		100%	55%	38%	42%	91%
	COVERAGE	100%	101%	98%		100%	99%	94%	92%	100%
KPN107776	Seq ID	10222		11132		11771	11810			13936
	IDENTITY	78%		37%		100%	35%			80%
	COVERAGE	98%		89%		102%	87%			98%
SAU100968	Seq ID	10064	10781	10993	11499		11959	12643	13614	13915
	IDENTITY	45%	62%	44%	36%		46%	100%	62%	46%
	COVERAGE	97%	97%	100%	99%		97%	100%	98%	97%
SAU201145	Seq ID	10064	10781	10993	11499		11959	12884	13614	13915
	IDENTITY	45%	62%	44%	36%		46%	100%	62%	46%
	COVERAGE	97%	97%	100%	99%		97%	100%	98%	97%
SPN101971	Seq ID	10064	10781	10993	11499		11959	12884	13287	13915
	IDENTITY	46%	77%	42%	36%		48%	62%	100%	46%
	COVERAGE	100%	99%	102%	100%		100%	99%	100%	100%
SPN201024	Seq ID	10064	10781	10993	11499		11959	12884	13614	13915
	IDENTITY	46%	77%	43%	36%		49%	62%	100%	46%
	COVERAGE	99%	99%	102%	101%		99%	99%	100%	99%

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
STY000277	Seq ID IDENTITY COVERAGE	10475 95% 100%	10607 44% 91%					12370 42% 99%	13166 38% 96%	13707 100% 100%
STY000625	Seq ID IDENTITY COVERAGE	10421 93% 100%								13784 100% 101%
STY000773	Seq ID IDENTITY COVERAGE	10315 94% 100%	10763 36% 74%	11215 71% 100%	11454 26% 77%	11716 93% 100%	12052 62% 100%		13662 31% 74%	13764 100% 100%
STY001430	Seq ID IDENTITY COVERAGE	10064 94% 100%	10781 49% 96%	10993 70% 101%	11499 37% 98%		11959 70% 98%	12884 46% 97%	13614 47% 98%	13915 100% 100%
STY001433	Seq ID IDENTITY COVERAGE	10065 98% 99%	10653 53% 94%	10992 82% 100%	11311 46% 97%		11958 72% 99%	12883 58% 94%	13177 50% 94%	13916 100% 100%
STY001867	Seq ID IDENTITY COVERAGE	10247 99% 98%					11812 47% 96%			13948 100% 100%
STY002995	Seq ID IDENTITY COVERAGE	10023 97% 94%		11256 67% 92%		11742 95% 101%	12044 65% 94%		13595 40% 91%	14018 100% 101%
STY003357	Seq ID IDENTITY COVERAGE	10228 87% 100%		11204 42% 100%		11631 85% 81%	12038 49% 101%	13132 36% 100%		13963 100% 100%

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
PA0028	SeqID COVERAGE IDENTITY						5053 100% 100%			
PA0120	SeqID COVERAGE IDENTITY	10386 96% 28%		10959 94% 28%			5054 100% 100%			13899 95% 28%
PA0129	SeqID COVERAGE IDENTITY	10265 93% 67%			11388 91% 32%		5055 100% 100%	12844 94% 36%		14048 91% 67%
PA0141	SeqID COVERAGE IDENTITY						5056 100% 100%			
PA0221	SeqID COVERAGE IDENTITY			11250 73% 32%	11386 77% 26%	11701 83% 28%	5057 100% 100%	12781 96% 28%		13778 77% 29%
PA0265	SeqID COVERAGE IDENTITY	10264 100% 81%	10550 97% 35%		11466 99% 26%		5058 100% 100%	12375 96% 38%	13316 91% 34%	14047 100% 80%
PA0321	SeqID COVERAGE IDENTITY						5059 100% 100%			
PA0337	SeqID COVERAGE IDENTITY	10278 99% 43%	10785 73% 35%	11275 72% 37%			5060 100% 100%	12351 72% 36%	13281 73% 35%	13880 99% 42%
PA0353	SeqID COVERAGE IDENTITY	10408 97% 74%		11088 100% 75%	11397 88% 28%	11749 101% 74%	5061 100% 100%	12159 100% 45%	13511 96% 38%	14034 101% 74%
PA0378	SeqID COVERAGE IDENTITY	10324 94% 52%		11130 80% 49%			5062 100% 100%			13730 95% 53%

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
PA0401	SeqID COVERAGE IDENTITY	10078 99% 26%	10858 100% 31%				5063 100% 100%	12993 96% 33%	13560 100% 33%	13723 99% 26%
PA0413	SeqID COVERAGE IDENTITY						5064 100% 100%			
PA0414	SeqID COVERAGE IDENTITY						5065 100% 100%			
PA0419	SeqID COVERAGE IDENTITY	10296 100% 46%	10871 93% 29%	11003 102% 45%		11660 78% 47%	5066 100% 100%	12971 100% 27%	13461 91% 29%	13738 100% 47%
PA0423	SeqID COVERAGE IDENTITY	10123 99% 75%			11424 97% 32%		5067 100% 100%	12708 75% 32%		14038 99% 76%
PA0469	SeqID COVERAGE IDENTITY						5068 100% 100%			
PA0472	SeqID COVERAGE IDENTITY	10471 88% 47%					5069 100% 100%			
PA0506	SeqID COVERAGE IDENTITY						5070 100% 100%			
PA0600	SeqID COVERAGE IDENTITY						5071 100% 100%			
PA0642	SeqID COVERAGE IDENTITY						5072 100% 100%			
PA0650	SeqID COVERAGE IDENTITY	10150 95% 38%		11237 83% 38%	11581 93% 35%		5073 100% 100%	12153 76% 34%	13459 95% 38%	13846 95% 39%
PA0715	SeqID COVERAGE IDENTITY						5074 100% 100%			

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
PA0788	SeqID COVERAGE IDENTITY						5075 100% 100%			
PA0882	SeqID COVERAGE IDENTITY	10233 85% 33%					5076 100% 100%			14013 101% 28%
PA0934	SeqID COVERAGE IDENTITY	10276 101% 47%	10876 93% 40%	11006 101% 46%		11753 80% 37%	5077 100% 100%	12646 92% 39%	13483 94% 38%	
PA0938	SeqID COVERAGE IDENTITY						5078 100% 100%			
PA1019	SeqID COVERAGE IDENTITY	10467 88% 26%	10592 84% 25%	11180 88% 28%			5079 100% 100%			
PA1072	SeqID COVERAGE IDENTITY	10377 100% 62%					5080 100% 100%		13410 71% 36%	13813 100% 61%
PA1115	SeqID COVERAGE IDENTITY						5081 100% 100%			
PA1270	SeqID COVERAGE IDENTITY	10328 76% 26%				11751 79% 25%	5082 100% 100%			13946 76% 26%
PA1301	SeqID COVERAGE IDENTITY	10470 96% 28%					5083 100% 100%			
PA1360	SeqID COVERAGE IDENTITY	10104 92% 63%					5084 100% 100%		13282 97% 25%	14000 92% 63%
PA1365	SeqID COVERAGE IDENTITY						5085 100% 100%			
PA1398	SeqID COVERAGE IDENTITY						5086 100% 100%			

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
PA1462	SeqID COVERAGE IDENTITY		10915 98% 29%		11559 101% 30%		5087 100% 100%			
PA1493	SeqID COVERAGE IDENTITY	10423 92% 56%				11718 97% 49%	5088 100% 100%			13786 92% 56%
PA1547	SeqID COVERAGE IDENTITY				11377 88% 28%		5089 100% 100%			
PA1636	SeqID COVERAGE IDENTITY	10091 101% 37%					5090 100% 100%	12990 96% 26%		13890 81% 32%
PA1684	SeqID COVERAGE IDENTITY					11693 99% 59%	5091 100% 100%			
PA1868	SeqID COVERAGE IDENTITY	10361 82% 35%					5092 100% 100%			
PA1876	SeqID COVERAGE IDENTITY					11746 76% 40%	5093 100% 100%			14036 93% 39%
PA1918	SeqID COVERAGE IDENTITY	10153 79% 31%		11033 82% 28%			5094 100% 100%			13745 79% 28%
PA1986	SeqID COVERAGE IDENTITY						5095 100% 100%			
PA2009	SeqID COVERAGE IDENTITY						5096 100% 100%			
PA2083	SeqID COVERAGE IDENTITY	10253 87% 31%				11692 85% 35%	5097 100% 100%			
PA2101	SeqID COVERAGE IDENTITY	10198 92% 30%					5098 100% 100%		13282 88% 25%	13861 95% 28%

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
PA2108	SeqID	10109		11257			5099	12943	13625	13996
	COVERAGE	96%		95%			100%	94%	90%	96%
	IDENTITY	37%		27%			100%	34%	29%	37%
PA2128	SeqID	10472	10865			11752	5100		13683	13893
	COVERAGE	97%	96%			86%	100%		80%	97%
	IDENTITY	27%	26%			25%	100%		27%	33%
PA2147	SeqID	10181					5101			13985
	COVERAGE	98%					100%			98%
	IDENTITY	60%					100%			59%
PA2196	SeqID	10169					5102			13852
	COVERAGE	99%					100%			99%
	IDENTITY	43%					100%			43%
PA2197	SeqID	10160					5103	12917		13830
	COVERAGE	100%					100%	97%		100%
	IDENTITY	74%					100%	44%		73%
PA2222	SeqID						5104			
	COVERAGE						100%			
	IDENTITY						100%			
PA2313	SeqID						5105			
	COVERAGE						100%			
	IDENTITY						100%			
PA2398	SeqID	10132					5106			
	COVERAGE	86%					100%			
	IDENTITY	35%					100%			
PA2424	SeqID						5107			
	COVERAGE						100%			
	IDENTITY						100%			
PA2461	SeqID						5108			
	COVERAGE						100%			
	IDENTITY						100%			
PA2470	SeqID						5109			13930
	COVERAGE						100%			98%
	IDENTITY						100%			60%
PA2488	SeqID	10189		11172			5110			13980
	COVERAGE	89%		70%			100%			87%
	IDENTITY	32%		28%			100%			29%

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
PA2494	SeqID	10331		11145	11516		5111			13719
	COVERAGE	99%		98%	100%		100%			98%
	IDENTITY	42%		31%	26%		100%			41%
PA2584	SeqID	10195	10899	10967	11504		5112	12330	13442	14058
	COVERAGE	94%	99%	94%	97%		100%	99%	92%	94%
	IDENTITY	60%	37%	57%	38%		100%	41%	42%	58%
PA2594	SeqID	10116				11714	5113			
	COVERAGE	97%				80%	100%			
	IDENTITY	41%				45%	100%			
PA2634	SeqID	10441					5114			
	COVERAGE	74%					100%			
	IDENTITY	28%					100%			
PA2641	SeqID	10226	10566				5115			13959
	COVERAGE	95%	89%				100%			95%
	IDENTITY	80%	37%				100%			80%
PA2671	SeqID						5116			
	COVERAGE						100%			
	IDENTITY						100%			
PA2680	SeqID	10444	10703			11730	5117			14029
	COVERAGE	101%	74%			90%	100%			101%
	IDENTITY	42%	30%			43%	100%			42%
PA2684	SeqID	10384					5118			
	COVERAGE	99%					100%			
	IDENTITY	33%					100%			
PA2726	SeqID						5119			
	COVERAGE						100%			
	IDENTITY						100%			
PA2742	SeqID	10177	10660	11222	11296		5120	12628	13302	
	COVERAGE	91%	97%	84%	89%		100%	97%	97%	
	IDENTITY	64%	50%	67%	47%		100%	55%	45%	
PA3006	SeqID						5121			
	COVERAGE						100%			
	IDENTITY						100%			
PA3011	SeqID	10151	10695	11233	11293		5122	12339		13848
	COVERAGE	100%	79%	100%	86%		100%	75%		100%
	IDENTITY	68%	40%	64%	39%		100%	42%		66%

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
PA3013	SeqID	10416	10494	11095	11525		5123	12461		13750
	COVERAGE	98%	80%	102%	102%		100%	102%		98%
	IDENTITY	64%	39%	43%	41%		100%	40%		64%
PA3041	SeqID	10307					5124			13777
	COVERAGE	88%					100%			88%
	IDENTITY	32%					100%			32%
PA3048	SeqID	10117		10966			5125			14005
	COVERAGE	99%		75%			100%			99%
	IDENTITY	47%		45%			100%			47%
PA3068	SeqID						5126			
	COVERAGE						100%			
	IDENTITY						100%			
PA3121	SeqID	10021		11164	11363		5127	12156		14017
	COVERAGE	99%		99%	81%		100%	99%		99%
	IDENTITY	63%		59%	26%		100%	56%		62%
PA3153	SeqID						5128			
	COVERAGE						100%			
	IDENTITY						100%			
PA3154	SeqID						5129			
	COVERAGE						100%			
	IDENTITY						100%			
PA3160	SeqID						5130			
	COVERAGE						100%			
	IDENTITY						100%			
PA3279	SeqID						5131			
	COVERAGE						100%			
	IDENTITY						100%			
PA3280	SeqID						5132			
	COVERAGE						100%			
	IDENTITY						100%			
PA3374	SeqID	10452					5133			
	COVERAGE	99%					100%			
	IDENTITY	55%					100%			
PA3479	SeqID						5134			
	COVERAGE						100%			
	IDENTITY						100%			

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
PA3484	SeqID COVERAGE IDENTITY						5135 100% 100%			
PA3522	SeqID COVERAGE IDENTITY	10331 98% 41%		11145 99% 30%	11516 99% 26%		5136 100% 100%			13719 99% 40%
PA3643	SeqID COVERAGE IDENTITY	10046 99% 53%		11173 100% 51%	11378 79% 30%		5137 100% 100%			13912 99% 52%
PA3703	SeqID COVERAGE IDENTITY	10194 100% 30%					5138 100% 100%			13751 100% 31%
PA3709	SeqID COVERAGE IDENTITY						5139 100% 100%			
PA3716	SeqID COVERAGE IDENTITY						5140 100% 100%			
PA3764	SeqID COVERAGE IDENTITY	10255 94% 38%		10991 91% 41%			5141 100% 100%			13793 82% 39%
PA3845	SeqID COVERAGE IDENTITY	10277 98% 34%		11200 98% 30%			5142 100% 100%			13882 98% 35%
PA3866	SeqID COVERAGE IDENTITY						5143 100% 100%			
PA3876	SeqID COVERAGE IDENTITY	10144 97% 61%					5144 100% 100%			13840 97% 58%
PA3877	SeqID COVERAGE IDENTITY	10161 98% 28%					5145 100% 100%	12699 92% 27%		13831 98% 27%
PA3931	SeqID COVERAGE IDENTITY	10050 82% 50%	10833 92% 43%	11067 103% 41%	11460 92% 49%	11656 82% 48%	5146 100% 100%	12548 96% 44%	13173 109% 36%	13720 95% 35%

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
PA3984	SeqID COVERAGE IDENTITY	10087 97% 40%		11002 98% 37%		11674 91% 39%	5147 100% 100%			14061 99% 40%
PA4024	SeqID COVERAGE IDENTITY	10244 95% 50%	10700 95% 50%			11736 71% 72%	5148 100% 100%			13951 95% 50%
PA4027	SeqID COVERAGE IDENTITY						5149 100% 100%			
PA4037	SeqID COVERAGE IDENTITY	10102 72% 35%	10563 83% 30%	11194 72% 33%	11527 72% 34%	11725 72% 33%	5150 100% 100%	12958 70% 35%	13296 71% 31%	14002 72% 34%
PA4067	SeqID COVERAGE IDENTITY	10149 98% 44%					5151 100% 100%			13845 99% 43%
PA4070	SeqID COVERAGE IDENTITY	10159 96% 28%					5152 100% 100%			
PA4081	SeqID COVERAGE IDENTITY						5153 100% 100%			
PA4105	SeqID COVERAGE IDENTITY						5154 100% 100%			
PA4124	SeqID COVERAGE IDENTITY						5155 100% 100%			14023 93% 64%
PA4125	SeqID COVERAGE IDENTITY						5156 100% 100%			14024 94% 67%
PA4158	SeqID COVERAGE IDENTITY	10080 98% 61%	10610 95% 38%	11009 88% 31%	11379 83% 28%	11769 74% 61%	5157 100% 100%	12297 96% 50%		13725 97% 61%
PA4237	SeqID COVERAGE IDENTITY	10333 91% 79%	10542 97% 43%	11123 98% 76%	11582 90% 43%		5158 100% 100%	12232 92% 45%	13224 97% 42%	14093 91% 79%

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
PA4242	SeqID	10338	10538	11117	11428		5159			
	COVERAGE	100%	100%	100%	100%		100%			
	IDENTITY	87%	68%	76%	74%		100%			
PA4244	SeqID	10340	10534	11116			5160	12225	13217	14099
	COVERAGE	100%	100%	100%			100%	100%	100%	100%
	IDENTITY	65%	46%	63%			100%	42%	43%	65%
PA4245	SeqID	10341	10532	11115			5161	12223	13216	13812
	COVERAGE	95%	98%	95%			100%	98%	98%	78%
	IDENTITY	56%	42%	58%			100%	42%	40%	33%
PA4246	SeqID	10342	10531	11114	11432		5162	12222	13215	14101
	COVERAGE	100%	92%	99%	88%		100%	99%	92%	100%
	IDENTITY	77%	52%	74%	49%		100%	52%	53%	77%
PA4247	SeqID	10343	10530	11113	11433		5163	12221	13214	14102
	COVERAGE	99%	98%	99%	97%		100%	98%	98%	99%
	IDENTITY	59%	52%	63%	37%		100%	48%	54%	59%
PA4248	SeqID	10344	10529	11112	11434		5164	12220	13571	14103
	COVERAGE	100%	99%	100%	99%		100%	99%	99%	100%
	IDENTITY	62%	49%	66%	50%		100%	43%	47%	62%
PA4249	SeqID	10345	10528	11111	11435		5165	13033	13212	14104
	COVERAGE	99%	102%	99%	100%		100%	102%	102%	99%
	IDENTITY	64%	46%	64%	40%		100%	44%	47%	64%
PA4250	SeqID	10346	10599	11110			5166	12737	13211	14105
	COVERAGE	100%	100%	100%			100%	100%	100%	100%
	IDENTITY	69%	43%	63%			100%	46%	53%	67%
PA4251	SeqID	10347	10527	11109	11589	11654	5167	12218	13210	14106
	COVERAGE	99%	99%	99%	99%	99%	100%	90%	98%	99%
	IDENTITY	69%	58%	68%	48%	69%	100%	63%	61%	68%
PA4252	SeqID	10348	10526	11108			5168	12217	13209	14107
	COVERAGE	97%	92%	94%			100%	98%	92%	96%
	IDENTITY	65%	49%	62%			100%	49%	46%	64%
PA4253	SeqID	10349	10525	11107	11436		5169	12216	13208	14108
	COVERAGE	101%	100%	101%	100%		100%	100%	100%	101%
	IDENTITY	85%	66%	85%	65%		100%	66%	66%	84%
PA4254	SeqID	10350	10524	11106	11437		5170	12215	13207	
	COVERAGE	90%	98%	90%	84%		100%	89%	89%	
	IDENTITY	71%	53%	62%	45%		100%	55%	56%	

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
PA4256	SeqID	10352	10560	11104	11439		5171	12260	13204	13968
	COVERAGE	100%	100%	100%	96%		100%	98%	98%	100%
	IDENTITY	77%	54%	77%	65%		100%	58%	57%	77%
PA4257	SeqID	10353	10559	11103	11592		5172	12259	13203	13969
	COVERAGE	99%	91%	100%	99%		100%	91%	93%	99%
	IDENTITY	74%	61%	72%	55%		100%	57%	59%	74%
PA4258	SeqID	10354	10558	11102	11593		5173	12258	13202	13970
	COVERAGE	100%	91%	100%	95%		100%	99%	91%	100%
	IDENTITY	69%	57%	70%	41%		100%	48%	58%	69%
PA4259	SeqID	10355	10557	11101	11594		5174	12255	13201	
	COVERAGE	100%	101%	100%	99%		100%	100%	100%	
	IDENTITY	82%	70%	84%	61%		100%	63%	67%	
PA4262	SeqID	10358	10549	11098	11595		5175	12240	13198	13973
	COVERAGE	100%	95%	100%	96%		100%	101%	97%	100%
	IDENTITY	68%	45%	72%	36%		100%	46%	44%	68%
PA4263	SeqID	10359		11097	11442		5176	12235	13197	13974
	COVERAGE	99%		98%	91%		100%	103%	99%	99%
	IDENTITY	75%		73%	35%		100%	46%	51%	75%
PA4264	SeqID	10360	10533	11096	11443	11643	5177		13196	13975
	COVERAGE	100%	75%	100%	95%	100%	100%		99%	100%
	IDENTITY	90%	58%	92%	57%	92%	100%		61%	91%
PA4268	SeqID	10365	10479	11062	11409		5178	12445	13231	13967
	COVERAGE	100%	111%	100%	100%		100%	111%	111%	100%
	IDENTITY	89%	70%	89%	75%		100%	68%	70%	89%
PA4269	SeqID	10439	10627	11036	11410		5179	12446	13646	14042
	COVERAGE	100%	100%	100%	109%		100%	101%	99%	100%
	IDENTITY	76%	46%	73%	47%		100%	46%	45%	75%
PA4271	SeqID	10437	10615	11072	11572		5180	12449	13247	14044
	COVERAGE	100%	101%	101%	102%		100%	98%	100%	100%
	IDENTITY	66%	65%	66%	54%		100%	58%	58%	64%
PA4272	SeqID	10436	10614	11071			5181	12450	13246	14045
	COVERAGE	99%	95%	100%			100%	99%	95%	99%
	IDENTITY	68%	40%	66%			100%	39%	42%	65%
PA4316	SeqID	10200		11235			5182			13821
	COVERAGE	88%		90%			100%			91%
	IDENTITY	51%		47%			100%			51%

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
PA4332	SeqID						5183			
	COVERAGE						100%			
	IDENTITY						100%			
PA4347	SeqID					11699	5184			
	COVERAGE					86%	100%			
	IDENTITY					27%	100%			
PA4363	SeqID	10292				11740	5185			13742
	COVERAGE	95%				81%	100%			95%
	IDENTITY	40%				36%	100%			41%
PA4375	SeqID	10072		11145	11516		5186			13719
	COVERAGE	101%		100%	100%		100%			101%
	IDENTITY	33%		45%	28%		100%			33%
PA4413	SeqID	10030	10805	11188	11458		5187	12360	13333	14077
	COVERAGE	90%	94%	92%	93%		100%	93%	98%	90%
	IDENTITY	45%	33%	41%	30%		100%	33%	32%	44%
PA4433	SeqID	10327	10602	11241	11289	11655	5188	12237	13356	13729
	COVERAGE	100%	99%	100%	94%	72%	100%	99%	99%	100%
	IDENTITY	75%	59%	73%	54%	76%	100%	55%	56%	72%
PA4473	SeqID	10463		11195			5189			13986
	COVERAGE	84%		81%			100%			84%
	IDENTITY	39%		37%			100%			39%
PA4506	SeqID	10381	10658	11198	11314	11717	5190	12850	13248	13800
	COVERAGE	99%	77%	98%	79%	91%	100%	99%	81%	99%
	IDENTITY	58%	48%	60%	51%	59%	100%	46%	42%	58%
PA4512	SeqID						5191			13815
	COVERAGE						100%			99%
	IDENTITY						100%			57%
PA4542	SeqID	10258	10628	11134	11489		5192	12526	13421	14088
	COVERAGE	100%	101%	100%	100%		100%	101%	80%	100%
	IDENTITY	71%	47%	70%	49%		100%	52%	46%	71%
PA4576	SeqID						5193			
	COVERAGE						100%			
	IDENTITY						100%			
PA4598	SeqID	10072		11145	11516		5194			13719
	COVERAGE	100%		100%	99%		100%			100%
	IDENTITY	50%		29%	28%		100%			50%

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
PA4665	SeqID COVERAGE IDENTITY	10143 100% 66%	10826 97% 54%	11251 101% 64%	11287 97% 52%	11675 100% 65%	5195 100% 100%	12380 98% 53%	13336 99% 50%	13979 100% 66%
PA4681	SeqID COVERAGE IDENTITY						5196 100% 100%			
PA4709	SeqID COVERAGE IDENTITY						5197 100% 100%			
PA4744	SeqID COVERAGE IDENTITY	10314 107% 58%		11216 98% 58%	11501 93% 39%		5198 100% 100%	12322 78% 48%	13663 91% 43%	13765 107% 58%
PA4771	SeqID COVERAGE IDENTITY	10387 100% 87%		11280 99% 75%			5199 100% 100%		13402 96% 33%	13828 97% 33%
PA4888	SeqID COVERAGE IDENTITY						5200 100% 100%			
PA4942	SeqID COVERAGE IDENTITY	10455 93% 48%		10972 91% 41%			5201 100% 100%			13856 95% 48%
PA4997	SeqID COVERAGE IDENTITY	10115 86% 43%	10619 82% 36%	10960 97% 44%	11394 83% 31%		5202 100% 100%	12501 96% 37%	13458 97% 32%	14006 86% 44%
PA5030	SeqID COVERAGE IDENTITY	10165 90% 64%					5203 100% 100%			
PA5076	SeqID COVERAGE IDENTITY	10197 94% 29%	10796 82% 33%	11176 97% 27%	11383 97% 26%	11694 90% 29%	5204 100% 100%		13292 98% 30%	14057 94% 30%
PA5088	SeqID COVERAGE IDENTITY						5205 100% 100%			
PA5193	SeqID COVERAGE IDENTITY	10373 100% 41%		11126 96% 39%		11709 77% 42%	5206 100% 100%			13808 100% 41%

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
PA5199	SeqID	10375	10596			11711	5207			13810
	COVERAGE	102%	71%			102%	100%			103%
	IDENTITY	33%	26%			34%	100%			32%
PA5207	SeqID			11260	11612		5208	12730		
	COVERAGE			100%	88%		100%	100%		
	IDENTITY			54%	39%		100%	28%		
PA5209	SeqID	10302					5209			13758
	COVERAGE	90%					100%			89%
	IDENTITY	29%					100%			28%
PA5248	SeqID						5210			
	COVERAGE						100%			
	IDENTITY						100%			
PA5299	SeqID						5211			
	COVERAGE						100%			
	IDENTITY						100%			
PA5316	SeqID	10391		11158	11327		5212	12129		
	COVERAGE	100%		99%	78%		100%	73%		
	IDENTITY	82%		79%	39%		100%	40%		
PA5388	SeqID		10503				5213			
	COVERAGE		85%				100%			
	IDENTITY		28%				100%			
PA5393	SeqID						5214			
	COVERAGE						100%			
	IDENTITY						100%			
PA5436	SeqID	10330	10924	11160	11321		5215	13127	13617	13885
	COVERAGE	94%	94%	94%	94%		100%	94%	94%	94%
	IDENTITY	52%	51%	52%	46%		100%	55%	54%	52%
PA5443	SeqID	10413	10788	11199	11452		5216	12489	13643	13748
	COVERAGE	100%	103%	100%	96%		100%	100%	105%	100%
	IDENTITY	64%	38%	56%	35%		100%	38%	39%	64%
PA5490	SeqID						5217			
	COVERAGE						100%			
	IDENTITY						100%			
PA5493	SeqID	10417	10668	11133	11609		5218	12623	13236	
	COVERAGE	102%	102%	102%	102%		100%	100%	101%	
	IDENTITY	62%	37%	58%	31%		100%	38%	37%	

TABLE VIIA

LOCUSID	Data	*Escherichia coli*	*Enterococcus faecalis*	*Haemophilus influenzae*	*Helicobacter pylori*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Salmonella typhi*
PA5507	SeqID COVERAGE IDENTITY	10119 99% 31%					5219 100% 100%			
PA5567	SeqID COVERAGE IDENTITY	10397 99% 67%	10911 103% 39%	11169 99% 64%	11450 100% 33%		5220 100% 100%	12703 102% 34%	13338 101% 37%	13923 99% 67%

TABLE VIIB

PathoSeq Cluster ID	Enterococcus faecalis	Escherichia coli	Pseudomonas aeruginosa	Staphylococcus aureus
15	EFA102326	ECO101796	PAE100280	SAU102515
55	EFA100151	ECO104157	PAE100416	SAU100633
57	EFA100617	ECO102690	PAE105434	SAU100158
1443	EFA100689	ECO103692	PAE101987	SAU100952
1861	EFA101412	ECO103231	PAE104331	SAU101793
2286	EFA103268	ECO103265	PAE104314	SAU101756
2362	EFA101425	ECO100662	PAE101537	SAU101236
2367	EFA101417	ECO103226	PAE103206	SAU101798
2549	EFA101410	ECO103233	PAE104329	SAU101791
3816	EFA101159	ECO103243	PAE104319	SAU100546
3857	EFA101415	ECO103228	PAE103204	SAU101796
4322	EFA101165	ECO103237	PAE104325	SAU100141
4569	EFA100955	ECO103217	PAE103215	SAU101808
4948	EFA101160	ECO103242	PAE104320	SAU100547
5818	EFA100742	ECO103224	PAE103208	SAU101800
8159	EFA101163	ECO103239	PAE104323	SAU100139
8296	EFA101164	ECO103238	PAE104324	SAU100140
8316	EFA101409	ECO103234	PAE104328	SAU101790
8494	EFA103062	ECO103884	PAE104311	SAU100433
8498	EFA101411	ECO103232	PAE104330	SAU101792
8499	EFA101416	ECO103227	PAE103205	SAU101797
7		ECO100071	PAE100837	SAU102674
8	EFA101340		PAE106580	SAU100118
28	EFA101403		PAE102647	SAU100514
41	EFA101753	ECO100148		SAU101565
63	EFA101685		PAE103857	SAU100331
147		ECO100645	PAE100543	SAU100053
548		ECO100377	PAE100604	SAU100747
730		ECO103592	PAE103108	SAU100061
1721	EFA101686	ECO100663		SAU101996
1749	EFA101477	ECO102557		SAU100613
2153	EFA102656	ECO100184		SAU101869
2790	EFA102764	ECO100500		SAU101578
3164	EFA101162	ECO103240		SAU102602
3312	EFA103174		PAE105008	SAU100521
3926	EFA100194	ECO103220		SAU101806
4441	EFA102541		PAE105364	SAU101814
5685	EFA100190	ECO103264		SAU100157
7417	EFA102788	ECO101684		SAU102992
7437	EFA102351	ECO100084		SAU100056
7579		ECO102470	PAE102641	SAU100607
7726	EFA102551	ECO103221		SAU101805
7727	EFA100978	ECO103218		SAU101807
8092		ECO102035	PAE102964	SAU100794
8158	EFA103365		PAE104318	SAU102880
8161	EFA100210		PAE104326	SAU102527
8162	EFA101414		PAE103203	SAU101795

TABLE VIIB

PathoSeq Cluster ID	Enterococcus faecalis	Escherichia coli	Pseudomonas aeruginosa	Staphylococcus aureus
8164	EFA100741	ECO103223		SAU101801
8493	EFA101141		PAE104310	SAU100432
10185	EFA102728	ECO104092		SAU102578
35		ECO102870		SAU100497
44			PAE101061	SAU101143
54			PAE100225	SAU100123
85		ECO101104		SAU101262
184			PAE104901	SAU101366
362	EFA102736			SAU100414
575	EFA101790			SAU100133
579	EFA102110			SAU101624
911			PAE105432	SAU102054
941		ECO101365		SAU102162
952	EFA100615			SAU100964
1084	EFA100289	ECO102819		
1141		ECO102255		SAU102356
1232		ECO100703		SAU101346
1274			PAE103655	SAU102264
1337		ECO102562		SAU100567
1350		ECO100930	PAE103901	
1374		ECO103659		SAU101385
1427	EFA100394			SAU100714
1535		ECO101207		SAU101561
1653	EFA102655			SAU101868
1849	EFA100642			SAU101653
1932	EFA100919			SAU101365
2156	EFA101150			SAU101271
2189		ECO102827	PAE100476	
2238		ECO101436		SAU101092
2338	EFA103038			SAU100518
2411	EFA102802			SAU102246
2501	EFA101121			SAU100996
2974			PAE102537	SAU102125
3027		ECO103959		SAU200242
3239	EFA103021			SAU100300
3244	EFA100399			SAU101891
3386	EFA100426			SAU100886
3447	EFA102915			SAU102112
3460	EFA102023			SAU101399
3682	EFA100740			SAU101802
3771	EFA101540			SAU100275
4424	EFA102542			SAU101815
4654		ECO100488	PAE106184	
5148	EFA100065			SAU100658
7227	EFA100023			SAU100436
7240		ECO103672		SAU101682
7278			PAE101620	SAU301370
7374			PAE106765	SAU103042
7375	EFA102051			SAU103038

PathoSeq Cluster ID	Enterococcus faecalis	Escherichia coli	Pseudomonas aeruginosa	Staphylococcus aureus
7402		ECO103572	PAE106044	
7419		ECO101686		SAU102693
7436	EFA101792			SAU101495
7504	EFA101670			SAU102603
7653	EFA100397			SAU100246
7660	EFA102352	ECO103698		
7719	EFA100756			SAU100496
7725	EFA100739			SAU101803
8040	EFA101736			SAU101197
8058	EFA103571			SAU101242
8077	EFA100200			SAU102231
8082	EFA101080			SAU100199
8116	EFA101963			SAU101028
8122	EFA101737			SAU101198
8141	EFA102780			SAU102433
8177	EFA103348			SAU202126
8178	EFA101022			SAU102283
8181	EFA101541			SAU102909
8191	EFA102022			SAU101398
8234	EFA103033			SAU100745
8237	EFA101682			SAU101266
8238	EFA103295			SAU100963
8251			PAE100662	SAU100596
8300	EFA101120			SAU100944
8539	EFA101339			SAU101400
8610		ECO103661		SAU102298
8874	EFA100748			SAU101155
9028	EFA103210			SAU100731
9996	EFA102338			SAU100175
10234	EFA102186			SAU102933
10248		ECO102828		SAU101220
10297			PAE105229	SAU101381
10328	EFA101079			SAU101547
10345	EFA100295			SAU100659
10365	EFA100641			SAU101655
10393	EFA103504			SAU100961
10402	EFA101833			SAU100880
12426	EFA101413			SAU101794
14277	EFA103081			SAU200088
14330	EFA101161			SAU102881
14455	EFA101424			SAU101771
14520	EFA100211			SAU101789
15660	EFA103375			SAU102694

EXAMPLE 13

Use of Identified Nucleic Acid Sequences as Probes

The sequences from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* described herein, homologous coding nucleic acids, or homologous antisense nucleic acids can be used as probes to obtain the sequence of additional genes of interest from a second cell or microorganism. For example, probes to genes encoding potential bacterial target proteins may be hybridized to nucleic acids from other organisms including other bacteria and higher organisms, to identify homologous sequences in these other organisms. For example, the identified sequences from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi*, homologous coding nucleic acids, or homologous antisense nucleic acids may be used to identify homologous sequences in *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species. In some embodiments of the present invention, the nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* described herein, homologous coding nucleic acids, or homologous antisense nucleic acids may be used to identify homologous nucleic acids from a heterologous organism other than *E. coli*.

Hybridization between the nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis,*

Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori, or *Salmonella typhi* described herein, homologous coding nucleic acids, or homologous antisense nucleic acids and nucleic acids from humans might indicate that the protein encoded by the gene to which the probe corresponds is found in humans and therefore not necessarily an optimal drug target. Alternatively, the gene can be conserved only in bacteria and therefore would be a good drug target for a broad spectrum antibiotic or antimicrobial. These probes can also be used in a known manner to isolate homologous nucleic acids from *Staphylococcus, Salmonella, Klebsiella, Pseudomonas, Enterococcus* or other cells or microorganisms, e.g. by screening a genomic or cDNA library.

Probes derived from the nucleic acid sequences from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* described herein, homologous coding nucleic acids, or homologous antisense nucleic acids, or portions thereof, can be labeled with detectable labels familiar to those skilled in the art, including radioisotopes and non-radioactive labels, to provide a detectable probe. The detectable probe can be single stranded or double stranded and can be made using techniques known in the art, including *in vitro* transcription, nick translation, or kinase reactions. A nucleic acid sample containing a sequence capable of hybridizing to the labeled probe is contacted with the labeled probe. If the nucleic acid in the sample is double stranded, it can be denatured prior to contacting the probe. In some applications, the nucleic acid sample can be immobilized on a surface such as a nitrocellulose or nylon membrane. The nucleic acid sample can comprise nucleic acids obtained from a variety of sources, including genomic DNA, cDNA libraries, RNA, or tissue samples.

Procedures used to detect the presence of nucleic acids capable of hybridizing to the detectable probe include well known techniques such as Southern blotting, Northern blotting, dot blotting, colony hybridization, and plaque hybridization. In some applications, the nucleic acid capable of hybridizing to the labeled probe can be cloned into vectors such as expression vectors, sequencing vectors, or in vitro transcription vectors to facilitate the characterization and expression of the hybridizing nucleic acids in the sample. For example, such techniques can be used to isolate, purify and clone sequences from a genomic library, made from a variety of bacterial species, which are capable of hybridizing to probes made from the sequences identified in Examples 5 and 6.

EXAMPLE 14

Preparation of PCR Primers and Amplification of DNA

The identified *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* genes corresponding directly to or located within the operon of nucleic acid sequences required for proliferation, homologous coding nucleic acids, or homologous antisense nucleic acids or portions thereof can be used to prepare PCR primers for a variety of applications, including the identification or isolation of homologous sequences

from other species. For example, the *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* genes may be used to prepare PCR primers to identify or isolate homologous sequences from *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* or any species falling within the genera of any of the above species. In some embodiments of the present invention, the PCR primers may be used to identify or isolate homologous nucleic acids from an organism other than *E. coli.*

The identified or isolated nucleic acids obtained using the PCR primers may contain part or all of the homologous nucleic acids. Because homologous nucleic acids are related but not identical in sequence, those skilled in the art will often employ degenerate sequence PCR primers. Such degenerate sequence primers are designed based on sequence regions that are either known to be conserved or suspected to be conserved such as conserved coding regions. The successful production of a PCR product using degenerate probes generated from the sequences identified herein would indicate the presence of a homologous gene sequence in the species being screened. The PCR primers are at least 10 nucleotides, and preferably at least 20 nucleotides in length. More preferably, the PCR primers are at least 20-30 nucleotides in length. In some embodiments, the PCR primers can be more than 30 nucleotides in length. It is preferred that the primer pairs have approximately the same G/C ratio, so that melting temperatures are approximately the same. A variety of PCR techniques are familiar to those skilled in the art. For a review of PCR technology, see Molecular Cloning to Genetic Engineering White, B.A. Ed. in **Methods in Molecular Biology** 67: Humana Press, Totowa 1997. When the entire coding sequence of the target gene is known, the 5' and 3' regions of the target gene can be used as the sequence source for PCR probe generation. In each of these PCR procedures, PCR

primers on either side of the nucleic acid sequences to be amplified are added to a suitably prepared nucleic acid sample along with dNTPs and a thermostable polymerase such as Taq polymerase, Pfu polymerase, or Vent polymerase. The nucleic acid in the sample is denatured and the PCR primers are specifically hybridized to complementary nucleic acid sequences in the sample. The hybridized primers are extended. Thereafter, another cycle of denaturation, hybridization, and extension is initiated. The cycles are repeated multiple times to produce an amplified fragment containing the nucleic acid sequence between the primer sites.

EXAMPLE 15

Inverse PCR

The technique of inverse polymerase chain reaction can be used to extend the known nucleic acid sequence identified in Examples 5 and 6. The inverse PCR reaction is described generally by Ochman et al., in Ch. 10 of **PCR Technology: Principles and Applications for DNA Amplification,** (Henry A. Erlich, Ed.) W.H. Freeman and Co. (1992). Traditional PCR requires two primers that are used to prime the synthesis of complementary strands of DNA. In inverse PCR, only a core sequence need be known.

Using the sequences identified as relevant from the techniques taught in Examples 5 and 6 and applied to other species of bacteria, a subset of nucleic sequences are identified that correspond to genes or operons that are required for bacterial proliferation. In species for which a genome sequence is not known, the technique of inverse PCR provides a method for obtaining the gene in order to determine the sequence or to place the probe sequences in full context to the target sequence to which the identified nucleic acid sequence binds.

To practice this technique, the genome of the target organism is digested with an appropriate restriction enzyme so as to create fragments of nucleic acid that contain the identified sequence as well as unknown sequences that flank the identified sequence. These fragments are then circularized and become the template for the PCR reaction. PCR primers are designed in accordance with the teachings of Example 15 and directed to the ends of the identified sequence.. The primers direct nucleic acid synthesis away from the known sequence and toward the unknown sequence contained within the circularized template. After the PCR reaction is complete, the resulting PCR products can be sequenced so as to extend the sequence of the identified gene past the core sequence of the identified exogenous nucleic acid sequence identified. In this manner, the full sequence of each novel gene can be identified. Additionally the sequences of adjacent coding and noncoding regions can be identified.

EXAMPLE 16

Identification of Genes Required for *Escherichia coli* Proliferation

Genes required for proliferation in *Escherichia coli* are identified according to the methods described above.

EXAMPLE 17

Identification of Genes Required for *Neisseria gonorrhoeae* Proliferation

Genes required for proliferation in *Neisseria gonorrhoeae* are identified according to the methods described above.

EXAMPLE 18

Identification of Genes Required for *Salmonella enterica* Proliferation

Genes required for proliferation in *Salmonella enterica* are identified according to the methods described above.

EXAMPLE 19

Identification of Genes Required for *Enterococcus faecium* Proliferation

Genes required for proliferation in *Enterococcus faecium* are identified according to the methods described above.

EXAMPLE 20

Identification of Genes Required for *Haemophilus influenzae* Proliferation

Genes required for proliferation in *Haemophilus influenzae* are identified according to the methods described above.

EXAMPLE 21

Identification of Genes Required for *Aspergillus fumigatus* Proliferation

Genes required for proliferation in *Aspergillus fumigatus* are identified according to the methods described above.

EXAMPLE 22

Identification of Genes Required for *Helicobacter pylori* Proliferation

Genes required for proliferation in *Helicobacter pylori* are identified according to the methods described above.

EXAMPLE 23

Identification of Genes Required for *Mycoplasma pneumoniae* Proliferation

Genes required for proliferation in *Mycoplasma pneumoniae* are identified according to the methods described above.

EXAMPLE 24

Identification of Genes Required for *Plasmodium ovale* Proliferation

Genes required for proliferation in *Plasmodium ovale* are identified according to the methods described above.

EXAMPLE 25

Identification of Genes Required for *Entamoeba histolytica* Proliferation

Genes required for proliferation in *Entamoeba histolytica* are identified according to the methods described above.

EXAMPLE 26

Identification of Genes Required for *Candida albicans* Proliferation

Genes required for proliferation in *Candida albicans* are identified according to the methods described above.

EXAMPLE 27

Identification of Genes Required for *Histoplasma capsulatum* Proliferation

Genes required for proliferation in *Histoplasma capsulatum* are identified according to the methods described above.

EXAMPLE 28

Identification of Genes Required for *Salmonella typhi* Proliferation

Genes required for proliferation in *Salmonella typhi* are identified according to the methods described above.

EXAMPLE 29

Identification of Genes Required for *Salmonella paratyphi* Proliferation

Genes required for proliferation in *Salmonella paratyphi* are identified according to the methods described above.

EXAMPLE 30

Identification of Genes Required for *Salmonella cholerasuis* Proliferation

Genes required for proliferation in *Salmonella cholerasuis* are identified according to the methods described above.

EXAMPLE 31

Identification of Genes Required for *Staphylococcus epidermis* Proliferation

Genes required for proliferation in *Staphylococcus epidermis* are identified according to the methods described above.

EXAMPLE 32

Identification of Genes Required for *Mycobacterium tuberculosis* Proliferation

Genes required for proliferation in *Mycobacterium tuberculosis* are identified according to the methods described above.

EXAMPLE 33

Identification of Genes Required for *Mycobacterium leprae* Proliferation

Genes required for proliferation in *Mycobacterium leprae* are identified according to the methods described above.

EXAMPLE 34

Identification of Genes Required for *Treponema pallidum* Proliferation

Genes required for proliferation in *Treponema pallidum* are identified according to the methods described above.

EXAMPLE 35

Identification of Genes Required for *Bacillus anthracis* Proliferation

Genes required for proliferation in *Bacillus anthracis* are identified according to the methods described above.

EXAMPLE 36

Identification of Genes Required for *Yersinia pestis* Proliferation

Genes required for proliferation in *Yersinia pestis* are identified according to the methods described above.

EXAMPLE 37

Identification of Genes Required for *Clostridium botulinum* Proliferation

Genes required for proliferation in *Clostridium botulinum* are identified according to the methods described above.

EXAMPLE 38

Identification of Genes Required for *Campylobacter jejuni* Proliferation

Genes required for proliferation in *Campylobacter jejuni* are identified according to the methods described above.

EXAMPLE 39

Identification of Genes Required for *Chlamydia trachomatis* Proliferation

Genes required for proliferation in *Chlamydia trachomatis* are identified according to the methods described above.

EXAMPLE 40

Identification of Genes Required for *Staphylococcus aureus* Proliferation

Genes required for proliferation in *Staphylococcus aureus* are identified according to the methods described above.

EXAMPLE 41

Identification of Genes Required for *Salmonella typhimurium* Proliferation

Genes required for proliferation in *Salmonella typhimurium* are identified according to the methods described above.

EXAMPLE 42

Identification of Genes Required for *Klebsiella Pneumoniae* Proliferation

Genes required for proliferation in *Klebsiella Pneumoniae* are identified according to the methods described above.

EXAMPLE 43

Identification of Genes Required for *Pseudomonas aeruginosa* Proliferation

Genes required for proliferation in *Pseudomonas aeruginosa* are identified according to the methods described above.

EXAMPLE 44

Identification of Genes Required for *Enterococcus faecalis* Proliferation

Genes required for proliferation in *Enterococcus faecalis* are identified according to the methods described above.

Use of Isolated Exogenous Nucleic Acid Fragments as Antisense Antibiotics

In addition to using the identified sequences to enable screening of molecule libraries to identify compounds useful to identify antibiotics, antisense nucleic acids complementary to the proliferation-required sequences or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids, or homologous antisense nucleic acids can be used as therapeutic agents. Specifically, the proliferation-required sequences or homolgous coding nucleic acids, or portions therof, in an antisense orientation or homologous antisense nucleic acids can be provided to an individual to inhibit the translation of a bacterial target gene or the processing, folding, or assembly into a protein/RNA complex of a nontranslated RNA.

EXAMPLE 45

Generation of Antisense Therapeutics from Identified Exogenous Sequences

Antisense nucleic acids complementary to the proliferation-required sequences described herein, or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids, or portions thereof, or homologous antisense nucleic acids or portions thereof can be used as antisense therapeutics for the treatment of bacterial infections or simply for inhibition of bacterial growth *in vitro* or *in vivo*. For example, the antisense therapeutics may be used to treat bacterial infections caused by *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* or to inhibit the growth of these organisms. The antisense therapeutics may also be used to treat infections caused by or to inhibit the growth of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae,*

Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis or any species falling within the genera of any of the above species. In some embodiments of the present invention, the antisense therapuetics may be used to treat infection by or inhibit the growth of an organism other than *E. coli.*

The therapy exploits the biological process in cells where genes are transcribed into messenger RNA (mRNA) that is then translated into proteins. Antisense RNA technology contemplates the use of antisense nucleic acids, including antisense oligonucleotides, complementary to a target gene that will bind to its target nucleic acid and decrease or inhibit the expression of the target gene. For example, the antisense nucleic acid may inhibit the translation or transcription of the target nucleic acid. In one embodiment, antisense oligonucleotides can be used to treat and control a bacterial infection of a cell culture containing a population of desired cells contaminated with bacteria. In another embodiment, the antisense oligonucleotides can be used to treat an organism with a bacterial infection.

Antisense oligonucleotides can be synthesized from any of the sequences of the present invention using methods well known in the art. In a preferred embodiment, antisense oligonucleotides are synthesized using artificial means. Uhlmann & Peymann, Chemical Rev. 90:543-584 (1990) review antisense oligonucleotide technology in detail. Modified or unmodified antisense oligonucleotides can be used as therapeutic agents. Modified antisense oligonucleotides are preferred. Modification of the phosphate backbones of the antisense oligonucleotides can be achieved by substituting the internucleotide phosphate residues with methylphosphonates, phosphorothioates, phosphoramidates, and phosphate esters. Nonphosphate internucleotide analogs such as siloxane bridges, carbonate brides, thioester bridges, as well as many others known in the art may also be used. The preparation of certain antisense oligonucleotides with modified internucleotide linkages is described in U.S. Patent No. 5,142,047.

Modifications to the nucleoside units of the antisense oligonucleotides are also contemplated. These modifications can increase the half-life and increase cellular rates of uptake for the oligonucleotides *in vivo*. For example, α-anomeric nucleotide units and modified nucleotides such as 1,2-dideoxy-d-ribofuranose, 1,2-dideoxy-1-phenylribofuranose, and N^4, N^4-ethano-5-methyl-cytosine are contemplated for use in the present invention.

An additional form of modified antisense molecules is found in peptide nucleic acids. Peptide nucleic acids (PNA) have been developed to hybridize to single and double stranded nucleic acids. PNA are nucleic acid analogs in which the entire deoxyribose-phosphate backbone has been exchanged with a chemically different, but structurally homologous, polyamide (peptide) backbone containing 2-aminoethyl glycine units. Unlike DNA, which is highly negatively charged, the PNA backbone is neutral. Therefore, there is much less repulsive energy between complementary strands in a PNA-DNA hybrid than in the comparable DNA-DNA hybrid, and consequently they are much more stable. PNA can hybridize to DNA in either a Watson/Crick or Hoogsteen fashion (Demidov et al., *Proc. Natl. Acad. Sci. U.S.A.* **92**:2637-2641, 1995; Egholm, *Nature* **365**:566-568, 1993; Nielsen et al., *Science* **254**:1497-1500, 1991; Dueholm et al., *New J. Chem.* **21**:19-31, 1997).

Molecules called PNA "clamps" have been synthesized which have two identical PNA sequences joined by a flexible hairpin linker containing three 8-amino-3,6-dioxaoctanoic acid units. When a PNA clamp is mixed with a complementary homopurine or homopyrimidine DNA target sequence, a PNA-DNA-PNA triplex hybrid can form which has been shown to be extremely stable (Bentin et al., *Biochemistry* **35**:8863-8869, 1996; Egholm et al., *Nucleic Acids Res.* **23**:217-222, 1995; Griffith et al., *J. Am. Chem. Soc.* **117**:831-832, 1995).

The sequence-specific and high affinity duplex and triplex binding of PNA have been extensively described (Nielsen et al., *Science* **254**:1497-1500, 1991; Egholm et al., *J. Am. Chem. Soc.* **114**:9677-9678, 1992; Egholm et al., *Nature* **365**:566-568, 1993; Almarsson et al., *Proc. Natl. Acad. Sci. U.S.A.* **90**:9542-9546, 1993; Demidov et al., *Proc. Natl. Acad. Sci. U.S.A.* **92**:2637-2641, 1995). They have also been shown to be resistant to nuclease and protease digestion (Demidov et al., *Biochem. Pharm.* **48**:1010-1313, 1994). PNA has been used to inhibit gene expression (Hanvey et al., *Science* **258**:1481-1485,1992; Nielsen et al., *Nucl. Acids. Res.*, **21**:197-200, 1993; Nielsen et al., *Gene* **149**:139-145, 1994; Good & Nielsen, **Science**, 95: 2073-2076, 1998), to block restriction enzyme activity (Nielsen et al., *supra.*, 1993), to act as an artificial transcription promoter (Mollegaard, *Proc. Natl. Acad. Sci. U.S.A.* **91**:3892-3895, 1994) and as a pseudo restriction endonuclease (Demidov et al., *Nucl. Acids. Res.* **21**:2103-2107, 1993). Recently, PNA has also been shown to have antiviral and antitumoral activity mediated through an antisense mechanism (Norton, *Nature Biotechnol.*, **14**:615-619, 1996; Hirschman et al., *J. Investig. Med.* **44**:347-351, 1996). PNAs have been linked to various peptides in order to promote PNA entry into cells (Basu et al., *Bioconj. Chem.* **8**:481-488, 1997; Pardridge et al., *Proc. Natl. Acad. Sci. U.S.A.* **92**:5592-5596, 1995).

The antisense oligonucleotides contemplated by the present invention can be administered by direct application of oligonucleotides to a target using standard techniques well known in the art. The antisense oligonucleotides can be generated within the target using a plasmid, or a phage. Alternatively, the antisense nucleic acid may be expressed from a sequence in the chromosome of the target cell. For example, a promoter may be introduced into the chromosome of the target cell near the target gene such that the promoter directs the transcription of the antisense nucleic acid.

Alternatively, a nucleic acid containing the antisense sequence operably linked to a promoter may be introduced into the chromosome of the target cell. It is further contemplated that the antisense oligonucleotides are incorporated in a ribozyme sequence to enable the antisense to specifically bind and cleave its target mRNA. For technical applications of ribozyme and antisense oligonucleotides see Rossi et al., **Pharmacol. Ther. 50(2)**:245-254, (1991). The present invention also contemplates using a retron to introduce an antisense oligonucleotide to a cell. Retron technology is exemplified by U.S. Patent No. 5,405,775. Antisense oligonucleotides can also be delivered using liposomes or by electroporation techniques which are well known in the art.

The antisense nucleic acids described above can also be used to design antibiotic compounds comprising nucleic acids which function by intracellular triple helix formation. Triple helix oligonucleotides are used to inhibit transcription from a genome. The antisense nucleic acids can be used to inhibit cell or microorganism gene expression in individuals infected with such microorganisms or containing such cells. Traditionally, homopurine sequences were considered the most useful for triple helix strategies. However, homopyrimidine sequences can also inhibit gene expression. Such homopyrimidine oligonucleotides bind to the major groove at homopurine:homopyrimidine sequences. Thus, both types of sequences based on the sequences from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* or homologous nucleic acids that are required for proliferation are contemplated for use as antibiotic compound templates.

The antisense nucleic acids, such as antisense oligonucleotides, which are complementary to the proliferation-required nucleic acids from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* or to homologous coding nucleic acids, or portions thereof, may be used to induce bacterial cell death or at least bacterial stasis by inhibiting target nucleic acid transcription or translation. Antisense oligonucleotides complementary to about 8 to 40 nucleotides of the proliferation-required nucleic acids described herein or homologous coding nucleic acids have sufficient complementarity to form a duplex with the target sequence under physiological conditions.

To kill bacterial cells or inhibit their growth, the antisense oligonucleotides are applied to the bacteria or to the target cells under conditions that facilitate their uptake. These conditions include sufficient incubation times of cells and oligonucleotides so that the antisense oligonucleotides are taken up by the cells. In one embodiment, an incubation period of 7-10 days is sufficient to kill bacteria in a sample. An optimum concentration of antisense oligonucleotides is selected for use.

The concentration of antisense oligonucleotides to be used can vary depending on the type of bacteria sought to be controlled, the nature of the antisense oligonucleotide to be used, and the

relative toxicity of the antisense oligonucleotide to the desired cells in the treated culture. Antisense oligonucleotides can be introduced to cell samples at a number of different concentrations preferably between 1×10^{-10}M to 1×10^{-4}M. Once the minimum concentration that can adequately control gene expression is identified, the optimized dose is translated into a dosage suitable for use *in vivo*. For example, an inhibiting concentration in culture of 1×10^{-7} translates into a dose of approximately 0.6 mg/kg body weight. Levels of oligonucleotide approaching 100 mg/kg body weight or higher may be possible after testing the toxicity of the oligonucleotide in laboratory animals. It is additionally contemplated that cells from the subject are removed, treated with the antisense oligonucleotide, and reintroduced into the subject. This range is merely illustrative and one of skill in the art are able to determine the optimal concentration to be used in a given case.

After the bacterial cells have been killed or controlled in a desired culture, the desired cell population may be used for other purposes.

EXAMPLE 46

Use of Antisense Oligonucleotides to Treat Contaminated Cell Cultures

The following example demonstrates the ability of an *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* antisense oligonucleotide or an antisense oligonucleotide complementary to a homologous coding nucleic acid, or portions thereof, to act as a bacteriocidal or bacteriostatic agent to treat a contaminated cell culture system. The application of the antisense oligonucleotides of the present invention are thought to inhibit the translation of bacterial gene products required for proliferation. The antisense nucleic acids may also inhibit the transcription, folding or processing of the target RNA.

In one embodiment of the present invention, the antisense oligonucleotide may comprise a phosphorothioate modified nucleic acid comprising at least about 15, at least about 20, at least about 25, at least about 30, at least about 35, at least about 40, or more than 40 consecutive nucleotides of an antisense nucleic acid listed in Table IA. A sense oligodeoxynucleotide complementary to the antisense sequence is synthesized and used as a control. The oligonucleotides are synthesized and purified according to the procedures of Matsukura, et al., Gene 72:343 (1988). The test oligonucleotides are dissolved in a small volume of autoclaved water and added to culture medium to make a 100 micromolar stock solution.

Human bone marrow cells are obtained from the peripheral blood of two patients and cultured according standard procedures well known in the art. The culture is contaminated with *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* or an organism containing a homologous nucleic acid and incubated at 37°C overnight to establish bacterial infection.

The control and antisense oligonucleotide containing solutions are added to the contaminated cultures and monitored for bacterial growth. After a 10 hour incubation of culture and oligonucleotides, samples from the control and experimental cultures are drawn and analyzed for the translation of the target bacterial gene using standard microbiological techniques well known in the art. The target *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* gene or an organism containing the homologous coding nucleic acid is found to be translated in the control culture treated with the control oligonucleotide, however, translation of the target gene in the experimental culture treated with the antisense oligonucleotide of the present invention is not detected or reduced, indicating that the culture is no longer contaminated or is contaminated at a reduced level.

EXAMPLE 47

Use of Antisense Oligonucleotides to Treat Infections

A subject suffering from a *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* infection or an infection with an organism containing a homologous coding nucleic acid is treated with the antisense oligonucleotide preparation above. The antisense oligonucleotide is provided in a pharmaceutically acceptable carrier at a concentration effective to inhibit the transcription or translation of the target nucleic acid. The present subject is treated with a concentration of antisense oligonucleotide sufficient to achieve a blood concentration of about 0.1-100 micromolar. The patient receives daily injections of antisense oligonucleotide to maintain this concentration for a period of 1 week. At the end of the week a blood sample is drawn and analyzed for the presence or absence of the organism using standard techniques well known in the art. There is no detectable evidence of *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* or an organim containing a homologous coding nucleic acid and the treatment is terminated.

Antisense nucleic acids complementary to a homologous coding nucleic acid or a portion thereof may be used in the preceding method to treat individuals infected with an organism containing the homologous coding nucleic acid.

EXAMPLE 48

Preparation and Use of Triple Helix Forming Oligonucleotides

The sequences of proliferation-required nucleic acids, homologous coding nucleic acids, or homologous antisense nucleic acids are scanned to identify 10-mer to 20-mer homopyrimidine or homopurine stretches that could be used in triple-helix based strategies for inhibiting gene expression. Following identification of candidate homopyrimidine or homopurine stretches, their efficiency in

inhibiting gene expression is assessed by introducing varying amounts of oligonucleotides containing the candidate sequences into a population of bacterial cells that normally express the target gene. The oligonucleotides may be prepared on an oligonucleotide synthesizer or they may be purchased commercially from a company specializing in custom oligonucleotide synthesis.

The oligonucleotides can be introduced into the cells using a variety of methods known to those skilled in the art, including but not limited to calcium phosphate precipitation, DEAE-Dextran, electroporation, liposome-mediated transfection or native uptake.

Treated cells are monitored for a reduction in proliferation using techniques such as monitoring growth levels as compared to untreated cells using optical density measurements. The oligonucleotides that are effective in inhibiting gene expression in cultured cells can then be introduced *in vivo* using the techniques well known in that art at a dosage level shown to be effective.

In some embodiments, the natural (beta) anomers of the oligonucleotide units can be replaced with alpha anomers to render the oligonucleotide more resistant to nucleases. Further, an intercalating agent such as ethidium bromide, or the like, can be attached to the 3' end of the alpha oligonucleotide to stabilize the triple helix. For information on the generation of oligonucleotides suitable for triple helix formation see Griffin et al. (**Science 245**:967-971 (1989)).

EXAMPLE 49

Identification of Bacterial Strains from Isolated Specimens by PCR

Classical bacteriological methods for the detection of various bacterial species are time consuming and costly. These methods include growing the bacteria isolated from a subject in specialized medium, cultivation on selective agar medium, followed by a set of confirmation assays that can take from 8 to 10 days or longer to complete. Use of the identified sequences of the present invention provides a method to dramatically reduce the time necessary to detect and identify specific bacterial species present in a sample.

In one exemplary method, bacteria are grown in enriched medium and DNA samples are isolated from specimens of, for example, blood, urine, stool, saliva or central nervous system fluid by conventional methods. A panel of PCR primers based on identified sequences unique to various species or types of cells or microorganisms are then utilized in accordance with Example 12 to amplify DNA of approximately 100-200 nucleotides in length from the specimen. A separate PCR reaction is set up for each pair of PCR primers and after the PCR reaction is complete, the reaction mixtures are assayed for the presence of PCR product. The presence or absence of bacteria from the species to which the PCR primer pairs belong is determined by the presence or absence of a PCR product in the various test PCR reaction tubes.

Although the PCR reaction is used to assay the isolated sample for the presence of various bacterial species, other assays such as the Southern blot hybridization are also contemplated.

Compounds which inhibit the activity or reduce the amount of gene products required for proliferation may be identified using rational drug design. These methods may be used with the

proliferation-required polypeptides described herein or homologous polypeptides. In such methods, the structure of the gene product is determined using methods such as x-ray crystallography, NMR, or computer modelling. Compounds are screened to identify those which have a structure which allows them to interact with the gene product. In some embodiments, the compounds are screened to identify those which have structures which allow them to interact with regions of the gene product which are important for its activity. For example, the compounds may be screened to identify those which have structures which allow them to bind to the active site of the gene product to inhibit its activity. For example, the compound may be a suicide substrate which binds to the active site with high affinity, thereby preventing the gene product from acting on its natural substrate. Alternatively, the compound may bind to a region of the gene product which is involved in complex formation with other biomolecules. In such instances, the activity of the gene product is inhibited by blocking the interaction between the gene product and other members of the complex.

Thus, one embodiment of the present invention comprises a method of using a crystal of the gene products of the present invention and/or a dataset comprising the three-dimensional coordinates obtained from the crystal in a drug-screening assay. The present invention also includes agents (modulators or drugs) that are identified by the methods of the present invention, along with the method of using agents (modulators or drugs) identified by a method of the present invention, for inhibiting the activity of or modulating the amount of an essential gene product. The present invention also includes crystals comprising the gene products of the present invention or portions thereof.

In some embodiments of the present invention, the three-dimensional structure of the polypeptides required for proliferation is determined using X-ray crystallography or NMR. The coordinates of the determined structure are used in computer-assisted modeling programs to identify compounds that bind to and/or modulate the activity or amount of the encoded polypeptide. The method may include the following steps: 1) the generation of high-purity crystals of the encoded recombinant (or endogenous) polypeptide for analysis; 2) determination of the three-dimensional structure of the polypeptide; and, 3) the use of computer-assisted "docking" programs to analyze the molecular interaction of compound structure and the polypeptide (i.e., drug screening).

General methods for performing each of the above steps are described below and are also well known to those of skill in the art. Any method known to those of skill in the art, including those described herein, may be employed for generating the three-dimensional structure for each identified essential gene product and its use in the drug-screening assays.

Crystals of the gene products required for proliferation may be obtained as follows. Under certain conditions, molecules condense from solution into a highly-ordered crystalline lattice, which is defined by a unit cell, the smallest repeating volume of the crystalline array. The contents of such a cell can interact with and diffract certain electromagnetic and particle waves (e.g., X-rays,

neutron beams, electron beams etc.). Due to the symmetry of the lattice, the diffracted waves interact to create a diffraction pattern. By measuring the diffraction pattern, crystallographers are able to reconstruct the three-dimensional structure of the atoms in the crystal.

Any method known to those of skill in the art, including those set forth below, may be employed to prepare high-purity crystals. For example, crystals of the product of the identified essential gene can be grown by a number of techniques including batch crystallization, vapor diffusion (either by sitting drop or hanging drop) and by microdialysis. Seeding of the crystals in some instances is required to obtain X-ray quality crystals. Standard micro and/or macro seeding of crystals may therefore be used. Exemplified below is the hanging-drop vapor diffusion procedure. Hanging drops of an essential gene product (2.5 µl, 10 mg/ml) in 20 mM Tris, pH=8.0, 100 mM NaCl are mixed with an equal amount of reservoir buffer containing 2.7-3.2 M sodium formate and 100 mM Tris buffer, pH=8.0, and kept at 4°C. Crystal showers may appear after 1-2 days with large single crystals growing to full size (0.3 X 0.3 X 0.15 mm^3) within 2-3 weeks. Crystals are harvested in 3.5 M sodium formate and 100 mM Tris buffer, pH=8.0 and cryoprotected in 3.5 M sodium formate, 100 mM Tris buffer, pH=8.0, 10% (w/v) sucrose, and 10% (v/v) ethylene glycol before flash freezing in liquid propane. In some embodiments, the crystal may be obtained using the methods described in U.S. Patent No. 5,869,604. The method involves (a) contacting a mixture containing uncrystallized polypeptides with an exogenous nucleating agent that has an areal lattice match of at least 90.4% to the polypeptide,(b) crystallizing the polypeptides, thereby forming at least one crystal of the polypeptide attached to the nucleating agent, the attached crystal being of a high purity, and at least one polypeptide crystal unattached to the nucleating agent, the unattached crystal being of a lower purity than the attached crystal, and (c) separating the crystal attached to the nucleating agent from the crystal unattached to the nucleating agent. The crystallized polypeptide may also be purified from contaminants by (a) contacting a mixture containing uncrystallized polypeptides and a contaminant with an exogenous nucleating agent that has an areal lattice match of at least 90.4% to the polypeptide, (b) crystallizing the polypeptides, thereby forming at least one crystal of the polypeptide attached to the nucleating agent, the attached crystal being of a high purity and produced in a high yield, and at least one crystal unattached to the nucleating agent, the unattached crystal being of a lower purity than the attached crystal, and (c) separating the crystal attached to the nucleating agent from the crystal unattached to the nucleating agent.

Once a crystal of the present invention is grown, X-ray diffraction data can be collected using methods familiar to those skilled in the art. Therefore, any person with skill in the art of protein crystallization having the present teachings and without undue experimentation can crystallize a large number of alternative forms of the essential gene products from a variety of different organisms, or polypeptides having conservative substitutions in their amino acid sequence.

A crystal lattice is defined by the symmetry of its unit cell and any structural motifs the unit cell contains. For example, there are 230 possible symmetry groups for an arbitrary crystal lattice, while the unit cell of the crystal lattice group may have an arbitrary dimension that depends on the molecules making up the lattice. Biological macromolecules, however, have asymmetric centers and are limited to 65 of the 230 symmetry groups. See Cantor et al., Biophysical Chemistry, Vol. III, W. H. Freeman & Company (1980).

A crystal lattice interacts with electromagnetic or particle waves, such as X-rays or electron beams respectively, that have a wavelength with the same order of magnitude as the spacing between atoms in the unit cell. The diffracted waves are measured as an array of spots on a detection surface positioned adjacent to the crystal. Each spot has a three-dimensional position, hkl, and an intensity, I(hkl), both of which are used to reconstruct the three-dimensional electron density of the crystal with the so-called Electron Density Equation. The Electron Density Equation states that the three-dimensional electron density of the unit cell is the Fourier transform of the structure factors. Thus, in theory, if the structure factors are known for a sufficient number of spots in the detection space, then the three-dimensional electron density of the unit cell could be calculated using the Electron Density Equation.

In some embodiments of the present invention, an image of a crystal of a gene product required for proliferation or a portion thereof is obtained with the aid of a digital computer and the crystal's diffraction pattern as described in U.S. Patent No. 5,353,236. The diffraction pattern contains a plurality of reflections, each having an associated resolution. The image is obtained by (a) converting the diffraction pattern of the crystal into computer usable normalized amplitudes, the pattern being produced with a diffractometer; (b) determining from the diffraction pattern a dimension of a unit cell of the crystal; (c) providing an envelope defining the region of the unit cell occupied by the gene product or portion thereof in the crystal; (d) distributing a collection of scattering bodies within said envelope, the collection of scattering bodies having various arrangements, each of which has an associated pattern of Fourier amplitudes; (e) condensing the collection of scattering bodies to a condensed arrangement that results in a high correlation between a diffraction pattern and the pattern of Fourier amplitudes for said collection of scattering bodies; (f) determining the phase associated with at least one of the reflections of said diffraction pattern from the condensed arrangement of scattering bodies; (g) calculating an electron density distribution of the gene product or portion thereof within the unit cell from the phase determined in procedure f; and (h) displaying a graphical image of the gene product or portion thereof constructed from said electron density distribution.

The crystals of the gene products required for proliferation may be used in drug screening methods such as those described in U.S. Patent Number 6,156,526. Briefly, in such methods, a compound which inhibits the formation of a complex comprising the gene product or a portion thereof is identified as follows. A set of atomic coordinates defining the three-dimensional

structure of a complex including the gene product of interest or a portion thereof are determined. A potential compound that binds to the gene product or a portion thereof involved in complex formation is selected using the atomic coordinates obtained above. The compound is contacted with the gene product or portion thereof and its binding partner(s) in the complex under conditions which would permit the complex to form in the absence of the potential compound. The binding affinity of the gene product or portion thereof for its binding partner(s) is determined and a potential compound is identified as a compound that inhibits the formation of the complex when there is a decrease in the binding affinity of the gene product or portion thereof for its binding partner(s).

In some embodiments of the present invention, the three dimensional structure of the essential gene product is determined and potential agonists and/or potential antagonists are designed with the aid of computer modeling [Bugg et al., Scientific American, Dec.:92-98 (1993); West et al., TIPS, 16:67-74 (1995); Dunbrack et al., Folding & Design, 2:27-42 (1997)].

Computer analysis may be performed with one or more of the computer programs including: QUANTA, CHARMM, INSIGHT, SYBYL, MACROMODEL and ICM [Dunbrack et al., Folding & Design, 2:27-42 (1997)]. In a further embodiment of this aspect of the invention, an initial drug-screening assay is performed using the three-dimensional structure so obtained, preferably along with a docking computer program. Such computer modeling can be performed with one or more Docking programs such as FlexX, DOC, GRAM and AUTO DOCK [Dunbrack et al., Folding & Design, 2:27-42 (1997)].

It should be understood that for each drug screening assay provided herein, a number of iterative cycles of any or all of the steps may be performed to optimize the selection. The drug screening assays of the present invention may use any of a number of means for determining the interaction between an agent or drug and an essential gene product.

In some embodiments of the present invention, a drug can be specifically designed to bind to an essential gene product of the present invention through NMR based methodology. [Shuker et al., pi Science 274:1531-1534 (1996).] NMR spectra may be recorded using devices familiar to those skilled in the art, such as the Varian Unity Plus 500 and unity 600 spectrometers, each equipped with a pulsed-field gradient triple resonance probe as analyzed as described in Bagby et al., [Cell 82:857-867 (1995)]. Sequential resonance assignments of backbone ^{1}H, .^{15}N, and .^{13}C atoms may be made using a combination of triple resonance experiments similar to those previously described [Bagby et al., Biochemistry, 33:2409-2421 (1994a)], except with enhanced sensitivity [Muhandiram and Kay, J. Magn. Reson., 103: 203-216 (1994)] and minimal H_2O saturation [Kay et al., J. Magn. Reson., 109:129-133 (1994)]. Side chain ^{1}H and ^{13}C assignments may be made using HCCH-TOCSY [Bax et al., J. Magn. Reson., 87:620-627 (1990)] experiments with mixing times of 8 ms and 16 ms.in solution but need not be included in structure calculations. Nuclear Overhauser effect (NOE) cross peaks in two-dimensional ^{1}H--^{1}H NOE spectroscopy (NOESY), three-dimensional ^{15}N-edited NOESY-HSQC [Zhang et al., J. Biomol, NMR, 4:845-858 (1994)] and

three-dimensional simultaneous acquisition $^{15}N/^{13}C$-edited NOE [Pascal et al., J. Magn. Reson., 103:197-201 (1994)] spectra may be obtained with 100 ms NOE mixing times. Standard pseudo-atom distance corrections [Wuthrich et al., J. Mol. Biol., 169:949-961 (1983)] may be incorporated to account for center averaging. An additional 0.5 .ANG. may be added to the upper limits for distances involving methyl groups [Wagner et al., J. Mol. Biol., 196:611-639 (1987); Clore et al., Biochemistry, 26:8012-8023 (1987)].

The structures can be calculated using a simulated annealing protocol [Nilges et al., In computational Aspects of the Study of Biological Macromolecules by Nuclear Magnetic Resonance Spectroscopy, J. C. Hoch, F. M. Poulsen, and C. Redfield, eds., New York: Plenum Press, pp. 451-455 (1991)] within X-PLOR [Brunger, X-PLOR Manual, Version 3.1, New Haven, Conn.: Department of Molecular Biophysics and Biochemistry, Yale University (1993)] using the previously described strategy [Bagby et al., Structure, 2:107-122 (1994b)]. Interhelical anges may be calculated using a program written by K. Yap. Accessible surface areas were calculated using the program Naccess, available from Prof. J. Thornton, University College, London.

Compounds capable of reducing the activity or amount of gene products required for cellular proliferation may be identified using the methods described in US Pat. No. 6,077,682. Briefly, the three-dimensional structure of the gene product or portion thereof may be used in a drug screening assay by (a) selecting a potential drug by performing rational drug design with the three-dimensional structure determined from one or more sets of atomic coordinates of the gene product or portion thereof in conjunction with computer modeling; (b) contacting the potential drug with a polypeptide comprising the gene product or portion thereof and (c) detecting the binding of the potential drug with said polypeptide; wherein a potential drug is selected as a drug if the potential drug binds to the polypeptide. In some methods, the three-dimensional structure of the gene product or portion thereof is used in a drug screening assay involving (a) selecting a potential drug by performing structural based rotational drug design with the three-dimensional structure of the gene product or portion thereof; wherein said selecting is performed in conjunction with computer modeling; (b) contacting the potential drug with a polypeptide comprising the gene product or portion thereof in the presence of a substrate of the gene product; wherein in the absence of the potential drug the substrate is acted upon by the gene product; and (c) determining the extent to which the gene product acted upon the substrate; wherein a drug is selected when a decrease in the action of the gene product on the substrate is determined in the presence of the potential drug relative to in its absence. In some embodiments, the preceding method further involves(d) contacting the potential drug with the gene product or portion thereof for NMR analysis; wherein a binding complex forms between the potential drug and said gene product or portion thereof for NMR analysis; wherein the gene product or portion thereof for NMR analysis comprises a conservative amino acid substitution; (e) determining the three-dimensional structure of the binding complex by NMR; and (f) selecting a candidate drug by performing structural based rational drug

design with the three-dimensional structure determined for the binding complex; wherein said selecting is performed in conjunction with computer modeling; (g) contacting the candidate drug with a second polypeptide comprising the gene product or portion thereof in the presence of a substrate of the gene product or portion thereof; wherein in the absence of the candidate drug the substrate is acted upon by the second polypeptide; and (h) determining the amount of action of the second polypeptide on the substrate; wherein a drug is selected when a decrease in the amount of action of the second polypeptide is determined in the presence of the candidate drug relative to in its absence.

Once the three-dimensional structure of a crystal comprising an essential gene product is determined, a potential modulator of its activity, can be examined through the use of computer modeling using a docking program such as FlexX, GRAM, DOCK, or AUTODOCK [Dunbrack et al., 1997, supra], to identify potential modulators. This procedure can include computer fitting of potential modulators to the polypeptide or fragments thereof to ascertain how well the shape and the chemical structure of the potential modulator will bind. Computer programs can also be employed to estimate the attraction, repulsion, and steric hindrance of the two binding partners (e.g., the essential gene product and a potential modulator). Generally the tighter the fit, the lower the steric hindrances, and the greater the attractive forces, the more potent the potential modulator since these properties are consistent with a tighter binding constant. Furthermore, the more specificity in the design of a potential drug the more likely that the drug will not interact as well with other proteins. This will minimize potential side-effects due to unwanted interactions with other proteins.

Compound and compound analogs can be systematically modified by computer modeling programs until one or more promising potential analogs is identified. In addition systematic modification of selected analogs can then be systematically modified by computer modeling programs until one or more potential analogs are identified. Such analysis has been shown to be effective in the development of HIV protease inhibitors [Lam et al., Science 263:380-384 (1994); Wlodawer et al., Ann. Rev. Biochem. 62:543-585 (1993); Appelt, Perspectives in Drug Discovery and Design 1:23-48 (1993); Erickson, Perspectives in Drug Discovery and Design 1:109-128 (1993)]. Alternatively a potential modulator could be obtained by initially screening a random peptide library produced by recombinant bacteriophage for example, [Scott and Smith, Science, 249:386-390 (1990); Cwirla et al., Proc. Natl. Acad. Sci., 87:6378-6382 (1990); Devlin et al., Science, 249:404-406 (1990)]. A peptide selected in this manner would then be systematically modified by computer modeling programs as described above, and then treated analogously to a structural analog.

Example 45 describes computer modelling of the structures of gene products required for proliferation.

EXAMPLE 50

Determination of the Structure of Gene Products Required for Proliferation Using Computer Modelling

Three dimensional models were built by applying computer modelling methods to some of the gene products required for proliferation of *Staphylococcus aureus* using the amino acid sequences of the encoded proteins as follows. Sir Tom Blundell's program COMPOSER as provided by Tripos Associates in their BIOPOLYMER module to SYBYL was used to build the models. Skolnik's method of topology fingerprinting as implemented in Matchmaker was used to score the average mutation free energy. This number is in Boltzmans (units of kT) and should be negative (the more negative, the better the model.

Composer uses a Needleman Wunsch alignment with jumbling to find significant alignments. The reported parameters are percent identity and significance as measured from the jumbling. Those matches which were 30% identical and had a significance greater that 4 on the scale were judged to be good candidates for model building templates. If no three dimensional structures met these criteria, then a BLAST search was conducted against the most recent PDB sequence database. Any significant hits discovered in this manner were then added to the binary protein structure database and the candidate search was repeated in the manner discussed above.

In the next phase, Composer assigned structurally conserved and structurally variable regions and built the backbone structure and then searched the database for structures of the variable loops. These were then spliced in and a model of the protein resulted. Any loops (variable regions) which were unassignable were manually built and refined with a combination of dynamics.

The structure was then refined. Hydrogen atoms were added and a non-active aggregate was defined. 1000pS of dynamics using AMBER ALL-ATOM and Kollman charges are performed. Next a minimization cycle of up 5000 steepest decent steps were performed and then the aggregate was thawed and the process was repeated on the entire protein.

The resulting structure was then validated in MATCHMAKER. The topologicaly scanned free energy determined from empirically derived protein topologies was computed and the average energy/residue is reported in Boltzamans was reported. As this number represents a free energy the more negative it is the more favorable it is.

Sixty six proteins required for the proliferation of *Staphylococcus aureus* were modelled as described above. MATCHMAKER energies were computed for these. The distribution of the models built by class is shown in the table below.

Classification	Number of Models	Average Matchmaker Energy
Acylases	1	-0.10
Dehydrogenases	3	-0.12
DNA Related	3	-0.12
Heat Shock Protein	2	-0.16
Hydrolases	3	-0.16
Isomerases	1	0.05
Ligases	7	-0.07
Lyases	1	-0.09
Membrane Anchored	1	-0.12
Misc	18	-0.21
Oxidoreductases	6	-0.09
Proteases	1	-0.03
Ribosome	3	-0.11
Synthases	4	-0.14
Transferases	6	-0.12

Table 1. Distribution of models built with their MATCHMAKER energies in kT

The validity of the above method was confirmed using FtsZ. In the case of FtsZ, a crystal structure from M. Janeschi was available. Examination of the gross structural features determined using the above modelling showed all of the folds in the correct place, although there were some minor differences from the structure determined by x-ray crystallography.

EXAMPLE 51

FUNCTIONAL COMPLEMENTATION

In another embodiment, gene products whose activities may be complemented by a proliferation-required gene product from *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa, Enterococcus faecalis, Escherichia coli, Enterococcus faecalis, Haemophilus influenzae, Helicobacter pylori,* or *Salmonella typhi* or homologous polypeptides are identified using merodiploids, created by introducing a plasmid or Bacterial Artificial Chromosome into an organism having a mutation in the essential gene which reduces or eliminates the activity of the gene product. In some embodiments, the mutation may be a conditional mutation, such as a temperature sensitive mutation, such that the organism proliferates under permissive conditions but is unable to proliferate under non-permissive conditions in the absence of complementation by the gene on the plasmid or Bacterial Artificial Chromosome. Alternatively, duplications may be constructed as described in Roth et al. (1987) Biosynthesis of Aromatic Amino Acids in Escherichia coli and Salmonella typhimurium, F. C. *Neidhardt,* ed., American Society for Microbiology, publisher, pp. 2269-2270. Such methods are familiar to those skilled in the art.

Table VIII provides a cross reference for SEQ ID NOs. of the nucleotide sequences discussed herein and the SEQ ID NOs. of the polypeptides encoded by these nucleotide.

TABLE VIII

Nucleotide SeqID	Protein SeqID
5916	10013
5917	10014
5918	10015
5919	10016
5920	10017
5921	10018
5922	10019
5923	10020
5924	10021
5925	10022
5926	10023
5927	10024
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5948	10045
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5950	10047
5951	10048
5952	10049
5953	10050
5954	10051
5955	10052
5956	10053
5957	10054
5958	10055
5959	10056
5960	10057
5961	10058
5962	10059

Nucleotide SeqID	Protein SeqID
5963	10060
5964	10061
5965	10062
5966	10063
5967	10064
5968	10065
5969	10066
5970	10067
5971	10068
5972	10069
5973	10070
5974	10071
5975	10072
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5978	10075
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5981	10078
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5984	10081
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5986	10083
5987	10084
5988	10085
5989	10086
5990	10087
5991	10088
5992	10089
5993	10090
5994	10091
5995	10092
5996	10093
5997	10094
5998	10095
5999	10096
6000	10097
6001	10098
6002	10099
6003	10100
6004	10101
6005	10102
6006	10103
6007	10104
6008	10105
6009	10106

TABLE VIII

Nucleotide SeqID	Protein SeqID
6010	10107
6011	10108
6012	10109
6013	10110
6014	10111
6015	10112
6016	10113
6017	10114
6018	10115
6019	10116
6020	10117
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6096	10193
6097	10194
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6099	10196
6100	10197
6101	10198
6102	10199
6103	10200
6104	10201
6105	10202

Nucleotide SeqID	Protein SeqID
6106	10203
6107	10204
6108	10205
6109	10206
6110	10207
6111	10208
6112	10209
6113	10210
6114	10211
6115	10212
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6118	10215
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6126	10223
6127	10224
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6129	10226
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6133	10230
6134	10231
6135	10232
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6137	10234
6138	10235
6139	10236
6140	10237
6141	10238
6142	10239
6143	10240
6144	10241
6145	10242
6146	10243
6147	10244
6148	10245
6149	10246
6150	10247
6151	10248
6152	10249
6153	10250

Nucleotide SeqID	Protein SeqID
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6155	10252
6156	10253
6157	10254
6158	10255
6159	10256
6160	10257
6161	10258
6162	10259
6163	10260
6164	10261
6165	10262
6166	10263
6167	10264
6168	10265
6169	10266
6170	10267
6171	10268
6172	10269
6173	10270
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6176	10273
6177	10274
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6179	10276
6180	10277
6181	10278
6182	10279
6183	10280
6184	10281
6185	10282
6186	10283
6187	10284
6188	10285
6189	10286
6190	10287
6191	10288
6192	10289
6193	10290
6194	10291
6195	10292
6196	10293
6197	10294
6198	10295
6199	10296
6200	10297
6201	10298

Nucleotide SeqID	Protein SeqID
6202	10299
6203	10300
6204	10301
6205	10302
6206	10303
6207	10304
6208	10305
6209	10306
6210	10307
6211	10308
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6217	10314
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6239	10336
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Nucleotide SeqID	Protein SeqID
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6257	10354
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6286	10383
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6288	10385
6289	10386
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6293	10390
6294	10391
6295	10392
6296	10393
6297	10394

Nucleotide SeqID	Protein SeqID
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6300	10397
6301	10398
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6303	10400
6304	10401
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6343	10440
6344	10441
6345	10442

Nucleotide SeqID	Protein SeqID
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6393	10490

TABLE VIII

Nucleotide SeqID	Protein SeqID
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TABLE VIII

Nucleotide SeqID	Protein SeqID
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Nucleotide SeqID	Protein SeqID
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Nucleotide SeqID	Protein SeqID
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TABLE VIII

Nucleotide SeqID	Protein SeqID
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Nucleotide SeqID	Protein SeqID
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TABLE VIII

Nucleotide SeqID	Protein SeqID
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Nucleotide SeqID	Protein SeqID
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Nucleotide SeqID	Protein SeqID
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Nucleotide SeqID	Protein SeqID
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Nucleotide SeqID	Protein SeqID
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Nucleotide SeqID	Protein SeqID
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TABLE VIII

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8362	12460
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8366	12464
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8368	12466
8369	12467
8370	12468
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8374	12472
8375	12473
8376	12474
8377	12475
8378	12476
8379	12477
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8381	12479
8382	12480
8383	12481
8384	12482

Nucleotide SeqID	Protein SeqID
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8401	12499
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Nucleotide SeqID	Protein SeqID
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Nucleotide SeqID	Protein SeqID
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TABLE VIII

Nucleotide SeqID	Protein SeqID
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8562	12660
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8566	12664
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8568	12666
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8570	12668
8571	12669
8572	12670
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8574	12672
8575	12673
8576	12674

Nucleotide SeqID	Protein SeqID
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TABLE VIII

Nucleotide SeqID	Protein SeqID
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TABLE VIII

Nucleotide SeqID	Protein SeqID
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Nucleotide SeqID	Protein SeqID
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Nucleotide SeqID	Protein SeqID
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TABLE VIII

Nucleotide SeqID	Protein SeqID
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8955	13053
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8958	13056
8959	13057
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Nucleotide SeqID	Protein SeqID
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Nucleotide SeqID	Protein SeqID
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Nucleotide SeqID	Protein SeqID
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Nucleotide SeqID	Protein SeqID
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Nucleotide SeqID	Protein SeqID
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Nucleotide SeqID	Protein SeqID
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TABLE VIII

Nucleotide SeqID	Protein SeqID
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Nucleotide SeqID	Protein SeqID
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Nucleotide SeqID	Protein SeqID
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Nucleotide SeqID	Protein SeqID
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TABLE VIII

Nucleotide SeqID	Protein SeqID
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Nucleotide SeqID	Protein SeqID
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Nucleotide SeqID	Protein SeqID
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9632	13730

Nucleotide SeqID	Protein SeqID
9633	13731
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9661	13759
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9663	13761
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9665	13763
9666	13764
9667	13765
9668	13766
9669	13767
9670	13768
9671	13769
9672	13770
9673	13771
9674	13772
9675	13773
9676	13774
9677	13775
9678	13776
9679	13777
9680	13778

Nucleotide SeqID	Protein SeqID
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9727	13825
9728	13826

Nucleotide SeqID	Protein SeqID
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9774	13872
9775	13873
9776	13874

Nucleotide SeqID	Protein SeqID
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9778	13876
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9792	13890
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9803	13901
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9823	13921
9824	13922

Nucleotide SeqID	Protein SeqID
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9866	13964
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9868	13966
9869	13967
9870	13968
9871	13969
9872	13970

Nucleotide SeqID	Protein SeqID	Nucleotide SeqID	Protein SeqID
9873	13971	9921	14019
9874	13972	9922	14020
9875	13973	9923	14021
9876	13974	9924	14022
9877	13975	9925	14023
9878	13976	9926	14024
9879	13977	9927	14025
9880	13978	9928	14026
9881	13979	9929	14027
9882	13980	9930	14028
9883	13981	9931	14029
9884	13982	9932	14030
9885	13983	9933	14031
9886	13984	9934	14032
9887	13985	9935	14033
9888	13986	9936	14034
9889	13987	9937	14035
9890	13988	9938	14036
9891	13989	9939	14037
9892	13990	9940	14038
9893	13991	9941	14039
9894	13992	9942	14040
9895	13993	9943	14041
9896	13994	9944	14042
9897	13995	9945	14043
9898	13996	9946	14044
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9901	13999	9949	14047
9902	14000	9950	14048
9903	14001	9951	14049
9904	14002	9952	14050
9905	14003	9953	14051
9906	14004	9954	14052
9907	14005	9955	14053
9908	14006	9956	14054
9909	14007	9957	14055
9910	14008	9958	14056
9911	14009	9959	14057
9912	14010	9960	14058
9913	14011	9961	14059
9914	14012	9962	14060
9915	14013	9963	14061
9916	14014	9964	14062
9917	14015	9965	14063
9918	14016	9966	14064
9919	14017	9967	14065
9920	14018	9968	14066

TABLE VIII

Nucleotide SeqID	Protein SeqID
9969	14067
9970	14068
9971	14069
9972	14070
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9982	14080
9983	14081
9984	14082
9985	14083
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9990	14088
9991	14089
9992	14090
9993	14091
9994	14092
9995	14093
9996	14094
9997	14095
9998	14096
9999	14097
10000	14098
10001	14099
10002	14100
10003	14101
10004	14102
10005	14103
10006	14104
10007	14105
10008	14106
10009	14107
10010	14108
10011	14109
10012	14110

SeqID	Clone name	Organism
8	E3M10000001A02	*Enterococcus faecalis*
9	E3M10000001A06	*Enterococcus faecalis*
10	E3M10000001B01	*Enterococcus faecalis*
11	E3M10000001B02	*Enterococcus faecalis*
12	E3M10000001B05	*Enterococcus faecalis*
13	E3M10000001B06	*Enterococcus faecalis*
14	E3M10000001B08	*Enterococcus faecalis*
15	E3M10000001B10	*Enterococcus faecalis*
16	E3M10000001C02	*Enterococcus faecalis*
17	E3M10000001C09	*Enterococcus faecalis*
18	E3M10000001D02	*Enterococcus faecalis*
19	E3M10000001D04	*Enterococcus faecalis*
20	E3M10000001D05	*Enterococcus faecalis*
21	E3M10000001D09	*Enterococcus faecalis*
22	E3M10000001E01	*Enterococcus faecalis*
23	E3M10000001E02	*Enterococcus faecalis*
24	E3M10000001E03	*Enterococcus faecalis*
25	E3M10000001E04	*Enterococcus faecalis*
26	E3M10000001E08	*Enterococcus faecalis*
27	E3M10000001E09	*Enterococcus faecalis*
28	E3M10000001F02	*Enterococcus faecalis*
29	E3M10000001F04	*Enterococcus faecalis*
30	E3M10000001F06	*Enterococcus faecalis*
31	E3M10000001F07	*Enterococcus faecalis*
32	E3M10000001G02	*Enterococcus faecalis*
33	E3M10000001G03	*Enterococcus faecalis*
34	E3M10000001G04	*Enterococcus faecalis*
35	E3M10000001G05	*Enterococcus faecalis*
36	E3M10000001H02	*Enterococcus faecalis*
37	E3M10000001H03	*Enterococcus faecalis*
38	E3M10000001H04	*Enterococcus faecalis*
39	E3M10000004A04	*Enterococcus faecalis*
40	E3M10000004C03	*Enterococcus faecalis*
41	E3M10000004D01	*Enterococcus faecalis*
42	E3M10000004D02	*Enterococcus faecalis*
43	E3M10000004D10	*Enterococcus faecalis*
44	E3M10000004E11	*Enterococcus faecalis*
45	E3M10000004F08	*Enterococcus faecalis*
46	E3M10000004F10	*Enterococcus faecalis*
47	E3M10000004G01	*Enterococcus faecalis*
48	E3M10000004H11	*Enterococcus faecalis*
49	E3M10000005A07	*Enterococcus faecalis*
50	E3M10000005B01	*Enterococcus faecalis*
51	E3M10000005B08	*Enterococcus faecalis*
52	E3M10000005C01	*Enterococcus faecalis*
53	E3M10000005C03	*Enterococcus faecalis*
54	E3M10000005C04	*Enterococcus faecalis*
55	E3M10000005D03	*Enterococcus faecalis*

TABLE IA

SeqID	Clone name	Organism
56	E3M10000005D04	*Enterococcus faecalis*
57	E3M10000005D10	*Enterococcus faecalis*
58	E3M10000005E01	*Enterococcus faecalis*
59	E3M10000005E02	*Enterococcus faecalis*
60	E3M10000005E03	*Enterococcus faecalis*
61	E3M10000005E08	*Enterococcus faecalis*
62	E3M10000005F07	*Enterococcus faecalis*
63	E3M10000005F10	*Enterococcus faecalis*
64	E3M10000005G05	*Enterococcus faecalis*
65	E3M10000005H04	*Enterococcus faecalis*
66	E3M10000006B03	*Enterococcus faecalis*
67	E3M10000006C01	*Enterococcus faecalis*
68	E3M10000006C12	*Enterococcus faecalis*
69	E3M10000006D03	*Enterococcus faecalis*
70	E3M10000006E11	*Enterococcus faecalis*
71	E3M10000006F04	*Enterococcus faecalis*
72	E3M10000006G04	*Enterococcus faecalis*
73	E3M10000006G12	*Enterococcus faecalis*
74	E3M10000006H09	*Enterococcus faecalis*
75	E3M10000007A02	*Enterococcus faecalis*
76	E3M10000007B02	*Enterococcus faecalis*
77	E3M10000007B03	*Enterococcus faecalis*
78	E3M10000007C03	*Enterococcus faecalis*
79	E3M10000007C04	*Enterococcus faecalis*
80	E3M10000007D03	*Enterococcus faecalis*
81	E3M10000007E05	*Enterococcus faecalis*
82	E3M10000007F01	*Enterococcus faecalis*
83	E3M10000007F06	*Enterococcus faecalis*
84	E3M10000007G01	*Enterococcus faecalis*
85	E3M10000008C03	*Enterococcus faecalis*
86	E3M10000008C08	*Enterococcus faecalis*
87	E3M10000008C09	*Enterococcus faecalis*
88	E3M10000008D08	*Enterococcus faecalis*
89	E3M10000008E02	*Enterococcus faecalis*
90	E3M10000008G05	*Enterococcus faecalis*
91	E3M10000008G09	*Enterococcus faecalis*
92	E3M10000008H02	*Enterococcus faecalis*
93	E3M10000009C07	*Enterococcus faecalis*
94	E3M10000009C09	*Enterococcus faecalis*
95	E3M10000009D01	*Enterococcus faecalis*
96	E3M10000009E02	*Enterococcus faecalis*
97	E3M10000009E03	*Enterococcus faecalis*
98	E3M10000009E05	*Enterococcus faecalis*
99	E3M10000009G02	*Enterococcus faecalis*
100	E3M10000010C08	*Enterococcus faecalis*
101	E3M10000010D05	*Enterococcus faecalis*
102	E3M10000010F01	*Enterococcus faecalis*
103	E3M10000010G05	*Enterococcus faecalis*
104	E3M10000010G07	*Enterococcus faecalis*

SeqID	Clone name	Organism
105	E3M10000010G09	*Enterococcus faecalis*
106	E3M10000010G10	*Enterococcus faecalis*
107	E3M10000010H02	*Enterococcus faecalis*
108	E3M10000011A09	*Enterococcus faecalis*
109	E3M10000011B03	*Enterococcus faecalis*
110	E3M10000011B09	*Enterococcus faecalis*
111	E3M10000011C07	*Enterococcus faecalis*
112	E3M10000011D03	*Enterococcus faecalis*
113	E3M10000011H02	*Enterococcus faecalis*
114	E3M10000011H05	*Enterococcus faecalis*
115	E3M10000012B01	*Enterococcus faecalis*
116	E3M10000012B02	*Enterococcus faecalis*
117	E3M10000012B07	*Enterococcus faecalis*
118	E3M10000012B08	*Enterococcus faecalis*
119	E3M10000012C01	*Enterococcus faecalis*
120	E3M10000012D10	*Enterococcus faecalis*
121	E3M10000012E08	*Enterococcus faecalis*
122	E3M10000012F05	*Enterococcus faecalis*
123	E3M10000012F06	*Enterococcus faecalis*
124	E3M10000012F07	*Enterococcus faecalis*
125	E3M10000012F10	*Enterococcus faecalis*
126	E3M10000012G02	*Enterococcus faecalis*
127	E3M10000012G07	*Enterococcus faecalis*
128	E3M10000013A06	*Enterococcus faecalis*
129	E3M10000013A07	*Enterococcus faecalis*
130	E3M10000013C05	*Enterococcus faecalis*
131	E3M10000013D02	*Enterococcus faecalis*
132	E3M10000013D08	*Enterococcus faecalis*
133	E3M10000013D10	*Enterococcus faecalis*
134	E3M10000013E02	*Enterococcus faecalis*
135	E3M10000013E08	*Enterococcus faecalis*
136	E3M10000013F05	*Enterococcus faecalis*
137	E3M10000013F12	*Enterococcus faecalis*
138	E3M10000013G10	*Enterococcus faecalis*
139	E3M10000013H03	*Enterococcus faecalis*
140	E3M10000013H05	*Enterococcus faecalis*
141	E3M10000013H10	*Enterococcus faecalis*
142	E3M10000014B12	*Enterococcus faecalis*
143	E3M10000014E12	*Enterococcus faecalis*
144	E3M10000014G09	*Enterococcus faecalis*
145	E3M10000015B04	*Enterococcus faecalis*
146	E3M10000015B12	*Enterococcus faecalis*
147	E3M10000015E12	*Enterococcus faecalis*
148	E3M10000016A03	*Enterococcus faecalis*
149	E3M10000016A04	*Enterococcus faecalis*
150	E3M10000016C11	*Enterococcus faecalis*
151	E3M10000016D03	*Enterococcus faecalis*
152	E3M10000016F06	*Enterococcus faecalis*
153	E3M10000016F10	*Enterococcus faecalis*

TABLE IA

SeqID	Clone name	Organism
154	E3M10000016H05	*Enterococcus faecalis*
155	E3M10000016H10	*Enterococcus faecalis*
156	E3M10000017A09	*Enterococcus faecalis*
157	E3M10000017D09	*Enterococcus faecalis*
158	E3M10000018A07	*Enterococcus faecalis*
159	E3M10000018C02	*Enterococcus faecalis*
160	E3M10000018E01	*Enterococcus faecalis*
161	E3M10000018G09	*Enterococcus faecalis*
162	E3M10000018H06	*Enterococcus faecalis*
163	E3M10000019B06	*Enterococcus faecalis*
164	E3M10000019D02	*Enterococcus faecalis*
165	E3M10000019E03	*Enterococcus faecalis*
166	E3M10000019E04	*Enterococcus faecalis*
167	E3M10000020G04	*Enterococcus faecalis*
168	E3M10000020H05	*Enterococcus faecalis*
169	E3M10000021A08	*Enterococcus faecalis*
170	E3M10000021A11	*Enterococcus faecalis*
171	E3M10000021B10	*Enterococcus faecalis*
172	E3M10000021C03	*Enterococcus faecalis*
173	E3M10000021C04	*Enterococcus faecalis*
174	E3M10000021C08	*Enterococcus faecalis*
175	E3M10000021D04	*Enterococcus faecalis*
176	E3M10000021E10	*Enterococcus faecalis*
177	E3M10000021G04	*Enterococcus faecalis*
178	E3M10000021G10	*Enterococcus faecalis*
179	E3M10000021G11	*Enterococcus faecalis*
180	E3M10000021H11	*Enterococcus faecalis*
181	E3M10000022A04	*Enterococcus faecalis*
182	E3M10000022A11	*Enterococcus faecalis*
183	E3M10000022B04	*Enterococcus faecalis*
184	E3M10000022B05	*Enterococcus faecalis*
185	E3M10000022B07	*Enterococcus faecalis*
186	E3M10000022C05	*Enterococcus faecalis*
187	E3M10000022C06	*Enterococcus faecalis*
188	E3M10000022C09	*Enterococcus faecalis*
189	E3M10000022D04	*Enterococcus faecalis*
190	E3M10000022F05	*Enterococcus faecalis*
191	E3M10000022F06	*Enterococcus faecalis*
192	E3M10000022F08	*Enterococcus faecalis*
193	E3M10000022G02	*Enterococcus faecalis*
194	E3M10000022G12	*Enterococcus faecalis*
195	E3M10000023A03	*Enterococcus faecalis*
196	E3M10000023A06	*Enterococcus faecalis*
197	E3M10000023A07	*Enterococcus faecalis*
198	E3M10000023A09	*Enterococcus faecalis*
199	E3M10000023B02	*Enterococcus faecalis*
200	E3M10000023B06	*Enterococcus faecalis*
201	E3M10000023C03	*Enterococcus faecalis*
202	E3M10000023C04	*Enterococcus faecalis*

SeqID	Clone name	Organism
203	E3M10000023C06	*Enterococcus faecalis*
204	E3M10000023C08	*Enterococcus faecalis*
205	E3M10000023C09	*Enterococcus faecalis*
206	E3M10000023D02	*Enterococcus faecalis*
207	E3M10000023D04	*Enterococcus faecalis*
208	E3M10000023D10	*Enterococcus faecalis*
209	E3M10000023E04	*Enterococcus faecalis*
210	E3M10000023E07	*Enterococcus faecalis*
211	E3M10000023E09	*Enterococcus faecalis*
212	E3M10000023F02	*Enterococcus faecalis*
213	E3M10000023F10	*Enterococcus faecalis*
214	E3M10000023G02	*Enterococcus faecalis*
215	E3M10000023G04	*Enterococcus faecalis*
216	E3M10000023G10	*Enterococcus faecalis*
217	E3M10000023H08	*Enterococcus faecalis*
218	E3M10000024A03	*Enterococcus faecalis*
219	E3M10000024A04	*Enterococcus faecalis*
220	E3M10000024A08	*Enterococcus faecalis*
221	E3M10000024C06	*Enterococcus faecalis*
222	E3M10000025A06	*Enterococcus faecalis*
223	E3M10000025B01	*Enterococcus faecalis*
224	E3M10000025B03	*Enterococcus faecalis*
225	E3M10000025B05	*Enterococcus faecalis*
226	E3M10000025B10	*Enterococcus faecalis*
227	E3M10000025C01	*Enterococcus faecalis*
228	E3M10000025C04	*Enterococcus faecalis*
229	E3M10000025C05	*Enterococcus faecalis*
230	E3M10000025C07	*Enterococcus faecalis*
231	E3M10000025C08	*Enterococcus faecalis*
232	E3M10000025C09	*Enterococcus faecalis*
233	E3M10000025C11	*Enterococcus faecalis*
234	E3M10000025D01	*Enterococcus faecalis*
235	E3M10000025D10	*Enterococcus faecalis*
236	E3M10000025E07	*Enterococcus faecalis*
237	E3M10000025E08	*Enterococcus faecalis*
238	E3M10000025E12	*Enterococcus faecalis*
239	E3M10000025F04	*Enterococcus faecalis*
240	E3M10000025F06	*Enterococcus faecalis*
241	E3M10000025F08	*Enterococcus faecalis*
242	E3M10000025F09	*Enterococcus faecalis*
243	E3M10000025F10	*Enterococcus faecalis*
244	E3M10000025F11	*Enterococcus faecalis*
245	E3M10000025F12	*Enterococcus faecalis*
246	E3M10000025G02	*Enterococcus faecalis*
247	E3M10000025G07	*Enterococcus faecalis*
248	E3M10000025G09	*Enterococcus faecalis*
249	E3M10000027A02	*Enterococcus faecalis*
250	E3M10000027A07	*Enterococcus faecalis*
251	E3M10000027A09	*Enterococcus faecalis*

SeqID	Clone name	Organism
252	E3M10000027B07	*Enterococcus faecalis*
253	E3M10000027B08	*Enterococcus faecalis*
254	E3M10000027B09	*Enterococcus faecalis*
255	E3M10000027C02	*Enterococcus faecalis*
256	E3M10000027C03	*Enterococcus faecalis*
257	E3M10000027C08	*Enterococcus faecalis*
258	E3M10000027D03	*Enterococcus faecalis*
259	E3M10000027D05	*Enterococcus faecalis*
260	E3M10000027D08	*Enterococcus faecalis*
261	E3M10000027D10	*Enterococcus faecalis*
262	E3M10000027G01	*Enterococcus faecalis*
263	E3M10000027G08	*Enterococcus faecalis*
264	E3M10000027H04	*Enterococcus faecalis*
265	E3M10000027H07	*Enterococcus faecalis*
266	E3M10000028A02	*Enterococcus faecalis*
267	E3M10000028A03	*Enterococcus faecalis*
268	E3M10000028A04	*Enterococcus faecalis*
269	E3M10000028A05	*Enterococcus faecalis*
270	E3M10000028A06	*Enterococcus faecalis*
271	E3M10000028A08	*Enterococcus faecalis*
272	E3M10000028B01	*Enterococcus faecalis*
273	E3M10000028B02	*Enterococcus faecalis*
274	E3M10000028B03	*Enterococcus faecalis*
275	E3M10000028B04	*Enterococcus faecalis*
276	E3M10000028B05	*Enterococcus faecalis*
277	E3M10000028B06	*Enterococcus faecalis*
278	E3M10000028B07	*Enterococcus faecalis*
279	E3M10000028B08	*Enterococcus faecalis*
280	E3M10000028C01	*Enterococcus faecalis*
281	E3M10000028C02	*Enterococcus faecalis*
282	E3M10000028C04	*Enterococcus faecalis*
283	E3M10000028C05	*Enterococcus faecalis*
284	E3M10000028C06	*Enterococcus faecalis*
285	E3M10000028C07	*Enterococcus faecalis*
286	E3M10000028C08	*Enterococcus faecalis*
287	E3M10000028D01	*Enterococcus faecalis*
288	E3M10000028D02	*Enterococcus faecalis*
289	E3M10000028D05	*Enterococcus faecalis*
290	E3M10000028D06	*Enterococcus faecalis*
291	E3M10000028D08	*Enterococcus faecalis*
292	E3M10000028E01	*Enterococcus faecalis*
293	E3M10000028E04	*Enterococcus faecalis*
294	E3M10000028E07	*Enterococcus faecalis*
295	E3M10000028F02	*Enterococcus faecalis*
296	E3M10000028F03	*Enterococcus faecalis*
297	E3M10000028F04	*Enterococcus faecalis*
298	E3M10000028F05	*Enterococcus faecalis*
299	E3M10000028F06	*Enterococcus faecalis*
300	E3M10000028F07	*Enterococcus faecalis*

SeqID	Clone name	Organism
301	E3M10000028G05	*Enterococcus faecalis*
302	E3M10000028G06	*Enterococcus faecalis*
303	E3M10000028G07	*Enterococcus faecalis*
304	E3M10000028H04	*Enterococcus faecalis*
305	E3M10000028H07	*Enterococcus faecalis*
306	E3M10000029A02	*Enterococcus faecalis*
307	E3M10000029A04	*Enterococcus faecalis*
308	E3M10000029A05	*Enterococcus faecalis*
309	E3M10000029A10	*Enterococcus faecalis*
310	E3M10000029A11	*Enterococcus faecalis*
311	E3M10000029B01	*Enterococcus faecalis*
312	E3M10000029B02	*Enterococcus faecalis*
313	E3M10000029B05	*Enterococcus faecalis*
314	E3M10000029B06	*Enterococcus faecalis*
315	E3M10000029B08	*Enterococcus faecalis*
316	E3M10000029B11	*Enterococcus faecalis*
317	E3M10000029B12	*Enterococcus faecalis*
318	E3M10000029C01	*Enterococcus faecalis*
319	E3M10000029C02	*Enterococcus faecalis*
320	E3M10000029C03	*Enterococcus faecalis*
321	E3M10000029C04	*Enterococcus faecalis*
322	E3M10000029C05	*Enterococcus faecalis*
323	E3M10000029C06	*Enterococcus faecalis*
324	E3M10000029C07	*Enterococcus faecalis*
325	E3M10000029C08	*Enterococcus faecalis*
326	E3M10000029C09	*Enterococcus faecalis*
327	E3M10000029C10	*Enterococcus faecalis*
328	E3M10000029C12	*Enterococcus faecalis*
329	E3M10000029D01	*Enterococcus faecalis*
330	E3M10000029D03	*Enterococcus faecalis*
331	E3M10000029D04	*Enterococcus faecalis*
332	E3M10000029D05	*Enterococcus faecalis*
333	E3M10000029D06	*Enterococcus faecalis*
334	E3M10000029D08	*Enterococcus faecalis*
335	E3M10000029D12	*Enterococcus faecalis*
336	E3M10000029E01	*Enterococcus faecalis*
337	E3M10000029E02	*Enterococcus faecalis*
338	E3M10000029E03	*Enterococcus faecalis*
339	E3M10000029E05	*Enterococcus faecalis*
340	E3M10000029E07	*Enterococcus faecalis*
341	E3M10000029E08	*Enterococcus faecalis*
342	E3M10000029E09	*Enterococcus faecalis*
343	E3M10000029E12	*Enterococcus faecalis*
344	E3M10000029F01	*Enterococcus faecalis*
345	E3M10000029F05	*Enterococcus faecalis*
346	E3M10000029F06	*Enterococcus faecalis*
347	E3M10000029F09	*Enterococcus faecalis*
348	E3M10000029F10	*Enterococcus faecalis*
349	E3M10000029F11	*Enterococcus faecalis*

TABLE IA

SeqID	Clone name	Organism
350	E3M10000029F12	*Enterococcus faecalis*
351	E3M10000029G01	*Enterococcus faecalis*
352	E3M10000029G04	*Enterococcus faecalis*
353	E3M10000029G05	*Enterococcus faecalis*
354	E3M10000029G07	*Enterococcus faecalis*
355	E3M10000029G08	*Enterococcus faecalis*
356	E3M10000029G09	*Enterococcus faecalis*
357	E3M10000029G10	*Enterococcus faecalis*
358	E3M10000029G11	*Enterococcus faecalis*
359	E3M10000029G12	*Enterococcus faecalis*
360	E3M10000029H02	*Enterococcus faecalis*
361	E3M10000029H04	*Enterococcus faecalis*
362	E3M10000029H05	*Enterococcus faecalis*
363	E3M10000029H07	*Enterococcus faecalis*
364	E3M10000029H08	*Enterococcus faecalis*
365	E3M10000029H11	*Enterococcus faecalis*
366	E3M10000030A05	*Enterococcus faecalis*
367	E3M10000030A08	*Enterococcus faecalis*
368	E3M10000030A09	*Enterococcus faecalis*
369	E3M10000030A11	*Enterococcus faecalis*
370	E3M10000030B03	*Enterococcus faecalis*
371	E3M10000030B04	*Enterococcus faecalis*
372	E3M10000030B05	*Enterococcus faecalis*
373	E3M10000030B06	*Enterococcus faecalis*
374	E3M10000030B07	*Enterococcus faecalis*
375	E3M10000030B08	*Enterococcus faecalis*
376	E3M10000030B10	*Enterococcus faecalis*
377	E3M10000030B11	*Enterococcus faecalis*
378	E3M10000030B12	*Enterococcus faecalis*
379	E3M10000030C03	*Enterococcus faecalis*
380	E3M10000030C04	*Enterococcus faecalis*
381	E3M10000030C12	*Enterococcus faecalis*
382	E3M10000030D02	*Enterococcus faecalis*
383	E3M10000030D05	*Enterococcus faecalis*
384	E3M10000030D08	*Enterococcus faecalis*
385	E3M10000030D09	*Enterococcus faecalis*
386	E3M10000030D10	*Enterococcus faecalis*
387	E3M10000030D12	*Enterococcus faecalis*
388	E3M10000030E01	*Enterococcus faecalis*
389	E3M10000030E02	*Enterococcus faecalis*
390	E3M10000030E04	*Enterococcus faecalis*
391	E3M10000030E08	*Enterococcus faecalis*
392	E3M10000030E09	*Enterococcus faecalis*
393	E3M10000030E10	*Enterococcus faecalis*
394	E3M10000030F01	*Enterococcus faecalis*
395	E3M10000030F04	*Enterococcus faecalis*
396	E3M10000030F06	*Enterococcus faecalis*
397	E3M10000030F07	*Enterococcus faecalis*
398	E3M10000030F10	*Enterococcus faecalis*

TABLE IA

SeqID	Clone name	Organism
399	E3M10000030F12	*Enterococcus faecalis*
400	E3M10000030G01	*Enterococcus faecalis*
401	E3M10000030G03	*Enterococcus faecalis*
402	E3M10000030G06	*Enterococcus faecalis*
403	E3M10000030G08	*Enterococcus faecalis*
404	E3M10000030G09	*Enterococcus faecalis*
405	E3M10000030G12	*Enterococcus faecalis*
406	E3M10000030H03	*Enterococcus faecalis*
407	E3M10000030H04	*Enterococcus faecalis*
408	E3M10000030H06	*Enterococcus faecalis*
409	E3M10000030H07	*Enterococcus faecalis*
410	E3M10000030H08	*Enterococcus faecalis*
411	E3M10000030H10	*Enterococcus faecalis*
412	E3M10000030H11	*Enterococcus faecalis*
413	E3M10000031A02	*Enterococcus faecalis*
414	E3M10000031A06	*Enterococcus faecalis*
415	E3M10000031A07	*Enterococcus faecalis*
416	E3M10000031A08	*Enterococcus faecalis*
417	E3M10000031B02	*Enterococcus faecalis*
418	E3M10000031B03	*Enterococcus faecalis*
419	E3M10000031B04	*Enterococcus faecalis*
420	E3M10000031B09	*Enterococcus faecalis*
421	E3M10000031B10	*Enterococcus faecalis*
422	E3M10000031B11	*Enterococcus faecalis*
423	E3M10000031B12	*Enterococcus faecalis*
424	E3M10000031C01	*Enterococcus faecalis*
425	E3M10000031C04	*Enterococcus faecalis*
426	E3M10000031C06	*Enterococcus faecalis*
427	E3M10000031C10	*Enterococcus faecalis*
428	E3M10000031C11	*Enterococcus faecalis*
429	E3M10000031C12	*Enterococcus faecalis*
430	E3M10000031D03	*Enterococcus faecalis*
431	E3M10000031D04	*Enterococcus faecalis*
432	E3M10000031D08	*Enterococcus faecalis*
433	E3M10000031E03	*Enterococcus faecalis*
434	E3M10000031E09	*Enterococcus faecalis*
435	E3M10000031F02	*Enterococcus faecalis*
436	E3M10000031F04	*Enterococcus faecalis*
437	E3M10000031F07	*Enterococcus faecalis*
438	E3M10000031F09	*Enterococcus faecalis*
439	E3M10000031F11	*Enterococcus faecalis*
440	E3M10000031G03	*Enterococcus faecalis*
441	E3M10000031G04	*Enterococcus faecalis*
442	E3M10000031G05	*Enterococcus faecalis*
443	E3M10000031G06	*Enterococcus faecalis*
444	E3M10000031G07	*Enterococcus faecalis*
445	E3M10000031G08	*Enterococcus faecalis*
446	E3M10000031G11	*Enterococcus faecalis*
447	E3M10000031H05	*Enterococcus faecalis*

TABLE IA

SeqID	Clone name	Organism
448	E3M10000031H06	*Enterococcus faecalis*
449	E3M10000031H07	*Enterococcus faecalis*
450	E3M10000031H08	*Enterococcus faecalis*
451	E3M10000031H10	*Enterococcus faecalis*
452	E3M10000031H11	*Enterococcus faecalis*
453	E3M10000032A02	*Enterococcus faecalis*
454	E3M10000032A04	*Enterococcus faecalis*
455	E3M10000032A06	*Enterococcus faecalis*
456	E3M10000032A07	*Enterococcus faecalis*
457	E3M10000032A08	*Enterococcus faecalis*
458	E3M10000032A09	*Enterococcus faecalis*
459	E3M10000032A10	*Enterococcus faecalis*
460	E3M10000032A11	*Enterococcus faecalis*
461	E3M10000032B03	*Enterococcus faecalis*
462	E3M10000032B04	*Enterococcus faecalis*
463	E3M10000032B07	*Enterococcus faecalis*
464	E3M10000032B08	*Enterococcus faecalis*
465	E3M10000032B09	*Enterococcus faecalis*
466	E3M10000032B11	*Enterococcus faecalis*
467	E3M10000032B12	*Enterococcus faecalis*
468	E3M10000032C01	*Enterococcus faecalis*
469	E3M10000032C02	*Enterococcus faecalis*
470	E3M10000032C03	*Enterococcus faecalis*
471	E3M10000032C04	*Enterococcus faecalis*
472	E3M10000032C06	*Enterococcus faecalis*
473	E3M10000032C09	*Enterococcus faecalis*
474	E3M10000032C11	*Enterococcus faecalis*
475	E3M10000032C12	*Enterococcus faecalis*
476	E3M10000032D01	*Enterococcus faecalis*
477	E3M10000032D02	*Enterococcus faecalis*
478	E3M10000032D03	*Enterococcus faecalis*
479	E3M10000032D06	*Enterococcus faecalis*
480	E3M10000032D09	*Enterococcus faecalis*
481	E3M10000032D12	*Enterococcus faecalis*
482	E3M10000032E04	*Enterococcus faecalis*
483	E3M10000032E05	*Enterococcus faecalis*
484	E3M10000032E08	*Enterococcus faecalis*
485	E3M10000032E10	*Enterococcus faecalis*
486	E3M10000032E11	*Enterococcus faecalis*
487	E3M10000032E12	*Enterococcus faecalis*
488	E3M10000032F02	*Enterococcus faecalis*
489	E3M10000032F03	*Enterococcus faecalis*
490	E3M10000032F05	*Enterococcus faecalis*
491	E3M10000032F07	*Enterococcus faecalis*
492	E3M10000032F08	*Enterococcus faecalis*
493	E3M10000032F11	*Enterococcus faecalis*
494	E3M10000032F12	*Enterococcus faecalis*
495	E3M10000032G01	*Enterococcus faecalis*
496	E3M10000032G02	*Enterococcus faecalis*

TABLE IA

SeqID	Clone name	Organism
497	E3M10000032G04	*Enterococcus faecalis*
498	E3M10000032G05	*Enterococcus faecalis*
499	E3M10000032G06	*Enterococcus faecalis*
500	E3M10000032G07	*Enterococcus faecalis*
501	E3M10000032H05	*Enterococcus faecalis*
502	E3M10000032H06	*Enterococcus faecalis*
503	E3M10000032H08	*Enterococcus faecalis*
504	E3M10000032H09	*Enterococcus faecalis*
505	E3M10000032H10	*Enterococcus faecalis*
506	E3M10000033A03	*Enterococcus faecalis*
507	E3M10000033A04	*Enterococcus faecalis*
508	E3M10000033A05	*Enterococcus faecalis*
509	E3M10000033A06	*Enterococcus faecalis*
510	E3M10000033A07	*Enterococcus faecalis*
511	E3M10000033A08	*Enterococcus faecalis*
512	E3M10000033A11	*Enterococcus faecalis*
513	E3M10000033B01	*Enterococcus faecalis*
514	E3M10000033B02	*Enterococcus faecalis*
515	E3M10000033B04	*Enterococcus faecalis*
516	E3M10000033B05	*Enterococcus faecalis*
517	E3M10000033B06	*Enterococcus faecalis*
518	E3M10000033B08	*Enterococcus faecalis*
519	E3M10000033B09	*Enterococcus faecalis*
520	E3M10000033C01	*Enterococcus faecalis*
521	E3M10000033C02	*Enterococcus faecalis*
522	E3M10000033C05	*Enterococcus faecalis*
523	E3M10000033C09	*Enterococcus faecalis*
524	E3M10000033C10	*Enterococcus faecalis*
525	E3M10000033C11	*Enterococcus faecalis*
526	E3M10000033C12	*Enterococcus faecalis*
527	E3M10000033D01	*Enterococcus faecalis*
528	E3M10000033D04	*Enterococcus faecalis*
529	E3M10000033D05	*Enterococcus faecalis*
530	E3M10000033D06	*Enterococcus faecalis*
531	E3M10000033D09	*Enterococcus faecalis*
532	E3M10000033D10	*Enterococcus faecalis*
533	E3M10000033D11	*Enterococcus faecalis*
534	E3M10000033E02	*Enterococcus faecalis*
535	E3M10000033E03	*Enterococcus faecalis*
536	E3M10000033E04	*Enterococcus faecalis*
537	E3M10000033E05	*Enterococcus faecalis*
538	E3M10000033E07	*Enterococcus faecalis*
539	E3M10000033E08	*Enterococcus faecalis*
540	E3M10000033E09	*Enterococcus faecalis*
541	E3M10000033E11	*Enterococcus faecalis*
542	E3M10000033F01	*Enterococcus faecalis*
543	E3M10000033F03	*Enterococcus faecalis*
544	E3M10000033F04	*Enterococcus faecalis*
545	E3M10000033F05	*Enterococcus faecalis*

TABLE IA

SeqID	Clone name	Organism
546	E3M10000033F07	*Enterococcus faecalis*
547	E3M10000033F08	*Enterococcus faecalis*
548	E3M10000033F10	*Enterococcus faecalis*
549	E3M10000033F12	*Enterococcus faecalis*
550	E3M10000033G01	*Enterococcus faecalis*
551	E3M10000033G02	*Enterococcus faecalis*
552	E3M10000033G03	*Enterococcus faecalis*
553	E3M10000033G04	*Enterococcus faecalis*
554	E3M10000033G06	*Enterococcus faecalis*
555	E3M10000033G07	*Enterococcus faecalis*
556	E3M10000033G08	*Enterococcus faecalis*
557	E3M10000033G09	*Enterococcus faecalis*
558	E3M10000033G12	*Enterococcus faecalis*
559	E3M10000033H02	*Enterococcus faecalis*
560	E3M10000033H04	*Enterococcus faecalis*
561	E3M10000033H05	*Enterococcus faecalis*
562	E3M10000033H07	*Enterococcus faecalis*
563	E3M10000033H08	*Enterococcus faecalis*
564	E3M10000033H09	*Enterococcus faecalis*
565	E3M10000033H10	*Enterococcus faecalis*
566	E3M10000033H11	*Enterococcus faecalis*
567	E3M10000034A02	*Enterococcus faecalis*
568	E3M10000034A03	*Enterococcus faecalis*
569	E3M10000034A04	*Enterococcus faecalis*
570	E3M10000034B02	*Enterococcus faecalis*
571	E3M10000034B04	*Enterococcus faecalis*
572	E3M10000034C04	*Enterococcus faecalis*
573	E3M10000034D01	*Enterococcus faecalis*
574	E3M10000034D02	*Enterococcus faecalis*
575	E3M10000034E01	*Enterococcus faecalis*
576	E3M10000034E04	*Enterococcus faecalis*
577	E3M10000034F02	*Enterococcus faecalis*
578	E3M10000034F03	*Enterococcus faecalis*
579	E3M10000034F04	*Enterococcus faecalis*
580	E3M10000034G02	*Enterococcus faecalis*
581	E3M10000034G03	*Enterococcus faecalis*
582	E3M10000034H02	*Enterococcus faecalis*
583	E3M10000034H03	*Enterococcus faecalis*
584	E3M10000035A02	*Enterococcus faecalis*
585	E3M10000035A04	*Enterococcus faecalis*
586	E3M10000035A05	*Enterococcus faecalis*
587	E3M10000035A06	*Enterococcus faecalis*
588	E3M10000035A08	*Enterococcus faecalis*
589	E3M10000035A09	*Enterococcus faecalis*
590	E3M10000035A11	*Enterococcus faecalis*
591	E3M10000035B01	*Enterococcus faecalis*
592	E3M10000035B03	*Enterococcus faecalis*
593	E3M10000035B06	*Enterococcus faecalis*
594	E3M10000035B07	*Enterococcus faecalis*

TABLE IA

SeqID	Clone name	Organism
595	E3M10000035B08	*Enterococcus faecalis*
596	E3M10000035B10	*Enterococcus faecalis*
597	E3M10000035B11	*Enterococcus faecalis*
598	E3M10000035B12	*Enterococcus faecalis*
599	E3M10000035C01	*Enterococcus faecalis*
600	E3M10000035C03	*Enterococcus faecalis*
601	E3M10000035C04	*Enterococcus faecalis*
602	E3M10000035C05	*Enterococcus faecalis*
603	E3M10000035C06	*Enterococcus faecalis*
604	E3M10000035C07	*Enterococcus faecalis*
605	E3M10000035C08	*Enterococcus faecalis*
606	E3M10000035C09	*Enterococcus faecalis*
607	E3M10000035C11	*Enterococcus faecalis*
608	E3M10000035C12	*Enterococcus faecalis*
609	E3M10000035D02	*Enterococcus faecalis*
610	E3M10000035D03	*Enterococcus faecalis*
611	E3M10000035D04	*Enterococcus faecalis*
612	E3M10000035D05	*Enterococcus faecalis*
613	E3M10000035D10	*Enterococcus faecalis*
614	E3M10000035D11	*Enterococcus faecalis*
615	E3M10000035E03	*Enterococcus faecalis*
616	E3M10000035E04	*Enterococcus faecalis*
617	E3M10000035E05	*Enterococcus faecalis*
618	E3M10000035E07	*Enterococcus faecalis*
619	E3M10000035E08	*Enterococcus faecalis*
620	E3M10000035E09	*Enterococcus faecalis*
621	E3M10000035E10	*Enterococcus faecalis*
622	E3M10000035E11	*Enterococcus faecalis*
623	E3M10000035E12	*Enterococcus faecalis*
624	E3M10000035F01	*Enterococcus faecalis*
625	E3M10000035F02	*Enterococcus faecalis*
626	E3M10000035F03	*Enterococcus faecalis*
627	E3M10000035F06	*Enterococcus faecalis*
628	E3M10000035F07	*Enterococcus faecalis*
629	E3M10000035F08	*Enterococcus faecalis*
630	E3M10000035F09	*Enterococcus faecalis*
631	E3M10000035F11	*Enterococcus faecalis*
632	E3M10000035F12	*Enterococcus faecalis*
633	E3M10000035G02	*Enterococcus faecalis*
634	E3M10000035G04	*Enterococcus faecalis*
635	E3M10000035G05	*Enterococcus faecalis*
636	E3M10000035G08	*Enterococcus faecalis*
637	E3M10000035G09	*Enterococcus faecalis*
638	E3M10000035G10	*Enterococcus faecalis*
639	E3M10000035G11	*Enterococcus faecalis*
640	E3M10000035H03	*Enterococcus faecalis*
641	E3M10000035H06	*Enterococcus faecalis*
642	E3M10000035H09	*Enterococcus faecalis*
643	E3M10000035H11	*Enterococcus faecalis*

TABLE IA

SeqID	Clone name	Organism
644	E3M10000036A03	*Enterococcus faecalis*
645	E3M10000036A04	*Enterococcus faecalis*
646	E3M10000036A05	*Enterococcus faecalis*
647	E3M10000036A06	*Enterococcus faecalis*
648	E3M10000036A07	*Enterococcus faecalis*
649	E3M10000036A08	*Enterococcus faecalis*
650	E3M10000036A09	*Enterococcus faecalis*
651	E3M10000036A10	*Enterococcus faecalis*
652	E3M10000036B01	*Enterococcus faecalis*
653	E3M10000036B03	*Enterococcus faecalis*
654	E3M10000036B06	*Enterococcus faecalis*
655	E3M10000036B07	*Enterococcus faecalis*
656	E3M10000036B08	*Enterococcus faecalis*
657	E3M10000036B09	*Enterococcus faecalis*
658	E3M10000036B11	*Enterococcus faecalis*
659	E3M10000036B12	*Enterococcus faecalis*
660	E3M10000036C01	*Enterococcus faecalis*
661	E3M10000036C03	*Enterococcus faecalis*
662	E3M10000036C06	*Enterococcus faecalis*
663	E3M10000036C07	*Enterococcus faecalis*
664	E3M10000036C08	*Enterococcus faecalis*
665	E3M10000036C09	*Enterococcus faecalis*
666	E3M10000036C10	*Enterococcus faecalis*
667	E3M10000036C11	*Enterococcus faecalis*
668	E3M10000036D03	*Enterococcus faecalis*
669	E3M10000036D04	*Enterococcus faecalis*
670	E3M10000036D06	*Enterococcus faecalis*
671	E3M10000036D08	*Enterococcus faecalis*
672	E3M10000036D09	*Enterococcus faecalis*
673	E3M10000036D10	*Enterococcus faecalis*
674	E3M10000036D11	*Enterococcus faecalis*
675	E3M10000036D12	*Enterococcus faecalis*
676	E3M10000036E01	*Enterococcus faecalis*
677	E3M10000036E04	*Enterococcus faecalis*
678	E3M10000036E05	*Enterococcus faecalis*
679	E3M10000036E07	*Enterococcus faecalis*
680	E3M10000036E08	*Enterococcus faecalis*
681	E3M10000036F03	*Enterococcus faecalis*
682	E3M10000036F04	*Enterococcus faecalis*
683	E3M10000036F05	*Enterococcus faecalis*
684	E3M10000036F08	*Enterococcus faecalis*
685	E3M10000036F09	*Enterococcus faecalis*
686	E3M10000036F10	*Enterococcus faecalis*
687	E3M10000036F12	*Enterococcus faecalis*
688	E3M10000036G01	*Enterococcus faecalis*
689	E3M10000036G02	*Enterococcus faecalis*
690	E3M10000036G03	*Enterococcus faecalis*
691	E3M10000036G04	*Enterococcus faecalis*
692	E3M10000036G06	*Enterococcus faecalis*

SeqID	Clone name	Organism
693	E3M10000036G10	*Enterococcus faecalis*
694	E3M10000036H02	*Enterococcus faecalis*
695	E3M10000036H03	*Enterococcus faecalis*
696	E3M10000036H04	*Enterococcus faecalis*
697	E3M10000036H05	*Enterococcus faecalis*
698	E3M10000036H06	*Enterococcus faecalis*
699	E3M10000036H07	*Enterococcus faecalis*
700	E3M10000036H08	*Enterococcus faecalis*
701	E3M10000036H09	*Enterococcus faecalis*
702	E3M10000036H10	*Enterococcus faecalis*
703	E3M10000037A03	*Enterococcus faecalis*
704	E3M10000037A06	*Enterococcus faecalis*
705	E3M10000037A08	*Enterococcus faecalis*
706	E3M10000037A09	*Enterococcus faecalis*
707	E3M10000037A10	*Enterococcus faecalis*
708	E3M10000037B02	*Enterococcus faecalis*
709	E3M10000037B07	*Enterococcus faecalis*
710	E3M10000037B08	*Enterococcus faecalis*
711	E3M10000037B11	*Enterococcus faecalis*
712	E3M10000037C01	*Enterococcus faecalis*
713	E3M10000037C02	*Enterococcus faecalis*
714	E3M10000037C04	*Enterococcus faecalis*
715	E3M10000037C05	*Enterococcus faecalis*
716	E3M10000037C07	*Enterococcus faecalis*
717	E3M10000037C11	*Enterococcus faecalis*
718	E3M10000037C12	*Enterococcus faecalis*
719	E3M10000037D02	*Enterococcus faecalis*
720	E3M10000037D03	*Enterococcus faecalis*
721	E3M10000037D04	*Enterococcus faecalis*
722	E3M10000037D05	*Enterococcus faecalis*
723	E3M10000037D06	*Enterococcus faecalis*
724	E3M10000037D09	*Enterococcus faecalis*
725	E3M10000037D11	*Enterococcus faecalis*
726	E3M10000037E01	*Enterococcus faecalis*
727	E3M10000037E02	*Enterococcus faecalis*
728	E3M10000037E03	*Enterococcus faecalis*
729	E3M10000037E05	*Enterococcus faecalis*
730	E3M10000037E07	*Enterococcus faecalis*
731	E3M10000037E08	*Enterococcus faecalis*
732	E3M10000037E10	*Enterococcus faecalis*
733	E3M10000037E12	*Enterococcus faecalis*
734	E3M10000037F01	*Enterococcus faecalis*
735	E3M10000037F02	*Enterococcus faecalis*
736	E3M10000037F06	*Enterococcus faecalis*
737	E3M10000037F07	*Enterococcus faecalis*
738	E3M10000037F12	*Enterococcus faecalis*
739	E3M10000037G01	*Enterococcus faecalis*
740	E3M10000037G02	*Enterococcus faecalis*
741	E3M10000037G03	*Enterococcus faecalis*

SeqID	Clone name	Organism
742	E3M10000037G05	*Enterococcus faecalis*
743	E3M10000037G06	*Enterococcus faecalis*
744	E3M10000037G07	*Enterococcus faecalis*
745	E3M10000037G08	*Enterococcus faecalis*
746	E3M10000037G10	*Enterococcus faecalis*
747	E3M10000037G11	*Enterococcus faecalis*
748	E3M10000037H02	*Enterococcus faecalis*
749	E3M10000037H05	*Enterococcus faecalis*
750	E3M10000037H07	*Enterococcus faecalis*
751	E3M10000037H10	*Enterococcus faecalis*
752	E3M10000037H11	*Enterococcus faecalis*
753	E3M10000038A02	*Enterococcus faecalis*
754	E3M10000038A03	*Enterococcus faecalis*
755	E3M10000038A05	*Enterococcus faecalis*
756	E3M10000038A06	*Enterococcus faecalis*
757	E3M10000038A07	*Enterococcus faecalis*
758	E3M10000038A09	*Enterococcus faecalis*
759	E3M10000038A10	*Enterococcus faecalis*
760	E3M10000038A11	*Enterococcus faecalis*
761	E3M10000038B02	*Enterococcus faecalis*
762	E3M10000038B03	*Enterococcus faecalis*
763	E3M10000038B04	*Enterococcus faecalis*
764	E3M10000038B05	*Enterococcus faecalis*
765	E3M10000038B07	*Enterococcus faecalis*
766	E3M10000038B08	*Enterococcus faecalis*
767	E3M10000038B09	*Enterococcus faecalis*
768	E3M10000038B11	*Enterococcus faecalis*
769	E3M10000038C02	*Enterococcus faecalis*
770	E3M10000038C03	*Enterococcus faecalis*
771	E3M10000038C05	*Enterococcus faecalis*
772	E3M10000038C07	*Enterococcus faecalis*
773	E3M10000038C10	*Enterococcus faecalis*
774	E3M10000038C12	*Enterococcus faecalis*
775	E3M10000038D01	*Enterococcus faecalis*
776	E3M10000038D02	*Enterococcus faecalis*
777	E3M10000038D04	*Enterococcus faecalis*
778	E3M10000038D08	*Enterococcus faecalis*
779	E3M10000038D10	*Enterococcus faecalis*
780	E3M10000038D11	*Enterococcus faecalis*
781	E3M10000038D12	*Enterococcus faecalis*
782	E3M10000038E02	*Enterococcus faecalis*
783	E3M10000038E03	*Enterococcus faecalis*
784	E3M10000038E04	*Enterococcus faecalis*
785	E3M10000038E05	*Enterococcus faecalis*
786	E3M10000038E07	*Enterococcus faecalis*
787	E3M10000038E08	*Enterococcus faecalis*
788	E3M10000038E11	*Enterococcus faecalis*
789	E3M10000038F02	*Enterococcus faecalis*
790	E3M10000038F04	*Enterococcus faecalis*

TABLE IA

SeqID	Clone name	Organism
791	E3M10000038F05	*Enterococcus faecalis*
792	E3M10000038F06	*Enterococcus faecalis*
793	E3M10000038F07	*Enterococcus faecalis*
794	E3M10000038F09	*Enterococcus faecalis*
795	E3M10000038F10	*Enterococcus faecalis*
796	E3M10000038F11	*Enterococcus faecalis*
797	E3M10000038G02	*Enterococcus faecalis*
798	E3M10000038G03	*Enterococcus faecalis*
799	E3M10000038G06	*Enterococcus faecalis*
800	E3M10000038G07	*Enterococcus faecalis*
801	E3M10000038G11	*Enterococcus faecalis*
802	E3M10000038H02	*Enterococcus faecalis*
803	E3M10000038H05	*Enterococcus faecalis*
804	E3M10000038H06	*Enterococcus faecalis*
805	E3M10000038H07	*Enterococcus faecalis*
806	E3M10000038H08	*Enterococcus faecalis*
807	E3M10000038H09	*Enterococcus faecalis*
808	E3M10000038H10	*Enterococcus faecalis*
809	E3M10000039A02	*Enterococcus faecalis*
810	E3M10000039A06	*Enterococcus faecalis*
811	E3M10000039A07	*Enterococcus faecalis*
812	E3M10000039A08	*Enterococcus faecalis*
813	E3M10000039A10	*Enterococcus faecalis*
814	E3M10000039A11	*Enterococcus faecalis*
815	E3M10000039B01	*Enterococcus faecalis*
816	E3M10000039B03	*Enterococcus faecalis*
817	E3M10000039B04	*Enterococcus faecalis*
818	E3M10000039B06	*Enterococcus faecalis*
819	E3M10000039B07	*Enterococcus faecalis*
820	E3M10000039B08	*Enterococcus faecalis*
821	E3M10000039B09	*Enterococcus faecalis*
822	E3M10000039B11	*Enterococcus faecalis*
823	E3M10000039C02	*Enterococcus faecalis*
824	E3M10000039C04	*Enterococcus faecalis*
825	E3M10000039C05	*Enterococcus faecalis*
826	E3M10000039C06	*Enterococcus faecalis*
827	E3M10000039C07	*Enterococcus faecalis*
828	E3M10000039C08	*Enterococcus faecalis*
829	E3M10000039C09	*Enterococcus faecalis*
830	E3M10000039C10	*Enterococcus faecalis*
831	E3M10000039D02	*Enterococcus faecalis*
832	E3M10000039D03	*Enterococcus faecalis*
833	E3M10000039D04	*Enterococcus faecalis*
834	E3M10000039D06	*Enterococcus faecalis*
835	E3M10000039E01	*Enterococcus faecalis*
836	E3M10000039E02	*Enterococcus faecalis*
837	E3M10000039E03	*Enterococcus faecalis*
838	E3M10000039E05	*Enterococcus faecalis*
839	E3M10000039E07	*Enterococcus faecalis*

TABLE IA

SeqID	Clone name	Organism
840	E3M10000039E08	*Enterococcus faecalis*
841	E3M10000039F01	*Enterococcus faecalis*
842	E3M10000039F02	*Enterococcus faecalis*
843	E3M10000039F03	*Enterococcus faecalis*
844	E3M10000039F06	*Enterococcus faecalis*
845	E3M10000039F07	*Enterococcus faecalis*
846	E3M10000039F08	*Enterococcus faecalis*
847	E3M10000039G01	*Enterococcus faecalis*
848	E3M10000039G02	*Enterococcus faecalis*
849	E3M10000039G05	*Enterococcus faecalis*
850	E3M10000039G07	*Enterococcus faecalis*
851	E3M10000039G09	*Enterococcus faecalis*
852	E3M10000039G10	*Enterococcus faecalis*
853	E3M10000039H02	*Enterococcus faecalis*
854	E3M10000039H07	*Enterococcus faecalis*
855	E3M10000039H08	*Enterococcus faecalis*
856	E3M10000039H10	*Enterococcus faecalis*
857	E3M10000039H11	*Enterococcus faecalis*
858	E3M10000040A03	*Enterococcus faecalis*
859	E3M10000040A05	*Enterococcus faecalis*
860	E3M10000040A07	*Enterococcus faecalis*
861	E3M10000040A09	*Enterococcus faecalis*
862	E3M10000040A10	*Enterococcus faecalis*
863	E3M10000040A11	*Enterococcus faecalis*
864	E3M10000040B01	*Enterococcus faecalis*
865	E3M10000040B02	*Enterococcus faecalis*
866	E3M10000040B05	*Enterococcus faecalis*
867	E3M10000040B06	*Enterococcus faecalis*
868	E3M10000040B08	*Enterococcus faecalis*
869	E3M10000040B09	*Enterococcus faecalis*
870	E3M10000040B10	*Enterococcus faecalis*
871	E3M10000040B11	*Enterococcus faecalis*
872	E3M10000040B12	*Enterococcus faecalis*
873	E3M10000040C02	*Enterococcus faecalis*
874	E3M10000040C05	*Enterococcus faecalis*
875	E3M10000040C06	*Enterococcus faecalis*
876	E3M10000040C07	*Enterococcus faecalis*
877	E3M10000040C08	*Enterococcus faecalis*
878	E3M10000040C09	*Enterococcus faecalis*
879	E3M10000040C10	*Enterococcus faecalis*
880	E3M10000040C11	*Enterococcus faecalis*
881	E3M10000040C12	*Enterococcus faecalis*
882	E3M10000040D03	*Enterococcus faecalis*
883	E3M10000040D04	*Enterococcus faecalis*
884	E3M10000040D08	*Enterococcus faecalis*
885	E3M10000040D12	*Enterococcus faecalis*
886	E3M10000040E02	*Enterococcus faecalis*
887	E3M10000040E10	*Enterococcus faecalis*
888	E3M10000040E11	*Enterococcus faecalis*

TABLE IA

SeqID	Clone name	Organism
889	E3M10000040E12	*Enterococcus faecalis*
890	E3M10000040F01	*Enterococcus faecalis*
891	E3M10000040F03	*Enterococcus faecalis*
892	E3M10000040F08	*Enterococcus faecalis*
893	E3M10000040F09	*Enterococcus faecalis*
894	E3M10000040F10	*Enterococcus faecalis*
895	E3M10000040G01	*Enterococcus faecalis*
896	E3M10000040G02	*Enterococcus faecalis*
897	E3M10000040G04	*Enterococcus faecalis*
898	E3M10000040G05	*Enterococcus faecalis*
899	E3M10000040G07	*Enterococcus faecalis*
900	E3M10000040G08	*Enterococcus faecalis*
901	E3M10000040G09	*Enterococcus faecalis*
902	E3M10000040G11	*Enterococcus faecalis*
903	E3M10000040H02	*Enterococcus faecalis*
904	E3M10000040H03	*Enterococcus faecalis*
905	E3M10000040H04	*Enterococcus faecalis*
906	E3M10000040H05	*Enterococcus faecalis*
907	E3M10000040H09	*Enterococcus faecalis*
908	E3M10000041A03	*Enterococcus faecalis*
909	E3M10000041A05	*Enterococcus faecalis*
910	E3M10000041A08	*Enterococcus faecalis*
911	E3M10000041A09	*Enterococcus faecalis*
912	E3M10000041A10	*Enterococcus faecalis*
913	E3M10000041A11	*Enterococcus faecalis*
914	E3M10000041B02	*Enterococcus faecalis*
915	E3M10000041B03	*Enterococcus faecalis*
916	E3M10000041B05	*Enterococcus faecalis*
917	E3M10000041B06	*Enterococcus faecalis*
918	E3M10000041B08	*Enterococcus faecalis*
919	E3M10000041B09	*Enterococcus faecalis*
920	E3M10000041B10	*Enterococcus faecalis*
921	E3M10000041B11	*Enterococcus faecalis*
922	E3M10000041B12	*Enterococcus faecalis*
923	E3M10000041C01	*Enterococcus faecalis*
924	E3M10000041C07	*Enterococcus faecalis*
925	E3M10000041C08	*Enterococcus faecalis*
926	E3M10000041C09	*Enterococcus faecalis*
927	E3M10000041C10	*Enterococcus faecalis*
928	E3M10000041C11	*Enterococcus faecalis*
929	E3M10000041C12	*Enterococcus faecalis*
930	E3M10000041D02	*Enterococcus faecalis*
931	E3M10000041D03	*Enterococcus faecalis*
932	E3M10000041D04	*Enterococcus faecalis*
933	E3M10000041D05	*Enterococcus faecalis*
934	E3M10000041D06	*Enterococcus faecalis*
935	E3M10000041D08	*Enterococcus faecalis*
936	E3M10000041D09	*Enterococcus faecalis*
937	E3M10000041D10	*Enterococcus faecalis*

SeqID	Clone name	Organism
938	E3M10000041D11	*Enterococcus faecalis*
939	E3M10000041D12	*Enterococcus faecalis*
940	E3M10000041E02	*Enterococcus faecalis*
941	E3M10000041E03	*Enterococcus faecalis*
942	E3M10000041E05	*Enterococcus faecalis*
943	E3M10000041E07	*Enterococcus faecalis*
944	E3M10000041E10	*Enterococcus faecalis*
945	E3M10000041E11	*Enterococcus faecalis*
946	E3M10000041F03	*Enterococcus faecalis*
947	E3M10000041F05	*Enterococcus faecalis*
948	E3M10000041F06	*Enterococcus faecalis*
949	E3M10000041F07	*Enterococcus faecalis*
950	E3M10000041F08	*Enterococcus faecalis*
951	E3M10000041F09	*Enterococcus faecalis*
952	E3M10000041F10	*Enterococcus faecalis*
953	E3M10000041F11	*Enterococcus faecalis*
954	E3M10000041G02	*Enterococcus faecalis*
955	E3M10000041G03	*Enterococcus faecalis*
956	E3M10000041G04	*Enterococcus faecalis*
957	E3M10000041G06	*Enterococcus faecalis*
958	E3M10000041G07	*Enterococcus faecalis*
959	E3M10000041G08	*Enterococcus faecalis*
960	E3M10000041G09	*Enterococcus faecalis*
961	E3M10000041G10	*Enterococcus faecalis*
962	E3M10000041G12	*Enterococcus faecalis*
963	E3M10000041H04	*Enterococcus faecalis*
964	E3M10000041H05	*Enterococcus faecalis*
965	E3M10000041H06	*Enterococcus faecalis*
966	E3M10000041H07	*Enterococcus faecalis*
967	E3M10000041H08	*Enterococcus faecalis*
968	E3M10000041H09	*Enterococcus faecalis*
969	E3M10000041H10	*Enterococcus faecalis*
970	E3M10000041H11	*Enterococcus faecalis*
971	E3M10000042A03	*Enterococcus faecalis*
972	E3M10000042A08	*Enterococcus faecalis*
973	E3M10000042A10	*Enterococcus faecalis*
974	E3M10000042B01	*Enterococcus faecalis*
975	E3M10000042B02	*Enterococcus faecalis*
976	E3M10000042B04	*Enterococcus faecalis*
977	E3M10000042B08	*Enterococcus faecalis*
978	E3M10000042B09	*Enterococcus faecalis*
979	E3M10000042B10	*Enterococcus faecalis*
980	E3M10000042B11	*Enterococcus faecalis*
981	E3M10000042C02	*Enterococcus faecalis*
982	E3M10000042C03	*Enterococcus faecalis*
983	E3M10000042C04	*Enterococcus faecalis*
984	E3M10000042C10	*Enterococcus faecalis*
985	E3M10000042D01	*Enterococcus faecalis*
986	E3M10000042D02	*Enterococcus faecalis*

TABLE IA

SeqID	Clone name	Organism
987	E3M10000042D03	*Enterococcus faecalis*
988	E3M10000042D06	*Enterococcus faecalis*
989	E3M10000042D09	*Enterococcus faecalis*
990	E3M10000042D11	*Enterococcus faecalis*
991	E3M10000042D12	*Enterococcus faecalis*
992	E3M10000042E05	*Enterococcus faecalis*
993	E3M10000042E12	*Enterococcus faecalis*
994	E3M10000042F11	*Enterococcus faecalis*
995	E3M10000042G01	*Enterococcus faecalis*
996	E3M10000042G05	*Enterococcus faecalis*
997	E3M10000042G07	*Enterococcus faecalis*
998	E3M10000042G08	*Enterococcus faecalis*
999	E3M10000042G11	*Enterococcus faecalis*
1000	E3M10000042G12	*Enterococcus faecalis*
1001	E3M10000042H06	*Enterococcus faecalis*
1002	E3M10000042H08	*Enterococcus faecalis*
1003	E3M10000042H11	*Enterococcus faecalis*
1004	E3M10000043A02	*Enterococcus faecalis*
1005	E3M10000043A03	*Enterococcus faecalis*
1006	E3M10000043A05	*Enterococcus faecalis*
1007	E3M10000043A08	*Enterococcus faecalis*
1008	E3M10000043A09	*Enterococcus faecalis*
1009	E3M10000043A10	*Enterococcus faecalis*
1010	E3M10000043A11	*Enterococcus faecalis*
1011	E3M10000043B01	*Enterococcus faecalis*
1012	E3M10000043B02	*Enterococcus faecalis*
1013	E3M10000043B03	*Enterococcus faecalis*
1014	E3M10000043B06	*Enterococcus faecalis*
1015	E3M10000043B08	*Enterococcus faecalis*
1016	E3M10000043B09	*Enterococcus faecalis*
1017	E3M10000043B10	*Enterococcus faecalis*
1018	E3M10000043B11	*Enterococcus faecalis*
1019	E3M10000043B12	*Enterococcus faecalis*
1020	E3M10000043C01	*Enterococcus faecalis*
1021	E3M10000043C08	*Enterococcus faecalis*
1022	E3M10000043C09	*Enterococcus faecalis*
1023	E3M10000043D01	*Enterococcus faecalis*
1024	E3M10000043D02	*Enterococcus faecalis*
1025	E3M10000043D09	*Enterococcus faecalis*
1026	E3M10000043D10	*Enterococcus faecalis*
1027	E3M10000043D12	*Enterococcus faecalis*
1028	E3M10000043E03	*Enterococcus faecalis*
1029	E3M10000043E07	*Enterococcus faecalis*
1030	E3M10000043E08	*Enterococcus faecalis*
1031	E3M10000043E10	*Enterococcus faecalis*
1032	E3M10000043E11	*Enterococcus faecalis*
1033	E3M10000043F03	*Enterococcus faecalis*
1034	E3M10000043F04	*Enterococcus faecalis*
1035	E3M10000043F06	*Enterococcus faecalis*

TABLE IA

SeqID	Clone name	Organism
1036	E3M10000043F08	*Enterococcus faecalis*
1037	E3M10000043F10	*Enterococcus faecalis*
1038	E3M10000043F12	*Enterococcus faecalis*
1039	E3M10000043G03	*Enterococcus faecalis*
1040	E3M10000043G04	*Enterococcus faecalis*
1041	E3M10000043G05	*Enterococcus faecalis*
1042	E3M10000043G07	*Enterococcus faecalis*
1043	E3M10000043G08	*Enterococcus faecalis*
1044	E3M10000043G10	*Enterococcus faecalis*
1045	E3M10000043G11	*Enterococcus faecalis*
1046	E3M10000043G12	*Enterococcus faecalis*
1047	E3M10000043H02	*Enterococcus faecalis*
1048	E3M10000043H05	*Enterococcus faecalis*
1049	E3M10000043H08	*Enterococcus faecalis*
1050	E3M10000043H09	*Enterococcus faecalis*
1051	E3M10000043H11	*Enterococcus faecalis*
1052	E3M10000044C02	*Enterococcus faecalis*
1053	E3M10000044E01	*Enterococcus faecalis*
1054	K1M10000002F02	*Klebsiella pneumoniae*
1055	K1M10000003C01	*Klebsiella pneumoniae*
1056	K1M10000004F06	*Klebsiella pneumoniae*
1057	K1M10000007F01	*Klebsiella pneumoniae*
1058	K1M10000008C02	*Klebsiella pneumoniae*
1059	K1M10000008C10	*Klebsiella pneumoniae*
1060	K1M10000008G10	*Klebsiella pneumoniae*
1061	K1M10000009D04	*Klebsiella pneumoniae*
1062	K1M10000013E04	*Klebsiella pneumoniae*
1063	K1M10000013E06	*Klebsiella pneumoniae*
1064	K1M10000019D06	*Klebsiella pneumoniae*
1065	K1M10000020B02	*Klebsiella pneumoniae*
1066	K1M10000021H06	*Klebsiella pneumoniae*
1067	K1M10000022C10	*Klebsiella pneumoniae*
1068	K1M10000023E09	*Klebsiella pneumoniae*
1069	K1M10000023E10	*Klebsiella pneumoniae*
1070	K1M10000030C07	*Klebsiella pneumoniae*
1071	K1M10000030E07	*Klebsiella pneumoniae*
1072	K1M10000031B11	*Klebsiella pneumoniae*
1073	K1M10000032E11	*Klebsiella pneumoniae*
1074	K1M10000033B02	*Klebsiella pneumoniae*
1075	K1M10000033E01	*Klebsiella pneumoniae*
1076	K1M10000036G08	*Klebsiella pneumoniae*
1077	K1M10000037D10	*Klebsiella pneumoniae*
1078	K1M10000038H09	*Klebsiella pneumoniae*
1079	K1M10000039H03	*Klebsiella pneumoniae*
1080	K1M10000043C01	*Klebsiella pneumoniae*
1081	K1M10000043D05	*Klebsiella pneumoniae*
1082	K1M10000043H10	*Klebsiella pneumoniae*
1083	K1M10000044D05	*Klebsiella pneumoniae*
1084	K1M10000044D08	*Klebsiella pneumoniae*

TABLE IA

SeqID	Clone name	Organism
1085	K1M10000044E05	*Klebsiella pneumoniae*
1086	K1M10000044G05	*Klebsiella pneumoniae*
1087	K1M10000045A07	*Klebsiella pneumoniae*
1088	K1M10000045D10	*Klebsiella pneumoniae*
1089	K1M10000003D03	*Klebsiella pneumoniae*
1090	K1M10000010C02	*Klebsiella pneumoniae*
1091	K1M10000021H10	*Klebsiella pneumoniae*
1092	P1M10000008C06	*Pseudomonas aeruginosa*
1093	P1M10000008G04	*Pseudomonas aeruginosa*
1094	P1M10000010C03	*Pseudomonas aeruginosa*
1095	P1M10000014H10	*Pseudomonas aeruginosa*
1096	P1M10000015C06	*Pseudomonas aeruginosa*
1097	P1M10000015C09	*Pseudomonas aeruginosa*
1098	P1M10000016C04	*Pseudomonas aeruginosa*
1099	P1M10000018B01	*Pseudomonas aeruginosa*
1100	P1M10000018C01	*Pseudomonas aeruginosa*
1101	P1M10000018E01	*Pseudomonas aeruginosa*
1102	P1M10000018G01	*Pseudomonas aeruginosa*
1103	P1M10000019F01	*Pseudomonas aeruginosa*
1104	P1M10000021G03	*Pseudomonas aeruginosa*
1105	P1M10000021G05	*Pseudomonas aeruginosa*
1106	P1M10000022D09	*Pseudomonas aeruginosa*
1107	P1M10000024D06	*Pseudomonas aeruginosa*
1108	P1M10000024E06	*Pseudomonas aeruginosa*
1109	P1M10000024H03	*Pseudomonas aeruginosa*
1110	P1M10000025A06	*Pseudomonas aeruginosa*
1111	P1M10000025G07	*Pseudomonas aeruginosa*
1112	P1M10000025H07	*Pseudomonas aeruginosa*
1113	P1M10000026E06	*Pseudomonas aeruginosa*
1114	P1M10000026F04	*Pseudomonas aeruginosa*
1115	P1M10000026G09	*Pseudomonas aeruginosa*
1116	P1M10000026H02	*Pseudomonas aeruginosa*
1117	P1M10000026H05	*Pseudomonas aeruginosa*
1118	P1M10000027A06	*Pseudomonas aeruginosa*
1119	P1M10000027B02	*Pseudomonas aeruginosa*
1120	P1M10000027G05	*Pseudomonas aeruginosa*
1121	P1M10000028A08	*Pseudomonas aeruginosa*
1122	P1M10000028B01	*Pseudomonas aeruginosa*
1123	P1M10000028E02	*Pseudomonas aeruginosa*
1124	P1M10000029A09	*Pseudomonas aeruginosa*
1125	P1M10000029G03	*Pseudomonas aeruginosa*
1126	P1M10000029H05	*Pseudomonas aeruginosa*
1127	P1M10000032F04	*Pseudomonas aeruginosa*
1128	P1M10000033A02	*Pseudomonas aeruginosa*
1129	P1M10000033B08	*Pseudomonas aeruginosa*
1130	P1M10000033E03	*Pseudomonas aeruginosa*
1131	P1M10000033F01	*Pseudomonas aeruginosa*
1132	P1M10000033G08	*Pseudomonas aeruginosa*
1133	P1M10000035A06	*Pseudomonas aeruginosa*

TABLE IA

SeqID	Clone name	Organism
1134	P1M10000037B12	*Pseudomonas aeruginosa*
1135	P1M10000037G12	*Pseudomonas aeruginosa*
1136	P1M10000038B08	*Pseudomonas aeruginosa*
1137	P1M10000038C03	*Pseudomonas aeruginosa*
1138	P1M10000038C06	*Pseudomonas aeruginosa*
1139	P1M10000038F04	*Pseudomonas aeruginosa*
1140	P1M10000038G02	*Pseudomonas aeruginosa*
1141	P1M10000039G05	*Pseudomonas aeruginosa*
1142	P1M10000039G12	*Pseudomonas aeruginosa*
1143	P1M10000040C01	*Pseudomonas aeruginosa*
1144	P1M10000040C04	*Pseudomonas aeruginosa*
1145	P1M10000040D04	*Pseudomonas aeruginosa*
1146	P1M10000040D05	*Pseudomonas aeruginosa*
1147	P1M10000040E10	*Pseudomonas aeruginosa*
1148	P1M10000040H03	*Pseudomonas aeruginosa*
1149	P1M10000041A12	*Pseudomonas aeruginosa*
1150	P1M10000041B02	*Pseudomonas aeruginosa*
1151	P1M10000041E01	*Pseudomonas aeruginosa*
1152	P1M10000041F01	*Pseudomonas aeruginosa*
1153	P1M10000042B12	*Pseudomonas aeruginosa*
1154	P1M10000042E08	*Pseudomonas aeruginosa*
1155	P1M10000043A03	*Pseudomonas aeruginosa*
1156	P1M10000043D06	*Pseudomonas aeruginosa*
1157	P1M10000044F07	*Pseudomonas aeruginosa*
1158	P1M10000046B03	*Pseudomonas aeruginosa*
1159	P1M10000046C07	*Pseudomonas aeruginosa*
1160	P1M10000046C08	*Pseudomonas aeruginosa*
1161	P1M10000046C09	*Pseudomonas aeruginosa*
1162	P1M10000046G11	*Pseudomonas aeruginosa*
1163	P1M10000047B04	*Pseudomonas aeruginosa*
1164	P1M10000047E11	*Pseudomonas aeruginosa*
1165	P1M10000047F07	*Pseudomonas aeruginosa*
1166	P1M10000047G10	*Pseudomonas aeruginosa*
1167	P1M10000048A03	*Pseudomonas aeruginosa*
1168	P1M10000049E08	*Pseudomonas aeruginosa*
1169	P1M10000049G10	*Pseudomonas aeruginosa*
1170	P1M10000050G11	*Pseudomonas aeruginosa*
1171	P1M10000051D11	*Pseudomonas aeruginosa*
1172	P1M10000051F01	*Pseudomonas aeruginosa*
1173	P1M10000052C03	*Pseudomonas aeruginosa*
1174	P1M10000052C12	*Pseudomonas aeruginosa*
1175	P1M10000052E04	*Pseudomonas aeruginosa*
1176	P1M10000053B12	*Pseudomonas aeruginosa*
1177	P1M10000053C02	*Pseudomonas aeruginosa*
1178	P1M10000053E07	*Pseudomonas aeruginosa*
1179	P1M10000053F08	*Pseudomonas aeruginosa*
1180	P1M10000055A11	*Pseudomonas aeruginosa*
1181	P1M10000055C08	*Pseudomonas aeruginosa*
1182	P1M10000055E05	*Pseudomonas aeruginosa*

SeqID	Clone name	Organism
1183	P1M10000056C07	*Pseudomonas aeruginosa*
1184	P1M10000056F05	*Pseudomonas aeruginosa*
1185	P1M10000056F06	*Pseudomonas aeruginosa*
1186	P1M10000056G01	*Pseudomonas aeruginosa*
1187	P1M10000058B07	*Pseudomonas aeruginosa*
1188	P1M10000059B04	*Pseudomonas aeruginosa*
1189	P1M10000059B10	*Pseudomonas aeruginosa*
1190	P1M10000059B11	*Pseudomonas aeruginosa*
1191	P1M10000059D11	*Pseudomonas aeruginosa*
1192	P1M10000059H08	*Pseudomonas aeruginosa*
1193	P1M10000059H09	*Pseudomonas aeruginosa*
1194	P1M10000060E03	*Pseudomonas aeruginosa*
1195	P1M10000060H02	*Pseudomonas aeruginosa*
1196	P1M10000060H04	*Pseudomonas aeruginosa*
1197	P1M10000061B04	*Pseudomonas aeruginosa*
1198	P1M10000061E04	*Pseudomonas aeruginosa*
1199	P1M10000061F04	*Pseudomonas aeruginosa*
1200	P1M10000062A12	*Pseudomonas aeruginosa*
1201	P1M10000062C03	*Pseudomonas aeruginosa*
1202	P1M10000062C04	*Pseudomonas aeruginosa*
1203	P1M10000062C07	*Pseudomonas aeruginosa*
1204	P1M10000062C12	*Pseudomonas aeruginosa*
1205	P1M10000062D07	*Pseudomonas aeruginosa*
1206	P1M10000062D08	*Pseudomonas aeruginosa*
1207	P1M10000062E08	*Pseudomonas aeruginosa*
1208	P1M10000062F06	*Pseudomonas aeruginosa*
1209	P1M10000062G11	*Pseudomonas aeruginosa*
1210	P1M10000062H01	*Pseudomonas aeruginosa*
1211	P1M10000062H04	*Pseudomonas aeruginosa*
1212	P1M10000063F02	*Pseudomonas aeruginosa*
1213	P1M10000063G02	*Pseudomonas aeruginosa*
1214	P1M10000063H02	*Pseudomonas aeruginosa*
1215	P1M10000064A10	*Pseudomonas aeruginosa*
1216	P1M10000064C02	*Pseudomonas aeruginosa*
1217	P1M10000064C03	*Pseudomonas aeruginosa*
1218	P1M10000064D03	*Pseudomonas aeruginosa*
1219	P1M10000064E05	*Pseudomonas aeruginosa*
1220	P1M10000064G12	*Pseudomonas aeruginosa*
1221	P1M10000064H07	*Pseudomonas aeruginosa*
1222	P1M10000065A04	*Pseudomonas aeruginosa*
1223	P1M10000065B07	*Pseudomonas aeruginosa*
1224	P1M10000065C03	*Pseudomonas aeruginosa*
1225	P1M10000065C05	*Pseudomonas aeruginosa*
1226	P1M10000065D06	*Pseudomonas aeruginosa*
1227	P1M10000065F01	*Pseudomonas aeruginosa*
1228	P1M10000065G06	*Pseudomonas aeruginosa*
1229	P1M10000065H07	*Pseudomonas aeruginosa*
1230	P1M10000066A10	*Pseudomonas aeruginosa*
1231	P1M10000066A11	*Pseudomonas aeruginosa*

TABLE IA

SeqID	Clone name	Organism
1232	P1M10000066F04	*Pseudomonas aeruginosa*
1233	P1M10000067A05	*Pseudomonas aeruginosa*
1234	P1M10000067A06	*Pseudomonas aeruginosa*
1235	P1M10000067A08	*Pseudomonas aeruginosa*
1236	P1M10000067C04	*Pseudomonas aeruginosa*
1237	P1M10000067C06	*Pseudomonas aeruginosa*
1238	P1M10000067D05	*Pseudomonas aeruginosa*
1239	P1M10000067F05	*Pseudomonas aeruginosa*
1240	P1M10000067G05	*Pseudomonas aeruginosa*
1241	P1M10000068A09	*Pseudomonas aeruginosa*
1242	P1M10000068D04	*Pseudomonas aeruginosa*
1243	P1M10000068F04	*Pseudomonas aeruginosa*
1244	P1M10000068F08	*Pseudomonas aeruginosa*
1245	P1M10000068G01	*Pseudomonas aeruginosa*
1246	P1M10000068H05	*Pseudomonas aeruginosa*
1247	P1M10000069D09	*Pseudomonas aeruginosa*
1248	P1M10000069G06	*Pseudomonas aeruginosa*
1249	P1M10000069H02	*Pseudomonas aeruginosa*
1250	P1M10000070A05	*Pseudomonas aeruginosa*
1251	P1M10000070B10	*Pseudomonas aeruginosa*
1252	P1M10000070C06	*Pseudomonas aeruginosa*
1253	P1M10000070D08	*Pseudomonas aeruginosa*
1254	P1M10000070E03	*Pseudomonas aeruginosa*
1255	P1M10000070G06	*Pseudomonas aeruginosa*
1256	P1M10000070G12	*Pseudomonas aeruginosa*
1257	P1M10000070H06	*Pseudomonas aeruginosa*
1258	P1M10000071A03	*Pseudomonas aeruginosa*
1259	P1M10000071C01	*Pseudomonas aeruginosa*
1260	P1M10000071E04	*Pseudomonas aeruginosa*
1261	P1M10000071F01	*Pseudomonas aeruginosa*
1262	P1M10000073A06	*Pseudomonas aeruginosa*
1263	P1M10000073B10	*Pseudomonas aeruginosa*
1264	P1M10000073D04	*Pseudomonas aeruginosa*
1265	P1M10000073D09	*Pseudomonas aeruginosa*
1266	P1M10000073G03	*Pseudomonas aeruginosa*
1267	P1M10000074B01	*Pseudomonas aeruginosa*
1268	P1M10000074B04	*Pseudomonas aeruginosa*
1269	P1M10000074E04	*Pseudomonas aeruginosa*
1270	P1M10000074E09	*Pseudomonas aeruginosa*
1271	P1M10000074F10	*Pseudomonas aeruginosa*
1272	P1M10000074G12	*Pseudomonas aeruginosa*
1273	P1M10000075A04	*Pseudomonas aeruginosa*
1274	P1M10000075B03	*Pseudomonas aeruginosa*
1275	P1M10000075F02	*Pseudomonas aeruginosa*
1276	P1M10000075G05	*Pseudomonas aeruginosa*
1277	P1M10000076D05	*Pseudomonas aeruginosa*
1278	P1M10000076D10	*Pseudomonas aeruginosa*
1279	P1M10000077A08	*Pseudomonas aeruginosa*
1280	P1M10000077C08	*Pseudomonas aeruginosa*

TABLE IA

SeqID	Clone name	Organism
1281	P1M10000077E04	*Pseudomonas aeruginosa*
1282	P1M10000077H05	*Pseudomonas aeruginosa*
1283	P1M10000079A10	*Pseudomonas aeruginosa*
1284	P1M10000079B10	*Pseudomonas aeruginosa*
1285	P1M10000079C10	*Pseudomonas aeruginosa*
1286	P1M10000079D01	*Pseudomonas aeruginosa*
1287	P1M10000079D10	*Pseudomonas aeruginosa*
1288	P1M10000079F06	*Pseudomonas aeruginosa*
1289	P1M10000080B01	*Pseudomonas aeruginosa*
1290	P1M10000080B06	*Pseudomonas aeruginosa*
1291	P1M10000080C01	*Pseudomonas aeruginosa*
1292	P1M10000080C06	*Pseudomonas aeruginosa*
1293	P1M10000080E04	*Pseudomonas aeruginosa*
1294	P1M10000081D12	*Pseudomonas aeruginosa*
1295	P1M10000081G05	*Pseudomonas aeruginosa*
1296	P1M10000081H05	*Pseudomonas aeruginosa*
1297	P1M10000082A05	*Pseudomonas aeruginosa*
1298	P1M10000082B04	*Pseudomonas aeruginosa*
1299	P1M10000082C05	*Pseudomonas aeruginosa*
1300	P1M10000082D05	*Pseudomonas aeruginosa*
1301	P1M10000082E05	*Pseudomonas aeruginosa*
1302	P1M10000083A11	*Pseudomonas aeruginosa*
1303	P1M10000083B01	*Pseudomonas aeruginosa*
1304	P1M10000083B12	*Pseudomonas aeruginosa*
1305	P1M10000083C11	*Pseudomonas aeruginosa*
1306	P1M10000083C12	*Pseudomonas aeruginosa*
1307	P1M10000084A04	*Pseudomonas aeruginosa*
1308	P1M10000084D03	*Pseudomonas aeruginosa*
1309	P1M10000084E04	*Pseudomonas aeruginosa*
1310	P1M10000084E11	*Pseudomonas aeruginosa*
1311	P1M10000084F08	*Pseudomonas aeruginosa*
1312	P1M10000085D06	*Pseudomonas aeruginosa*
1313	P1M10000086A02	*Pseudomonas aeruginosa*
1314	P1M10000086B01	*Pseudomonas aeruginosa*
1315	P1M10000086D02	*Pseudomonas aeruginosa*
1316	P1M10000086E05	*Pseudomonas aeruginosa*
1317	P1M10000087A11	*Pseudomonas aeruginosa*
1318	P1M10000087C09	*Pseudomonas aeruginosa*
1319	P1M10000087E04	*Pseudomonas aeruginosa*
1320	P1M10000087F04	*Pseudomonas aeruginosa*
1321	P1M10000087F09	*Pseudomonas aeruginosa*
1322	P1M10000088A07	*Pseudomonas aeruginosa*
1323	P1M10000088D06	*Pseudomonas aeruginosa*
1324	P1M10000089C08	*Pseudomonas aeruginosa*
1325	P1M10000089D11	*Pseudomonas aeruginosa*
1326	P1M10000089G08	*Pseudomonas aeruginosa*
1327	P1M10000090B11	*Pseudomonas aeruginosa*
1328	P1M10000090F06	*Pseudomonas aeruginosa*
1329	P1M10000090F08	*Pseudomonas aeruginosa*

TABLE IA

SeqID	Clone name	Organism
1330	P1M10000091D02	*Pseudomonas aeruginosa*
1331	P1M10000091E09	*Pseudomonas aeruginosa*
1332	P1M10000091G10	*Pseudomonas aeruginosa*
1333	P1M10000092B02	*Pseudomonas aeruginosa*
1334	P1M10000092B10	*Pseudomonas aeruginosa*
1335	P1M10000092D09	*Pseudomonas aeruginosa*
1336	P1M10000092E02	*Pseudomonas aeruginosa*
1337	P1M10000092F05	*Pseudomonas aeruginosa*
1338	P1M10000093A03	*Pseudomonas aeruginosa*
1339	P1M10000093B09	*Pseudomonas aeruginosa*
1340	P1M10000093C08	*Pseudomonas aeruginosa*
1341	P1M10000093E09	*Pseudomonas aeruginosa*
1342	P1M10000093F03	*Pseudomonas aeruginosa*
1343	P1M10000093H07	*Pseudomonas aeruginosa*
1344	P1M10000094F04	*Pseudomonas aeruginosa*
1345	P1M10000094H03	*Pseudomonas aeruginosa*
1346	P1M10000095C01	*Pseudomonas aeruginosa*
1347	P1M10000095C09	*Pseudomonas aeruginosa*
1348	P1M10000095E04	*Pseudomonas aeruginosa*
1349	P1M10000095G04	*Pseudomonas aeruginosa*
1350	P1M10000096E04	*Pseudomonas aeruginosa*
1351	P1M10000096E12	*Pseudomonas aeruginosa*
1352	ID2	*Pseudomonas aeruginosa*
1353	4.1	*Pseudomonas aeruginosa*
1354	S1M10000001A05	*Staphylococcus aureus*
1355	S1M10000001A08	*Staphylococcus aureus*
1356	S1M10000001A09	*Staphylococcus aureus*
1357	S1M10000001A10	*Staphylococcus aureus*
1358	S1M10000001C06	*Staphylococcus aureus*
1359	S1M10000001D01	*Staphylococcus aureus*
1360	S1M10000001D02	*Staphylococcus aureus*
1361	S1M10000001D06	*Staphylococcus aureus*
1362	S1M10000001D07	*Staphylococcus aureus*
1363	S1M10000001E02	*Staphylococcus aureus*
1364	S1M10000001E04	*Staphylococcus aureus*
1365	S1M10000001E05	*Staphylococcus aureus*
1366	S1M10000001E09	*Staphylococcus aureus*
1367	S1M10000001E10	*Staphylococcus aureus*
1368	S1M10000001E11	*Staphylococcus aureus*
1369	S1M10000001F02	*Staphylococcus aureus*
1370	S1M10000001F04	*Staphylococcus aureus*
1371	S1M10000001F08	*Staphylococcus aureus*
1372	S1M10000001F09	*Staphylococcus aureus*
1373	S1M10000001F10	*Staphylococcus aureus*
1374	S1M10000001F11	*Staphylococcus aureus*
1375	S1M10000001G01	*Staphylococcus aureus*
1376	S1M10000001G07	*Staphylococcus aureus*
1377	S1M10000001G08	*Staphylococcus aureus*
1378	S1M10000001G10	*Staphylococcus aureus*

SeqID	Clone name	Organism
1379	S1M10000002A02	*Staphylococcus aureus*
1380	S1M10000002A09	*Staphylococcus aureus*
1381	S1M10000002A10	*Staphylococcus aureus*
1382	S1M10000002A12	*Staphylococcus aureus*
1383	S1M10000002B01	*Staphylococcus aureus*
1384	S1M10000002B03	*Staphylococcus aureus*
1385	S1M10000002B04	*Staphylococcus aureus*
1386	S1M10000002B05	*Staphylococcus aureus*
1387	S1M10000002B06	*Staphylococcus aureus*
1388	S1M10000002B07	*Staphylococcus aureus*
1389	S1M10000002B09	*Staphylococcus aureus*
1390	S1M10000002B11	*Staphylococcus aureus*
1391	S1M10000002C02	*Staphylococcus aureus*
1392	S1M10000002C09	*Staphylococcus aureus*
1393	S1M10000002C10	*Staphylococcus aureus*
1394	S1M10000002C11	*Staphylococcus aureus*
1395	S1M10000002C12	*Staphylococcus aureus*
1396	S1M10000002D01	*Staphylococcus aureus*
1397	S1M10000002D02	*Staphylococcus aureus*
1398	S1M10000002D03	*Staphylococcus aureus*
1399	S1M10000002D05	*Staphylococcus aureus*
1400	S1M10000002D07	*Staphylococcus aureus*
1401	S1M10000002D08	*Staphylococcus aureus*
1402	S1M10000002D10	*Staphylococcus aureus*
1403	S1M10000002D12	*Staphylococcus aureus*
1404	S1M10000002E01	*Staphylococcus aureus*
1405	S1M10000002E02	*Staphylococcus aureus*
1406	S1M10000002E07	*Staphylococcus aureus*
1407	S1M10000002E09	*Staphylococcus aureus*
1408	S1M10000002E11	*Staphylococcus aureus*
1409	S1M10000002E12	*Staphylococcus aureus*
1410	S1M10000002F01	*Staphylococcus aureus*
1411	S1M10000002F02	*Staphylococcus aureus*
1412	S1M10000002F04	*Staphylococcus aureus*
1413	S1M10000002F09	*Staphylococcus aureus*
1414	S1M10000002F12	*Staphylococcus aureus*
1415	S1M10000002G01	*Staphylococcus aureus*
1416	S1M10000002G03	*Staphylococcus aureus*
1417	S1M10000002G05	*Staphylococcus aureus*
1418	S1M10000002G06	*Staphylococcus aureus*
1419	S1M10000002G07	*Staphylococcus aureus*
1420	S1M10000002G08	*Staphylococcus aureus*
1421	S1M10000002G09	*Staphylococcus aureus*
1422	S1M10000002G10	*Staphylococcus aureus*
1423	S1M10000002G11	*Staphylococcus aureus*
1424	S1M10000002G12	*Staphylococcus aureus*
1425	S1M10000003A01	*Staphylococcus aureus*
1426	S1M10000003A02	*Staphylococcus aureus*
1427	S1M10000003A03	*Staphylococcus aureus*

SeqID	Clone name	Organism
1428	S1M10000003A04	*Staphylococcus aureus*
1429	S1M10000003A06	*Staphylococcus aureus*
1430	S1M10000003A07	*Staphylococcus aureus*
1431	S1M10000003A08	*Staphylococcus aureus*
1432	S1M10000003A10	*Staphylococcus aureus*
1433	S1M10000003A11	*Staphylococcus aureus*
1434	S1M10000003B06	*Staphylococcus aureus*
1435	S1M10000003B08	*Staphylococcus aureus*
1436	S1M10000003B09	*Staphylococcus aureus*
1437	S1M10000003B12	*Staphylococcus aureus*
1438	S1M10000003C06	*Staphylococcus aureus*
1439	S1M10000003C07	*Staphylococcus aureus*
1440	S1M10000003C10	*Staphylococcus aureus*
1441	S1M10000003C12	*Staphylococcus aureus*
1442	S1M10000003D05	*Staphylococcus aureus*
1443	S1M10000003D06	*Staphylococcus aureus*
1444	S1M10000003D08	*Staphylococcus aureus*
1445	S1M10000003D10	*Staphylococcus aureus*
1446	S1M10000003E07	*Staphylococcus aureus*
1447	S1M10000003E09	*Staphylococcus aureus*
1448	S1M10000003E10	*Staphylococcus aureus*
1449	S1M10000003E11	*Staphylococcus aureus*
1450	S1M10000003F02	*Staphylococcus aureus*
1451	S1M10000003F05	*Staphylococcus aureus*
1452	S1M10000003F06	*Staphylococcus aureus*
1453	S1M10000003F07	*Staphylococcus aureus*
1454	S1M10000003F08	*Staphylococcus aureus*
1455	S1M10000003F12	*Staphylococcus aureus*
1456	S1M10000003G03	*Staphylococcus aureus*
1457	S1M10000003G04	*Staphylococcus aureus*
1458	S1M10000003G08	*Staphylococcus aureus*
1459	S1M10000003G10	*Staphylococcus aureus*
1460	S1M10000004A04	*Staphylococcus aureus*
1461	S1M10000004A06	*Staphylococcus aureus*
1462	S1M10000004A07	*Staphylococcus aureus*
1463	S1M10000004A11	*Staphylococcus aureus*
1464	S1M10000004A12	*Staphylococcus aureus*
1465	S1M10000004B03	*Staphylococcus aureus*
1466	S1M10000004B04	*Staphylococcus aureus*
1467	S1M10000004B06	*Staphylococcus aureus*
1468	S1M10000004B08	*Staphylococcus aureus*
1469	S1M10000004B09	*Staphylococcus aureus*
1470	S1M10000004B11	*Staphylococcus aureus*
1471	S1M10000004C01	*Staphylococcus aureus*
1472	S1M10000004C02	*Staphylococcus aureus*
1473	S1M10000004C03	*Staphylococcus aureus*
1474	S1M10000004C06	*Staphylococcus aureus*
1475	S1M10000004C07	*Staphylococcus aureus*
1476	S1M10000004C08	*Staphylococcus aureus*

SeqID	Clone name	Organism
1477	S1M10000004C09	*Staphylococcus aureus*
1478	S1M10000004C10	*Staphylococcus aureus*
1479	S1M10000004C12	*Staphylococcus aureus*
1480	S1M10000004D01	*Staphylococcus aureus*
1481	S1M10000004D03	*Staphylococcus aureus*
1482	S1M10000004D04	*Staphylococcus aureus*
1483	S1M10000004D06	*Staphylococcus aureus*
1484	S1M10000004D07	*Staphylococcus aureus*
1485	S1M10000004D08	*Staphylococcus aureus*
1486	S1M10000004D10	*Staphylococcus aureus*
1487	S1M10000004D12	*Staphylococcus aureus*
1488	S1M10000004E03	*Staphylococcus aureus*
1489	S1M10000004E04	*Staphylococcus aureus*
1490	S1M10000004E06	*Staphylococcus aureus*
1491	S1M10000004E07	*Staphylococcus aureus*
1492	S1M10000004E11	*Staphylococcus aureus*
1493	S1M10000004E12	*Staphylococcus aureus*
1494	S1M10000004F01	*Staphylococcus aureus*
1495	S1M10000004F02	*Staphylococcus aureus*
1496	S1M10000004F06	*Staphylococcus aureus*
1497	S1M10000004F07	*Staphylococcus aureus*
1498	S1M10000004F08	*Staphylococcus aureus*
1499	S1M10000004F09	*Staphylococcus aureus*
1500	S1M10000004F12	*Staphylococcus aureus*
1501	S1M10000004G01	*Staphylococcus aureus*
1502	S1M10000004G02	*Staphylococcus aureus*
1503	S1M10000004G03	*Staphylococcus aureus*
1504	S1M10000004G05	*Staphylococcus aureus*
1505	S1M10000004G06	*Staphylococcus aureus*
1506	S1M10000004G07	*Staphylococcus aureus*
1507	S1M10000004G09	*Staphylococcus aureus*
1508	S1M10000004G12	*Staphylococcus aureus*
1509	S1M10000005A01	*Staphylococcus aureus*
1510	S1M10000005A03	*Staphylococcus aureus*
1511	S1M10000005A05	*Staphylococcus aureus*
1512	S1M10000005A06	*Staphylococcus aureus*
1513	S1M10000005A07	*Staphylococcus aureus*
1514	S1M10000005A08	*Staphylococcus aureus*
1515	S1M10000005A09	*Staphylococcus aureus*
1516	S1M10000005A10	*Staphylococcus aureus*
1517	S1M10000005A11	*Staphylococcus aureus*
1518	S1M10000005B02	*Staphylococcus aureus*
1519	S1M10000005B04	*Staphylococcus aureus*
1520	S1M10000005B07	*Staphylococcus aureus*
1521	S1M10000005B08	*Staphylococcus aureus*
1522	S1M10000005B09	*Staphylococcus aureus*
1523	S1M10000005B12	*Staphylococcus aureus*
1524	S1M10000005C01	*Staphylococcus aureus*
1525	S1M10000005C05	*Staphylococcus aureus*

SeqID	Clone name	Organism
1526	S1M10000005C06	*Staphylococcus aureus*
1527	S1M10000005C09	*Staphylococcus aureus*
1528	S1M10000005C11	*Staphylococcus aureus*
1529	S1M10000005D01	*Staphylococcus aureus*
1530	S1M10000005D02	*Staphylococcus aureus*
1531	S1M10000005D03	*Staphylococcus aureus*
1532	S1M10000005D04	*Staphylococcus aureus*
1533	S1M10000005D05	*Staphylococcus aureus*
1534	S1M10000005D06	*Staphylococcus aureus*
1535	S1M10000005D07	*Staphylococcus aureus*
1536	S1M10000005D08	*Staphylococcus aureus*
1537	S1M10000005D09	*Staphylococcus aureus*
1538	S1M10000005D11	*Staphylococcus aureus*
1539	S1M10000005D12	*Staphylococcus aureus*
1540	S1M10000005E01	*Staphylococcus aureus*
1541	S1M10000005E02	*Staphylococcus aureus*
1542	S1M10000005E05	*Staphylococcus aureus*
1543	S1M10000005E06	*Staphylococcus aureus*
1544	S1M10000005E07	*Staphylococcus aureus*
1545	S1M10000005E08	*Staphylococcus aureus*
1546	S1M10000005E10	*Staphylococcus aureus*
1547	S1M10000005E11	*Staphylococcus aureus*
1548	S1M10000005E12	*Staphylococcus aureus*
1549	S1M10000005F02	*Staphylococcus aureus*
1550	S1M10000005F03	*Staphylococcus aureus*
1551	S1M10000005F04	*Staphylococcus aureus*
1552	S1M10000006A03	*Staphylococcus aureus*
1553	S1M10000006A04	*Staphylococcus aureus*
1554	S1M10000006A05	*Staphylococcus aureus*
1555	S1M10000006A07	*Staphylococcus aureus*
1556	S1M10000006A08	*Staphylococcus aureus*
1557	S1M10000006A10	*Staphylococcus aureus*
1558	S1M10000006A12	*Staphylococcus aureus*
1559	S1M10000006B02	*Staphylococcus aureus*
1560	S1M10000006B03	*Staphylococcus aureus*
1561	S1M10000006B04	*Staphylococcus aureus*
1562	S1M10000006B07	*Staphylococcus aureus*
1563	S1M10000006B10	*Staphylococcus aureus*
1564	S1M10000006B11	*Staphylococcus aureus*
1565	S1M10000006C02	*Staphylococcus aureus*
1566	S1M10000006C04	*Staphylococcus aureus*
1567	S1M10000006C06	*Staphylococcus aureus*
1568	S1M10000006C07	*Staphylococcus aureus*
1569	S1M10000006C08	*Staphylococcus aureus*
1570	S1M10000006C10	*Staphylococcus aureus*
1571	S1M10000006D03	*Staphylococcus aureus*
1572	S1M10000006D05	*Staphylococcus aureus*
1573	S1M10000006D06	*Staphylococcus aureus*
1574	S1M10000006D07	*Staphylococcus aureus*

SeqID	Clone name	Organism
1575	S1M10000006D08	*Staphylococcus aureus*
1576	S1M10000006E02	*Staphylococcus aureus*
1577	S1M10000006E03	*Staphylococcus aureus*
1578	S1M10000006E04	*Staphylococcus aureus*
1579	S1M10000006E07	*Staphylococcus aureus*
1580	S1M10000006E08	*Staphylococcus aureus*
1581	S1M10000006F01	*Staphylococcus aureus*
1582	S1M10000006F02	*Staphylococcus aureus*
1583	S1M10000006F03	*Staphylococcus aureus*
1584	S1M10000006F04	*Staphylococcus aureus*
1585	S1M10000006F06	*Staphylococcus aureus*
1586	S1M10000006G02	*Staphylococcus aureus*
1587	S1M10000006G03	*Staphylococcus aureus*
1588	S1M10000006G05	*Staphylococcus aureus*
1589	S1M10000006G06	*Staphylococcus aureus*
1590	S1M10000006G07	*Staphylococcus aureus*
1591	S1M10000006G09	*Staphylococcus aureus*
1592	S1M10000006G10	*Staphylococcus aureus*
1593	S1M10000006G11	*Staphylococcus aureus*
1594	S1M10000007A02	*Staphylococcus aureus*
1595	S1M10000007A03	*Staphylococcus aureus*
1596	S1M10000007B02	*Staphylococcus aureus*
1597	S1M10000007B11	*Staphylococcus aureus*
1598	S1M10000007C02	*Staphylococcus aureus*
1599	S1M10000007C04	*Staphylococcus aureus*
1600	S1M10000007C05	*Staphylococcus aureus*
1601	S1M10000007C06	*Staphylococcus aureus*
1602	S1M10000007C07	*Staphylococcus aureus*
1603	S1M10000007C08	*Staphylococcus aureus*
1604	S1M10000007C09	*Staphylococcus aureus*
1605	S1M10000007D03	*Staphylococcus aureus*
1606	S1M10000007D06	*Staphylococcus aureus*
1607	S1M10000007D08	*Staphylococcus aureus*
1608	S1M10000007D10	*Staphylococcus aureus*
1609	S1M10000007D11	*Staphylococcus aureus*
1610	S1M10000007E04	*Staphylococcus aureus*
1611	S1M10000007E06	*Staphylococcus aureus*
1612	S1M10000007E07	*Staphylococcus aureus*
1613	S1M10000007F01	*Staphylococcus aureus*
1614	S1M10000007F02	*Staphylococcus aureus*
1615	S1M10000007F04	*Staphylococcus aureus*
1616	S1M10000007F08	*Staphylococcus aureus*
1617	S1M10000007F09	*Staphylococcus aureus*
1618	S1M10000007F10	*Staphylococcus aureus*
1619	S1M10000007F11	*Staphylococcus aureus*
1620	S1M10000007F12	*Staphylococcus aureus*
1621	S1M10000007G02	*Staphylococcus aureus*
1622	S1M10000007G03	*Staphylococcus aureus*
1623	S1M10000007G05	*Staphylococcus aureus*

SeqID	Clone name	Organism
1624	S1M10000007G07	*Staphylococcus aureus*
1625	S1M10000007G08	*Staphylococcus aureus*
1626	S1M10000008A03	*Staphylococcus aureus*
1627	S1M10000008A04	*Staphylococcus aureus*
1628	S1M10000008A05	*Staphylococcus aureus*
1629	S1M10000008A08	*Staphylococcus aureus*
1630	S1M10000008A09	*Staphylococcus aureus*
1631	S1M10000008A12	*Staphylococcus aureus*
1632	S1M10000008B03	*Staphylococcus aureus*
1633	S1M10000008B04	*Staphylococcus aureus*
1634	S1M10000008B06	*Staphylococcus aureus*
1635	S1M10000008B08	*Staphylococcus aureus*
1636	S1M10000008B09	*Staphylococcus aureus*
1637	S1M10000008B10	*Staphylococcus aureus*
1638	S1M10000008C05	*Staphylococcus aureus*
1639	S1M10000008C06	*Staphylococcus aureus*
1640	S1M10000008C07	*Staphylococcus aureus*
1641	S1M10000008C08	*Staphylococcus aureus*
1642	S1M10000008C09	*Staphylococcus aureus*
1643	S1M10000008D05	*Staphylococcus aureus*
1644	S1M10000008D09	*Staphylococcus aureus*
1645	S1M10000008E05	*Staphylococcus aureus*
1646	S1M10000008E08	*Staphylococcus aureus*
1647	S1M10000008E09	*Staphylococcus aureus*
1648	S1M10000008E10	*Staphylococcus aureus*
1649	S1M10000008F01	*Staphylococcus aureus*
1650	S1M10000008F02	*Staphylococcus aureus*
1651	S1M10000008F03	*Staphylococcus aureus*
1652	S1M10000008F06	*Staphylococcus aureus*
1653	S1M10000008F08	*Staphylococcus aureus*
1654	S1M10000008F09	*Staphylococcus aureus*
1655	S1M10000008F10	*Staphylococcus aureus*
1656	S1M10000008F11	*Staphylococcus aureus*
1657	S1M10000008G02	*Staphylococcus aureus*
1658	S1M10000008G03	*Staphylococcus aureus*
1659	S1M10000008G05	*Staphylococcus aureus*
1660	S1M10000009A02	*Staphylococcus aureus*
1661	S1M10000009A04	*Staphylococcus aureus*
1662	S1M10000009A07	*Staphylococcus aureus*
1663	S1M10000009A08	*Staphylococcus aureus*
1664	S1M10000009A09	*Staphylococcus aureus*
1665	S1M10000009A10	*Staphylococcus aureus*
1666	S1M10000009A11	*Staphylococcus aureus*
1667	S1M10000009B01	*Staphylococcus aureus*
1668	S1M10000009B02	*Staphylococcus aureus*
1669	S1M10000009B03	*Staphylococcus aureus*
1670	S1M10000009B04	*Staphylococcus aureus*
1671	S1M10000009B05	*Staphylococcus aureus*
1672	S1M10000009B06	*Staphylococcus aureus*

TABLE IA

SeqID	Clone name	Organism
1673	S1M10000009B07	*Staphylococcus aureus*
1674	S1M10000009B10	*Staphylococcus aureus*
1675	S1M10000009B11	*Staphylococcus aureus*
1676	S1M10000009B12	*Staphylococcus aureus*
1677	S1M10000009C01	*Staphylococcus aureus*
1678	S1M10000009C02	*Staphylococcus aureus*
1679	S1M10000009C05	*Staphylococcus aureus*
1680	S1M10000009C06	*Staphylococcus aureus*
1681	S1M10000009C07	*Staphylococcus aureus*
1682	S1M10000009C08	*Staphylococcus aureus*
1683	S1M10000009C09	*Staphylococcus aureus*
1684	S1M10000009C10	*Staphylococcus aureus*
1685	S1M10000009C11	*Staphylococcus aureus*
1686	S1M10000009D01	*Staphylococcus aureus*
1687	S1M10000009D02	*Staphylococcus aureus*
1688	S1M10000009D03	*Staphylococcus aureus*
1689	S1M10000009D04	*Staphylococcus aureus*
1690	S1M10000009D05	*Staphylococcus aureus*
1691	S1M10000009D07	*Staphylococcus aureus*
1692	S1M10000009D09	*Staphylococcus aureus*
1693	S1M10000009D11	*Staphylococcus aureus*
1694	S1M10000009E02	*Staphylococcus aureus*
1695	S1M10000009E06	*Staphylococcus aureus*
1696	S1M10000009E08	*Staphylococcus aureus*
1697	S1M10000009E09	*Staphylococcus aureus*
1698	S1M10000009E11	*Staphylococcus aureus*
1699	S1M10000009E12	*Staphylococcus aureus*
1700	S1M10000009F01	*Staphylococcus aureus*
1701	S1M10000009F02	*Staphylococcus aureus*
1702	S1M10000009F03	*Staphylococcus aureus*
1703	S1M10000009F05	*Staphylococcus aureus*
1704	S1M10000009F06	*Staphylococcus aureus*
1705	S1M10000009F07	*Staphylococcus aureus*
1706	S1M10000009F09	*Staphylococcus aureus*
1707	S1M10000009F10	*Staphylococcus aureus*
1708	S1M10000009G02	*Staphylococcus aureus*
1709	S1M10000009G03	*Staphylococcus aureus*
1710	S1M10000009G05	*Staphylococcus aureus*
1711	S1M10000009G06	*Staphylococcus aureus*
1712	S1M10000009G07	*Staphylococcus aureus*
1713	S1M10000009G09	*Staphylococcus aureus*
1714	S1M10000009G10	*Staphylococcus aureus*
1715	S1M10000009G11	*Staphylococcus aureus*
1716	S1M10000009H01	*Staphylococcus aureus*
1717	S1M10000009H02	*Staphylococcus aureus*
1718	S1M10000009H03	*Staphylococcus aureus*
1719	S1M10000009H05	*Staphylococcus aureus*
1720	S1M10000009H07	*Staphylococcus aureus*
1721	S1M10000009H09	*Staphylococcus aureus*

SeqID	Clone name	Organism
1722	S1M10000009H11	*Staphylococcus aureus*
1723	S1M10000011A02	*Staphylococcus aureus*
1724	S1M10000011A03	*Staphylococcus aureus*
1725	S1M10000011A04	*Staphylococcus aureus*
1726	S1M10000011A06	*Staphylococcus aureus*
1727	S1M10000011B01	*Staphylococcus aureus*
1728	S1M10000011B02	*Staphylococcus aureus*
1729	S1M10000011B03	*Staphylococcus aureus*
1730	S1M10000011B04	*Staphylococcus aureus*
1731	S1M10000011B05	*Staphylococcus aureus*
1732	S1M10000011C01	*Staphylococcus aureus*
1733	S1M10000011C05	*Staphylococcus aureus*
1734	S1M10000011C06	*Staphylococcus aureus*
1735	S1M10000011D01	*Staphylococcus aureus*
1736	S1M10000011D02	*Staphylococcus aureus*
1737	S1M10000011D04	*Staphylococcus aureus*
1738	S1M10000011D06	*Staphylococcus aureus*
1739	S1M10000011E02	*Staphylococcus aureus*
1740	S1M10000011E03	*Staphylococcus aureus*
1741	S1M10000011E04	*Staphylococcus aureus*
1742	S1M10000011F01	*Staphylococcus aureus*
1743	S1M10000011F03	*Staphylococcus aureus*
1744	S1M10000011F04	*Staphylococcus aureus*
1745	S1M10000011F06	*Staphylococcus aureus*
1746	S1M10000011G01	*Staphylococcus aureus*
1747	S1M10000011G03	*Staphylococcus aureus*
1748	S1M10000011G04	*Staphylococcus aureus*
1749	S1M10000011G05	*Staphylococcus aureus*
1750	S1M10000011G06	*Staphylococcus aureus*
1751	S1M10000011H01	*Staphylococcus aureus*
1752	S1M10000011H03	*Staphylococcus aureus*
1753	S1M10000011H04	*Staphylococcus aureus*
1754	S1M10000012A02	*Staphylococcus aureus*
1755	S1M10000012A06	*Staphylococcus aureus*
1756	S1M10000012A08	*Staphylococcus aureus*
1757	S1M10000012A09	*Staphylococcus aureus*
1758	S1M10000012A10	*Staphylococcus aureus*
1759	S1M10000012A11	*Staphylococcus aureus*
1760	S1M10000012B01	*Staphylococcus aureus*
1761	S1M10000012B05	*Staphylococcus aureus*
1762	S1M10000012B06	*Staphylococcus aureus*
1763	S1M10000012B07	*Staphylococcus aureus*
1764	S1M10000012B11	*Staphylococcus aureus*
1765	S1M10000012C01	*Staphylococcus aureus*
1766	S1M10000012C03	*Staphylococcus aureus*
1767	S1M10000012C04	*Staphylococcus aureus*
1768	S1M10000012C05	*Staphylococcus aureus*
1769	S1M10000012C06	*Staphylococcus aureus*
1770	S1M10000012C11	*Staphylococcus aureus*

SeqID	Clone name	Organism
1771	S1M10000012C12	*Staphylococcus aureus*
1772	S1M10000012D04	*Staphylococcus aureus*
1773	S1M10000012D06	*Staphylococcus aureus*
1774	S1M10000012D07	*Staphylococcus aureus*
1775	S1M10000012D08	*Staphylococcus aureus*
1776	S1M10000012D09	*Staphylococcus aureus*
1777	S1M10000012D12	*Staphylococcus aureus*
1778	S1M10000012E01	*Staphylococcus aureus*
1779	S1M10000012E02	*Staphylococcus aureus*
1780	S1M10000012E04	*Staphylococcus aureus*
1781	S1M10000012E07	*Staphylococcus aureus*
1782	S1M10000012E08	*Staphylococcus aureus*
1783	S1M10000012E12	*Staphylococcus aureus*
1784	S1M10000012F04	*Staphylococcus aureus*
1785	S1M10000012F07	*Staphylococcus aureus*
1786	S1M10000012F08	*Staphylococcus aureus*
1787	S1M10000012F09	*Staphylococcus aureus*
1788	S1M10000012F10	*Staphylococcus aureus*
1789	S1M10000012F11	*Staphylococcus aureus*
1790	S1M10000012F12	*Staphylococcus aureus*
1791	S1M10000012G01	*Staphylococcus aureus*
1792	S1M10000012G02	*Staphylococcus aureus*
1793	S1M10000012G03	*Staphylococcus aureus*
1794	S1M10000012G06	*Staphylococcus aureus*
1795	S1M10000012G07	*Staphylococcus aureus*
1796	S1M10000012G08	*Staphylococcus aureus*
1797	S1M10000012G10	*Staphylococcus aureus*
1798	S1M10000012H05	*Staphylococcus aureus*
1799	S1M10000012H08	*Staphylococcus aureus*
1800	S1M10000012H09	*Staphylococcus aureus*
1801	S1M10000012H10	*Staphylococcus aureus*
1802	S1M10000012H11	*Staphylococcus aureus*
1803	S1M10000013A02	*Staphylococcus aureus*
1804	S1M10000013A03	*Staphylococcus aureus*
1805	S1M10000013A05	*Staphylococcus aureus*
1806	S1M10000013A07	*Staphylococcus aureus*
1807	S1M10000013A08	*Staphylococcus aureus*
1808	S1M10000013A09	*Staphylococcus aureus*
1809	S1M10000013A10	*Staphylococcus aureus*
1810	S1M10000013A11	*Staphylococcus aureus*
1811	S1M10000013A12	*Staphylococcus aureus*
1812	S1M10000013B02	*Staphylococcus aureus*
1813	S1M10000013B03	*Staphylococcus aureus*
1814	S1M10000013B04	*Staphylococcus aureus*
1815	S1M10000013B05	*Staphylococcus aureus*
1816	S1M10000013B06	*Staphylococcus aureus*
1817	S1M10000013B07	*Staphylococcus aureus*
1818	S1M10000013B09	*Staphylococcus aureus*
1819	S1M10000013B11	*Staphylococcus aureus*

TABLE IA

SeqID	Clone name	Organism
1820	S1M10000013C03	*Staphylococcus aureus*
1821	S1M10000013C05	*Staphylococcus aureus*
1822	S1M10000013C07	*Staphylococcus aureus*
1823	S1M10000013C08	*Staphylococcus aureus*
1824	S1M10000013C09	*Staphylococcus aureus*
1825	S1M10000013C10	*Staphylococcus aureus*
1826	S1M10000013C11	*Staphylococcus aureus*
1827	S1M10000013C12	*Staphylococcus aureus*
1828	S1M10000013D08	*Staphylococcus aureus*
1829	S1M10000013D09	*Staphylococcus aureus*
1830	S1M10000013D11	*Staphylococcus aureus*
1831	S1M10000013E01	*Staphylococcus aureus*
1832	S1M10000013E02	*Staphylococcus aureus*
1833	S1M10000013E04	*Staphylococcus aureus*
1834	S1M10000013E06	*Staphylococcus aureus*
1835	S1M10000013E08	*Staphylococcus aureus*
1836	S1M10000013E09	*Staphylococcus aureus*
1837	S1M10000013E10	*Staphylococcus aureus*
1838	S1M10000013F02	*Staphylococcus aureus*
1839	S1M10000013F03	*Staphylococcus aureus*
1840	S1M10000013F06	*Staphylococcus aureus*
1841	S1M10000013F07	*Staphylococcus aureus*
1842	S1M10000013F08	*Staphylococcus aureus*
1843	S1M10000013F09	*Staphylococcus aureus*
1844	S1M10000013F12	*Staphylococcus aureus*
1845	S1M10000013G01	*Staphylococcus aureus*
1846	S1M10000013G04	*Staphylococcus aureus*
1847	S1M10000013G05	*Staphylococcus aureus*
1848	S1M10000013G06	*Staphylococcus aureus*
1849	S1M10000013G07	*Staphylococcus aureus*
1850	S1M10000013G10	*Staphylococcus aureus*
1851	S1M10000013G11	*Staphylococcus aureus*
1852	S1M10000013G12	*Staphylococcus aureus*
1853	S1M10000013H03	*Staphylococcus aureus*
1854	S1M10000013H04	*Staphylococcus aureus*
1855	S1M10000013H05	*Staphylococcus aureus*
1856	S1M10000013H07	*Staphylococcus aureus*
1857	S1M10000013H09	*Staphylococcus aureus*
1858	S1M10000013H10	*Staphylococcus aureus*
1859	S1M10000013H11	*Staphylococcus aureus*
1860	S1M10000014A02	*Staphylococcus aureus*
1861	S1M10000014A03	*Staphylococcus aureus*
1862	S1M10000014A05	*Staphylococcus aureus*
1863	S1M10000014A07	*Staphylococcus aureus*
1864	S1M10000014A08	*Staphylococcus aureus*
1865	S1M10000014A11	*Staphylococcus aureus*
1866	S1M10000014A12	*Staphylococcus aureus*
1867	S1M10000014B01	*Staphylococcus aureus*
1868	S1M10000014B02	*Staphylococcus aureus*

SeqID	Clone name	Organism
1869	S1M10000014B03	*Staphylococcus aureus*
1870	S1M10000014B04	*Staphylococcus aureus*
1871	S1M10000014B05	*Staphylococcus aureus*
1872	S1M10000014B06	*Staphylococcus aureus*
1873	S1M10000014B07	*Staphylococcus aureus*
1874	S1M10000014B08	*Staphylococcus aureus*
1875	S1M10000014B10	*Staphylococcus aureus*
1876	S1M10000014B11	*Staphylococcus aureus*
1877	S1M10000014B12	*Staphylococcus aureus*
1878	S1M10000014C01	*Staphylococcus aureus*
1879	S1M10000014C05	*Staphylococcus aureus*
1880	S1M10000014C06	*Staphylococcus aureus*
1881	S1M10000014C07	*Staphylococcus aureus*
1882	S1M10000014C09	*Staphylococcus aureus*
1883	S1M10000014C10	*Staphylococcus aureus*
1884	S1M10000014C11	*Staphylococcus aureus*
1885	S1M10000014C12	*Staphylococcus aureus*
1886	S1M10000014D03	*Staphylococcus aureus*
1887	S1M10000014D06	*Staphylococcus aureus*
1888	S1M10000014D08	*Staphylococcus aureus*
1889	S1M10000014D09	*Staphylococcus aureus*
1890	S1M10000014D10	*Staphylococcus aureus*
1891	S1M10000014E01	*Staphylococcus aureus*
1892	S1M10000014E04	*Staphylococcus aureus*
1893	S1M10000014E05	*Staphylococcus aureus*
1894	S1M10000014E07	*Staphylococcus aureus*
1895	S1M10000014E08	*Staphylococcus aureus*
1896	S1M10000014E09	*Staphylococcus aureus*
1897	S1M10000014E10	*Staphylococcus aureus*
1898	S1M10000014E12	*Staphylococcus aureus*
1899	S1M10000014F02	*Staphylococcus aureus*
1900	S1M10000014F03	*Staphylococcus aureus*
1901	S1M10000014F04	*Staphylococcus aureus*
1902	S1M10000014F05	*Staphylococcus aureus*
1903	S1M10000014F08	*Staphylococcus aureus*
1904	S1M10000014F09	*Staphylococcus aureus*
1905	S1M10000014F10	*Staphylococcus aureus*
1906	S1M10000014G02	*Staphylococcus aureus*
1907	S1M10000014G04	*Staphylococcus aureus*
1908	S1M10000014G06	*Staphylococcus aureus*
1909	S1M10000014G07	*Staphylococcus aureus*
1910	S1M10000014G08	*Staphylococcus aureus*
1911	S1M10000014G12	*Staphylococcus aureus*
1912	S1M10000014H02	*Staphylococcus aureus*
1913	S1M10000014H03	*Staphylococcus aureus*
1914	S1M10000014H04	*Staphylococcus aureus*
1915	S1M10000014H05	*Staphylococcus aureus*
1916	S1M10000014H06	*Staphylococcus aureus*
1917	S1M10000014H07	*Staphylococcus aureus*

SeqID	Clone name	Organism
1918	S1M10000014H08	*Staphylococcus aureus*
1919	S1M10000014H11	*Staphylococcus aureus*
1920	S1M10000015A02	*Staphylococcus aureus*
1921	S1M10000015A03	*Staphylococcus aureus*
1922	S1M10000015A05	*Staphylococcus aureus*
1923	S1M10000015A06	*Staphylococcus aureus*
1924	S1M10000015A09	*Staphylococcus aureus*
1925	S1M10000015A10	*Staphylococcus aureus*
1926	S1M10000015A11	*Staphylococcus aureus*
1927	S1M10000015A12	*Staphylococcus aureus*
1928	S1M10000015B02	*Staphylococcus aureus*
1929	S1M10000015B05	*Staphylococcus aureus*
1930	S1M10000015B08	*Staphylococcus aureus*
1931	S1M10000015B09	*Staphylococcus aureus*
1932	S1M10000015B10	*Staphylococcus aureus*
1933	S1M10000015C01	*Staphylococcus aureus*
1934	S1M10000015C02	*Staphylococcus aureus*
1935	S1M10000015C03	*Staphylococcus aureus*
1936	S1M10000015C05	*Staphylococcus aureus*
1937	S1M10000015C06	*Staphylococcus aureus*
1938	S1M10000015C08	*Staphylococcus aureus*
1939	S1M10000015C10	*Staphylococcus aureus*
1940	S1M10000015C12	*Staphylococcus aureus*
1941	S1M10000015D02	*Staphylococcus aureus*
1942	S1M10000015D03	*Staphylococcus aureus*
1943	S1M10000015D04	*Staphylococcus aureus*
1944	S1M10000015D05	*Staphylococcus aureus*
1945	S1M10000015D06	*Staphylococcus aureus*
1946	S1M10000015D12	*Staphylococcus aureus*
1947	S1M10000015E02	*Staphylococcus aureus*
1948	S1M10000015E03	*Staphylococcus aureus*
1949	S1M10000015E06	*Staphylococcus aureus*
1950	S1M10000015E07	*Staphylococcus aureus*
1951	S1M10000015E09	*Staphylococcus aureus*
1952	S1M10000015E10	*Staphylococcus aureus*
1953	S1M10000015E11	*Staphylococcus aureus*
1954	S1M10000015E12	*Staphylococcus aureus*
1955	S1M10000015F01	*Staphylococcus aureus*
1956	S1M10000015F02	*Staphylococcus aureus*
1957	S1M10000015F03	*Staphylococcus aureus*
1958	S1M10000015F04	*Staphylococcus aureus*
1959	S1M10000015F06	*Staphylococcus aureus*
1960	S1M10000015F07	*Staphylococcus aureus*
1961	S1M10000015F08	*Staphylococcus aureus*
1962	S1M10000015F09	*Staphylococcus aureus*
1963	S1M10000015F10	*Staphylococcus aureus*
1964	S1M10000015G01	*Staphylococcus aureus*
1965	S1M10000015G02	*Staphylococcus aureus*
1966	S1M10000015G03	*Staphylococcus aureus*

SeqID	Clone name	Organism
1967	S1M10000015G04	*Staphylococcus aureus*
1968	S1M10000015G05	*Staphylococcus aureus*
1969	S1M10000015G06	*Staphylococcus aureus*
1970	S1M10000015G07	*Staphylococcus aureus*
1971	S1M10000015G08	*Staphylococcus aureus*
1972	S1M10000015G09	*Staphylococcus aureus*
1973	S1M10000015G10	*Staphylococcus aureus*
1974	S1M10000015G11	*Staphylococcus aureus*
1975	S1M10000015H04	*Staphylococcus aureus*
1976	S1M10000015H06	*Staphylococcus aureus*
1977	S1M10000016A03	*Staphylococcus aureus*
1978	S1M10000016A04	*Staphylococcus aureus*
1979	S1M10000016A06	*Staphylococcus aureus*
1980	S1M10000016A07	*Staphylococcus aureus*
1981	S1M10000016A09	*Staphylococcus aureus*
1982	S1M10000016A10	*Staphylococcus aureus*
1983	S1M10000016A12	*Staphylococcus aureus*
1984	S1M10000016B02	*Staphylococcus aureus*
1985	S1M10000016B05	*Staphylococcus aureus*
1986	S1M10000016B06	*Staphylococcus aureus*
1987	S1M10000016B07	*Staphylococcus aureus*
1988	S1M10000016B08	*Staphylococcus aureus*
1989	S1M10000016B09	*Staphylococcus aureus*
1990	S1M10000016B10	*Staphylococcus aureus*
1991	S1M10000016B11	*Staphylococcus aureus*
1992	S1M10000016B12	*Staphylococcus aureus*
1993	S1M10000016C01	*Staphylococcus aureus*
1994	S1M10000016C02	*Staphylococcus aureus*
1995	S1M10000016C04	*Staphylococcus aureus*
1996	S1M10000016C05	*Staphylococcus aureus*
1997	S1M10000016C06	*Staphylococcus aureus*
1998	S1M10000016C08	*Staphylococcus aureus*
1999	S1M10000016C09	*Staphylococcus aureus*
2000	S1M10000016C10	*Staphylococcus aureus*
2001	S1M10000016C11	*Staphylococcus aureus*
2002	S1M10000016C12	*Staphylococcus aureus*
2003	S1M10000016D01	*Staphylococcus aureus*
2004	S1M10000016D02	*Staphylococcus aureus*
2005	S1M10000016D04	*Staphylococcus aureus*
2006	S1M10000016D05	*Staphylococcus aureus*
2007	S1M10000016D06	*Staphylococcus aureus*
2008	S1M10000016D08	*Staphylococcus aureus*
2009	S1M10000016D09	*Staphylococcus aureus*
2010	S1M10000016D10	*Staphylococcus aureus*
2011	S1M10000016D11	*Staphylococcus aureus*
2012	S1M10000016E04	*Staphylococcus aureus*
2013	S1M10000016E05	*Staphylococcus aureus*
2014	S1M10000016E06	*Staphylococcus aureus*
2015	S1M10000016E07	*Staphylococcus aureus*

SeqID	Clone name	Organism
2016	S1M10000016E08	*Staphylococcus aureus*
2017	S1M10000016E09	*Staphylococcus aureus*
2018	S1M10000016E10	*Staphylococcus aureus*
2019	S1M10000016E11	*Staphylococcus aureus*
2020	S1M10000016E12	*Staphylococcus aureus*
2021	S1M10000016F02	*Staphylococcus aureus*
2022	S1M10000016F03	*Staphylococcus aureus*
2023	S1M10000016F05	*Staphylococcus aureus*
2024	S1M10000016F06	*Staphylococcus aureus*
2025	S1M10000016F08	*Staphylococcus aureus*
2026	S1M10000016F09	*Staphylococcus aureus*
2027	S1M10000016F11	*Staphylococcus aureus*
2028	S1M10000016G01	*Staphylococcus aureus*
2029	S1M10000016G03	*Staphylococcus aureus*
2030	S1M10000016G04	*Staphylococcus aureus*
2031	S1M10000016G05	*Staphylococcus aureus*
2032	S1M10000016H03	*Staphylococcus aureus*
2033	S1M10000016H04	*Staphylococcus aureus*
2034	S1M10000016H08	*Staphylococcus aureus*
2035	S1M10000016H10	*Staphylococcus aureus*
2036	S1M10000017A02	*Staphylococcus aureus*
2037	S1M10000017A03	*Staphylococcus aureus*
2038	S1M10000017A04	*Staphylococcus aureus*
2039	S1M10000017A08	*Staphylococcus aureus*
2040	S1M10000017A11	*Staphylococcus aureus*
2041	S1M10000017A12	*Staphylococcus aureus*
2042	S1M10000017B02	*Staphylococcus aureus*
2043	S1M10000017B05	*Staphylococcus aureus*
2044	S1M10000017B07	*Staphylococcus aureus*
2045	S1M10000017B08	*Staphylococcus aureus*
2046	S1M10000017B09	*Staphylococcus aureus*
2047	S1M10000017B10	*Staphylococcus aureus*
2048	S1M10000017B11	*Staphylococcus aureus*
2049	S1M10000017B12	*Staphylococcus aureus*
2050	S1M10000017C01	*Staphylococcus aureus*
2051	S1M10000017C03	*Staphylococcus aureus*
2052	S1M10000017C05	*Staphylococcus aureus*
2053	S1M10000017C08	*Staphylococcus aureus*
2054	S1M10000017C09	*Staphylococcus aureus*
2055	S1M10000017C10	*Staphylococcus aureus*
2056	S1M10000017C11	*Staphylococcus aureus*
2057	S1M10000017C12	*Staphylococcus aureus*
2058	S1M10000017D03	*Staphylococcus aureus*
2059	S1M10000017D09	*Staphylococcus aureus*
2060	S1M10000017D10	*Staphylococcus aureus*
2061	S1M10000017E04	*Staphylococcus aureus*
2062	S1M10000017E05	*Staphylococcus aureus*
2063	S1M10000017E08	*Staphylococcus aureus*
2064	S1M10000017E11	*Staphylococcus aureus*

SeqID	Clone name	Organism
2065	S1M10000017F01	*Staphylococcus aureus*
2066	S1M10000017F04	*Staphylococcus aureus*
2067	S1M10000017F05	*Staphylococcus aureus*
2068	S1M10000017F06	*Staphylococcus aureus*
2069	S1M10000017F11	*Staphylococcus aureus*
2070	S1M10000017G02	*Staphylococcus aureus*
2071	S1M10000017G05	*Staphylococcus aureus*
2072	S1M10000017G06	*Staphylococcus aureus*
2073	S1M10000018A03	*Staphylococcus aureus*
2074	S1M10000018A04	*Staphylococcus aureus*
2075	S1M10000018A05	*Staphylococcus aureus*
2076	S1M10000018A06	*Staphylococcus aureus*
2077	S1M10000018A08	*Staphylococcus aureus*
2078	S1M10000018A09	*Staphylococcus aureus*
2079	S1M10000018A10	*Staphylococcus aureus*
2080	S1M10000018A11	*Staphylococcus aureus*
2081	S1M10000018B02	*Staphylococcus aureus*
2082	S1M10000018B03	*Staphylococcus aureus*
2083	S1M10000018B05	*Staphylococcus aureus*
2084	S1M10000018B09	*Staphylococcus aureus*
2085	S1M10000018B10	*Staphylococcus aureus*
2086	S1M10000018B11	*Staphylococcus aureus*
2087	S1M10000018C01	*Staphylococcus aureus*
2088	S1M10000018C02	*Staphylococcus aureus*
2089	S1M10000018C03	*Staphylococcus aureus*
2090	S1M10000018C04	*Staphylococcus aureus*
2091	S1M10000018C05	*Staphylococcus aureus*
2092	S1M10000018C06	*Staphylococcus aureus*
2093	S1M10000018C08	*Staphylococcus aureus*
2094	S1M10000018C09	*Staphylococcus aureus*
2095	S1M10000018C10	*Staphylococcus aureus*
2096	S1M10000018C11	*Staphylococcus aureus*
2097	S1M10000018C12	*Staphylococcus aureus*
2098	S1M10000018D01	*Staphylococcus aureus*
2099	S1M10000018D02	*Staphylococcus aureus*
2100	S1M10000018D03	*Staphylococcus aureus*
2101	S1M10000018D04	*Staphylococcus aureus*
2102	S1M10000018D09	*Staphylococcus aureus*
2103	S1M10000018D10	*Staphylococcus aureus*
2104	S1M10000018D11	*Staphylococcus aureus*
2105	S1M10000018D12	*Staphylococcus aureus*
2106	S1M10000018E01	*Staphylococcus aureus*
2107	S1M10000018E02	*Staphylococcus aureus*
2108	S1M10000018E03	*Staphylococcus aureus*
2109	S1M10000018E04	*Staphylococcus aureus*
2110	S1M10000018E05	*Staphylococcus aureus*
2111	S1M10000018E08	*Staphylococcus aureus*
2112	S1M10000018E09	*Staphylococcus aureus*
2113	S1M10000018E11	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2115	S1M10000018F03	*Staphylococcus aureus*
2116	S1M10000018F04	*Staphylococcus aureus*
2117	S1M10000018F07	*Staphylococcus aureus*
2118	S1M10000018F09	*Staphylococcus aureus*
2119	S1M10000018F10	*Staphylococcus aureus*
2120	S1M10000018F12	*Staphylococcus aureus*
2121	S1M10000018G03	*Staphylococcus aureus*
2122	S1M10000018G05	*Staphylococcus aureus*
2123	S1M10000018G07	*Staphylococcus aureus*
2124	S1M10000018G08	*Staphylococcus aureus*
2125	S1M10000018G09	*Staphylococcus aureus*
2126	S1M10000018G10	*Staphylococcus aureus*
2127	S1M10000018G12	*Staphylococcus aureus*
2128	S1M10000018H01	*Staphylococcus aureus*
2129	S1M10000018H02	*Staphylococcus aureus*
2130	S1M10000018H07	*Staphylococcus aureus*
2131	S1M10000018H09	*Staphylococcus aureus*
2132	S1M10000018H10	*Staphylococcus aureus*
2133	S1M10000019A02	*Staphylococcus aureus*
2134	S1M10000019A03	*Staphylococcus aureus*
2135	S1M10000019A05	*Staphylococcus aureus*
2136	S1M10000019A06	*Staphylococcus aureus*
2137	S1M10000019A07	*Staphylococcus aureus*
2138	S1M10000019A09	*Staphylococcus aureus*
2139	S1M10000019A11	*Staphylococcus aureus*
2140	S1M10000019A12	*Staphylococcus aureus*
2141	S1M10000019B03	*Staphylococcus aureus*
2142	S1M10000019B04	*Staphylococcus aureus*
2143	S1M10000019B07	*Staphylococcus aureus*
2144	S1M10000019B08	*Staphylococcus aureus*
2145	S1M10000019B09	*Staphylococcus aureus*
2146	S1M10000019B10	*Staphylococcus aureus*
2147	S1M10000019B11	*Staphylococcus aureus*
2148	S1M10000019B12	*Staphylococcus aureus*
2149	S1M10000019C01	*Staphylococcus aureus*
2150	S1M10000019C04	*Staphylococcus aureus*
2151	S1M10000019C05	*Staphylococcus aureus*
2152	S1M10000019C06	*Staphylococcus aureus*
2153	S1M10000019C07	*Staphylococcus aureus*
2154	S1M10000019C08	*Staphylococcus aureus*
2155	S1M10000019C11	*Staphylococcus aureus*
2156	S1M10000019C12	*Staphylococcus aureus*
2157	S1M10000019D01	*Staphylococcus aureus*
2158	S1M10000019D02	*Staphylococcus aureus*
2159	S1M10000019D04	*Staphylococcus aureus*
2160	S1M10000019D05	*Staphylococcus aureus*
2161	S1M10000019D06	*Staphylococcus aureus*
2162	S1M10000019D07	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2164	S1M10000019D12	*Staphylococcus aureus*
2165	S1M10000019E01	*Staphylococcus aureus*
2166	S1M10000019E02	*Staphylococcus aureus*
2167	S1M10000019E07	*Staphylococcus aureus*
2168	S1M10000019F01	*Staphylococcus aureus*
2169	S1M10000019F05	*Staphylococcus aureus*
2170	S1M10000019F06	*Staphylococcus aureus*
2171	S1M10000019F08	*Staphylococcus aureus*
2172	S1M10000019F09	*Staphylococcus aureus*
2173	S1M10000019F11	*Staphylococcus aureus*
2174	S1M10000019G04	*Staphylococcus aureus*
2175	S1M10000019G07	*Staphylococcus aureus*
2176	S1M10000019G09	*Staphylococcus aureus*
2177	S1M10000019G10	*Staphylococcus aureus*
2178	S1M10000019G11	*Staphylococcus aureus*
2179	S1M10000019H05	*Staphylococcus aureus*
2180	S1M10000019H08	*Staphylococcus aureus*
2181	S1M10000020A05	*Staphylococcus aureus*
2182	S1M10000020A06	*Staphylococcus aureus*
2183	S1M10000020A07	*Staphylococcus aureus*
2184	S1M10000020A11	*Staphylococcus aureus*
2185	S1M10000020A12	*Staphylococcus aureus*
2186	S1M10000020B02	*Staphylococcus aureus*
2187	S1M10000020B03	*Staphylococcus aureus*
2188	S1M10000020B05	*Staphylococcus aureus*
2189	S1M10000020B06	*Staphylococcus aureus*
2190	S1M10000020B07	*Staphylococcus aureus*
2191	S1M10000020B09	*Staphylococcus aureus*
2192	S1M10000020B12	*Staphylococcus aureus*
2193	S1M10000020C09	*Staphylococcus aureus*
2194	S1M10000020C10	*Staphylococcus aureus*
2195	S1M10000020C11	*Staphylococcus aureus*
2196	S1M10000020D03	*Staphylococcus aureus*
2197	S1M10000020D04	*Staphylococcus aureus*
2198	S1M10000020D06	*Staphylococcus aureus*
2199	S1M10000020D07	*Staphylococcus aureus*
2200	S1M10000020D08	*Staphylococcus aureus*
2201	S1M10000020D09	*Staphylococcus aureus*
2202	S1M10000020D12	*Staphylococcus aureus*
2203	S1M10000020E01	*Staphylococcus aureus*
2204	S1M10000020E03	*Staphylococcus aureus*
2205	S1M10000020E04	*Staphylococcus aureus*
2206	S1M10000020E06	*Staphylococcus aureus*
2207	S1M10000020E08	*Staphylococcus aureus*
2208	S1M10000020E11	*Staphylococcus aureus*
2209	S1M10000020E12	*Staphylococcus aureus*
2210	S1M10000020F01	*Staphylococcus aureus*
2211	S1M10000020F05	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2213	S1M10000020F07	*Staphylococcus aureus*
2214	S1M10000020F09	*Staphylococcus aureus*
2215	S1M10000020F11	*Staphylococcus aureus*
2216	S1M10000020F12	*Staphylococcus aureus*
2217	S1M10000020G01	*Staphylococcus aureus*
2218	S1M10000020G05	*Staphylococcus aureus*
2219	S1M10000020G07	*Staphylococcus aureus*
2220	S1M10000020G08	*Staphylococcus aureus*
2221	S1M10000020G09	*Staphylococcus aureus*
2222	S1M10000020G10	*Staphylococcus aureus*
2223	S1M10000020G11	*Staphylococcus aureus*
2224	S1M10000020G12	*Staphylococcus aureus*
2225	S1M10000020H01	*Staphylococcus aureus*
2226	S1M10000020H02	*Staphylococcus aureus*
2227	S1M10000020H04	*Staphylococcus aureus*
2228	S1M10000020H06	*Staphylococcus aureus*
2229	S1M10000020H08	*Staphylococcus aureus*
2230	S1M10000020H10	*Staphylococcus aureus*
2231	S1M10000020H11	*Staphylococcus aureus*
2232	S1M10000021A04	*Staphylococcus aureus*
2233	S1M10000021A05	*Staphylococcus aureus*
2234	S1M10000021A06	*Staphylococcus aureus*
2235	S1M10000021A07	*Staphylococcus aureus*
2236	S1M10000021A08	*Staphylococcus aureus*
2237	S1M10000021A09	*Staphylococcus aureus*
2238	S1M10000021A10	*Staphylococcus aureus*
2239	S1M10000021B05	*Staphylococcus aureus*
2240	S1M10000021B06	*Staphylococcus aureus*
2241	S1M10000021B07	*Staphylococcus aureus*
2242	S1M10000021B10	*Staphylococcus aureus*
2243	S1M10000021C04	*Staphylococcus aureus*
2244	S1M10000021C05	*Staphylococcus aureus*
2245	S1M10000021C07	*Staphylococcus aureus*
2246	S1M10000021C08	*Staphylococcus aureus*
2247	S1M10000021C10	*Staphylococcus aureus*
2248	S1M10000021C11	*Staphylococcus aureus*
2249	S1M10000021C12	*Staphylococcus aureus*
2250	S1M10000021D01	*Staphylococcus aureus*
2251	S1M10000021D03	*Staphylococcus aureus*
2252	S1M10000021D04	*Staphylococcus aureus*
2253	S1M10000021D06	*Staphylococcus aureus*
2254	S1M10000021D09	*Staphylococcus aureus*
2255	S1M10000021D10	*Staphylococcus aureus*
2256	S1M10000021E01	*Staphylococcus aureus*
2257	S1M10000021E02	*Staphylococcus aureus*
2258	S1M10000021E03	*Staphylococcus aureus*
2259	S1M10000021E05	*Staphylococcus aureus*
2260	S1M10000021E06	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2262	S1M10000021E12	*Staphylococcus aureus*
2263	S1M10000021F02	*Staphylococcus aureus*
2264	S1M10000021F04	*Staphylococcus aureus*
2265	S1M10000021F05	*Staphylococcus aureus*
2266	S1M10000021F06	*Staphylococcus aureus*
2267	S1M10000021F07	*Staphylococcus aureus*
2268	S1M10000021F09	*Staphylococcus aureus*
2269	S1M10000021F11	*Staphylococcus aureus*
2270	S1M10000021G01	*Staphylococcus aureus*
2271	S1M10000021G03	*Staphylococcus aureus*
2272	S1M10000021G08	*Staphylococcus aureus*
2273	S1M10000021H04	*Staphylococcus aureus*
2274	S1M10000021H05	*Staphylococcus aureus*
2275	S1M10000021H07	*Staphylococcus aureus*
2276	S1M10000021H08	*Staphylococcus aureus*
2277	S1M10000021H11	*Staphylococcus aureus*
2278	S1M10000022A02	*Staphylococcus aureus*
2279	S1M10000022A03	*Staphylococcus aureus*
2280	S1M10000022A05	*Staphylococcus aureus*
2281	S1M10000022A08	*Staphylococcus aureus*
2282	S1M10000022A09	*Staphylococcus aureus*
2283	S1M10000022A12	*Staphylococcus aureus*
2284	S1M10000022B02	*Staphylococcus aureus*
2285	S1M10000022B03	*Staphylococcus aureus*
2286	S1M10000022B05	*Staphylococcus aureus*
2287	S1M10000022B06	*Staphylococcus aureus*
2288	S1M10000022B08	*Staphylococcus aureus*
2289	S1M10000022B09	*Staphylococcus aureus*
2290	S1M10000022B10	*Staphylococcus aureus*
2291	S1M10000022B11	*Staphylococcus aureus*
2292	S1M10000022B12	*Staphylococcus aureus*
2293	S1M10000022C02	*Staphylococcus aureus*
2294	S1M10000022C03	*Staphylococcus aureus*
2295	S1M10000022C04	*Staphylococcus aureus*
2296	S1M10000022C06	*Staphylococcus aureus*
2297	S1M10000022C07	*Staphylococcus aureus*
2298	S1M10000022C08	*Staphylococcus aureus*
2299	S1M10000022C11	*Staphylococcus aureus*
2300	S1M10000022D03	*Staphylococcus aureus*
2301	S1M10000022D05	*Staphylococcus aureus*
2302	S1M10000022D06	*Staphylococcus aureus*
2303	S1M10000022D07	*Staphylococcus aureus*
2304	S1M10000022D08	*Staphylococcus aureus*
2305	S1M10000022D09	*Staphylococcus aureus*
2306	S1M10000022D11	*Staphylococcus aureus*
2307	S1M10000022E01	*Staphylococcus aureus*
2308	S1M10000022E03	*Staphylococcus aureus*
2309	S1M10000022E05	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2311	S1M10000022F04	*Staphylococcus aureus*
2312	S1M10000022F06	*Staphylococcus aureus*
2313	S1M10000022F07	*Staphylococcus aureus*
2314	S1M10000022F08	*Staphylococcus aureus*
2315	S1M10000022F11	*Staphylococcus aureus*
2316	S1M10000022G03	*Staphylococcus aureus*
2317	S1M10000022G04	*Staphylococcus aureus*
2318	S1M10000022G07	*Staphylococcus aureus*
2319	S1M10000022G08	*Staphylococcus aureus*
2320	S1M10000022G12	*Staphylococcus aureus*
2321	S1M10000022H03	*Staphylococcus aureus*
2322	S1M10000022H05	*Staphylococcus aureus*
2323	S1M10000022H06	*Staphylococcus aureus*
2324	S1M10000022H07	*Staphylococcus aureus*
2325	S1M10000022H08	*Staphylococcus aureus*
2326	S1M10000022H11	*Staphylococcus aureus*
2327	S1M10000023A05	*Staphylococcus aureus*
2328	S1M10000023A09	*Staphylococcus aureus*
2329	S1M10000023A11	*Staphylococcus aureus*
2330	S1M10000023A12	*Staphylococcus aureus*
2331	S1M10000023B01	*Staphylococcus aureus*
2332	S1M10000023B03	*Staphylococcus aureus*
2333	S1M10000023B07	*Staphylococcus aureus*
2334	S1M10000023B08	*Staphylococcus aureus*
2335	S1M10000023B09	*Staphylococcus aureus*
2336	S1M10000023B10	*Staphylococcus aureus*
2337	S1M10000023B11	*Staphylococcus aureus*
2338	S1M10000023B12	*Staphylococcus aureus*
2339	S1M10000023C02	*Staphylococcus aureus*
2340	S1M10000023C10	*Staphylococcus aureus*
2341	S1M10000023C11	*Staphylococcus aureus*
2342	S1M10000023C12	*Staphylococcus aureus*
2343	S1M10000023D01	*Staphylococcus aureus*
2344	S1M10000023D03	*Staphylococcus aureus*
2345	S1M10000023D04	*Staphylococcus aureus*
2346	S1M10000023D07	*Staphylococcus aureus*
2347	S1M10000023D08	*Staphylococcus aureus*
2348	S1M10000023D09	*Staphylococcus aureus*
2349	S1M10000023D10	*Staphylococcus aureus*
2350	S1M10000023D12	*Staphylococcus aureus*
2351	S1M10000023E01	*Staphylococcus aureus*
2352	S1M10000023E04	*Staphylococcus aureus*
2353	S1M10000023E07	*Staphylococcus aureus*
2354	S1M10000023E10	*Staphylococcus aureus*
2355	S1M10000023E11	*Staphylococcus aureus*
2356	S1M10000023F04	*Staphylococcus aureus*
2357	S1M10000023F07	*Staphylococcus aureus*
2358	S1M10000023F08	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2360	S1M10000023F11	*Staphylococcus aureus*
2361	S1M10000023F12	*Staphylococcus aureus*
2362	S1M10000023G02	*Staphylococcus aureus*
2363	S1M10000023G03	*Staphylococcus aureus*
2364	S1M10000023G06	*Staphylococcus aureus*
2365	S1M10000023G07	*Staphylococcus aureus*
2366	S1M10000023G08	*Staphylococcus aureus*
2367	S1M10000023G09	*Staphylococcus aureus*
2368	S1M10000023G11	*Staphylococcus aureus*
2369	S1M10000023H02	*Staphylococcus aureus*
2370	S1M10000023H06	*Staphylococcus aureus*
2371	S1M10000023H07	*Staphylococcus aureus*
2372	S1M10000023H09	*Staphylococcus aureus*
2373	S1M10000023H10	*Staphylococcus aureus*
2374	S1M10000024A02	*Staphylococcus aureus*
2375	S1M10000024A04	*Staphylococcus aureus*
2376	S1M10000024A07	*Staphylococcus aureus*
2377	S1M10000024A08	*Staphylococcus aureus*
2378	S1M10000024A11	*Staphylococcus aureus*
2379	S1M10000024B05	*Staphylococcus aureus*
2380	S1M10000024B06	*Staphylococcus aureus*
2381	S1M10000024B08	*Staphylococcus aureus*
2382	S1M10000024B09	*Staphylococcus aureus*
2383	S1M10000024B10	*Staphylococcus aureus*
2384	S1M10000024C02	*Staphylococcus aureus*
2385	S1M10000024C04	*Staphylococcus aureus*
2386	S1M10000024C07	*Staphylococcus aureus*
2387	S1M10000024D02	*Staphylococcus aureus*
2388	S1M10000024D03	*Staphylococcus aureus*
2389	S1M10000024D10	*Staphylococcus aureus*
2390	S1M10000024D11	*Staphylococcus aureus*
2391	S1M10000024E03	*Staphylococcus aureus*
2392	S1M10000024E05	*Staphylococcus aureus*
2393	S1M10000024E06	*Staphylococcus aureus*
2394	S1M10000024E07	*Staphylococcus aureus*
2395	S1M10000024E08	*Staphylococcus aureus*
2396	S1M10000024F02	*Staphylococcus aureus*
2397	S1M10000024F03	*Staphylococcus aureus*
2398	S1M10000024F05	*Staphylococcus aureus*
2399	S1M10000024F08	*Staphylococcus aureus*
2400	S1M10000024F10	*Staphylococcus aureus*
2401	S1M10000024G05	*Staphylococcus aureus*
2402	S1M10000024G06	*Staphylococcus aureus*
2403	S1M10000024G07	*Staphylococcus aureus*
2404	S1M10000024G08	*Staphylococcus aureus*
2405	S1M10000024G10	*Staphylococcus aureus*
2406	S1M10000024G12	*Staphylococcus aureus*
2407	S1M10000024H02	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2409	S1M10000024H07	*Staphylococcus aureus*
2410	S1M10000024H08	*Staphylococcus aureus*
2411	S1M10000025A03	*Staphylococcus aureus*
2412	S1M10000025A08	*Staphylococcus aureus*
2413	S1M10000025A09	*Staphylococcus aureus*
2414	S1M10000025A10	*Staphylococcus aureus*
2415	S1M10000025B01	*Staphylococcus aureus*
2416	S1M10000025B02	*Staphylococcus aureus*
2417	S1M10000025B03	*Staphylococcus aureus*
2418	S1M10000025B05	*Staphylococcus aureus*
2419	S1M10000025B06	*Staphylococcus aureus*
2420	S1M10000025B09	*Staphylococcus aureus*
2421	S1M10000025B12	*Staphylococcus aureus*
2422	S1M10000025C01	*Staphylococcus aureus*
2423	S1M10000025C03	*Staphylococcus aureus*
2424	S1M10000025C05	*Staphylococcus aureus*
2425	S1M10000025C09	*Staphylococcus aureus*
2426	S1M10000025C10	*Staphylococcus aureus*
2427	S1M10000025C11	*Staphylococcus aureus*
2428	S1M10000025D01	*Staphylococcus aureus*
2429	S1M10000025D03	*Staphylococcus aureus*
2430	S1M10000025D04	*Staphylococcus aureus*
2431	S1M10000025D06	*Staphylococcus aureus*
2432	S1M10000025D08	*Staphylococcus aureus*
2433	S1M10000025D09	*Staphylococcus aureus*
2434	S1M10000025D10	*Staphylococcus aureus*
2435	S1M10000025E01	*Staphylococcus aureus*
2436	S1M10000025E04	*Staphylococcus aureus*
2437	S1M10000025E09	*Staphylococcus aureus*
2438	S1M10000025E11	*Staphylococcus aureus*
2439	S1M10000025F03	*Staphylococcus aureus*
2440	S1M10000025F05	*Staphylococcus aureus*
2441	S1M10000025F08	*Staphylococcus aureus*
2442	S1M10000025F09	*Staphylococcus aureus*
2443	S1M10000025F10	*Staphylococcus aureus*
2444	S1M10000025F12	*Staphylococcus aureus*
2445	S1M10000025G04	*Staphylococcus aureus*
2446	S1M10000025G06	*Staphylococcus aureus*
2447	S1M10000025G10	*Staphylococcus aureus*
2448	S1M10000025H05	*Staphylococcus aureus*
2449	S1M10000025H06	*Staphylococcus aureus*
2450	S1M10000025H07	*Staphylococcus aureus*
2451	S1M10000025H10	*Staphylococcus aureus*
2452	S1M10000026A02	*Staphylococcus aureus*
2453	S1M10000026A04	*Staphylococcus aureus*
2454	S1M10000026A05	*Staphylococcus aureus*
2455	S1M10000026A06	*Staphylococcus aureus*
2456	S1M10000026A07	*Staphylococcus aureus*

SeqID	Clone name	Organism
2457	S1M10000026A08	*Staphylococcus aureus*
2458	S1M10000026A09	*Staphylococcus aureus*
2459	S1M10000026A10	*Staphylococcus aureus*
2460	S1M10000026A11	*Staphylococcus aureus*
2461	S1M10000026B02	*Staphylococcus aureus*
2462	S1M10000026B03	*Staphylococcus aureus*
2463	S1M10000026B05	*Staphylococcus aureus*
2464	S1M10000026B06	*Staphylococcus aureus*
2465	S1M10000026B07	*Staphylococcus aureus*
2466	S1M10000026B10	*Staphylococcus aureus*
2467	S1M10000026B11	*Staphylococcus aureus*
2468	S1M10000026B12	*Staphylococcus aureus*
2469	S1M10000026C01	*Staphylococcus aureus*
2470	S1M10000026C06	*Staphylococcus aureus*
2471	S1M10000026C07	*Staphylococcus aureus*
2472	S1M10000026C08	*Staphylococcus aureus*
2473	S1M10000026C11	*Staphylococcus aureus*
2474	S1M10000026C12	*Staphylococcus aureus*
2475	S1M10000026D04	*Staphylococcus aureus*
2476	S1M10000026D05	*Staphylococcus aureus*
2477	S1M10000026D06	*Staphylococcus aureus*
2478	S1M10000026D07	*Staphylococcus aureus*
2479	S1M10000026D08	*Staphylococcus aureus*
2480	S1M10000026D10	*Staphylococcus aureus*
2481	S1M10000026D12	*Staphylococcus aureus*
2482	S1M10000026E01	*Staphylococcus aureus*
2483	S1M10000026E07	*Staphylococcus aureus*
2484	S1M10000026E09	*Staphylococcus aureus*
2485	S1M10000026E10	*Staphylococcus aureus*
2486	S1M10000026E11	*Staphylococcus aureus*
2487	S1M10000026E12	*Staphylococcus aureus*
2488	S1M10000026F01	*Staphylococcus aureus*
2489	S1M10000026F03	*Staphylococcus aureus*
2490	S1M10000026F04	*Staphylococcus aureus*
2491	S1M10000026F05	*Staphylococcus aureus*
2492	S1M10000026F06	*Staphylococcus aureus*
2493	S1M10000026F07	*Staphylococcus aureus*
2494	S1M10000026F08	*Staphylococcus aureus*
2495	S1M10000026F09	*Staphylococcus aureus*
2496	S1M10000026F10	*Staphylococcus aureus*
2497	S1M10000026F11	*Staphylococcus aureus*
2498	S1M10000026F12	*Staphylococcus aureus*
2499	S1M10000026G01	*Staphylococcus aureus*
2500	S1M10000026G03	*Staphylococcus aureus*
2501	S1M10000026G04	*Staphylococcus aureus*
2502	S1M10000026G05	*Staphylococcus aureus*
2503	S1M10000026G06	*Staphylococcus aureus*
2504	S1M10000026G07	*Staphylococcus aureus*
2505	S1M10000026G09	*Staphylococcus aureus*

SeqID	Clone name	Organism
2506	S1M10000026G10	*Staphylococcus aureus*
2507	S1M10000026G12	*Staphylococcus aureus*
2508	S1M10000026H01	*Staphylococcus aureus*
2509	S1M10000026H02	*Staphylococcus aureus*
2510	S1M10000026H03	*Staphylococcus aureus*
2511	S1M10000026H04	*Staphylococcus aureus*
2512	S1M10000026H05	*Staphylococcus aureus*
2513	S1M10000026H07	*Staphylococcus aureus*
2514	S1M10000026H09	*Staphylococcus aureus*
2515	S1M10000026H10	*Staphylococcus aureus*
2516	S1M10000027A04	*Staphylococcus aureus*
2517	S1M10000027A05	*Staphylococcus aureus*
2518	S1M10000027A08	*Staphylococcus aureus*
2519	S1M10000027A11	*Staphylococcus aureus*
2520	S1M10000027B04	*Staphylococcus aureus*
2521	S1M10000027B06	*Staphylococcus aureus*
2522	S1M10000027B07	*Staphylococcus aureus*
2523	S1M10000027B08	*Staphylococcus aureus*
2524	S1M10000027B09	*Staphylococcus aureus*
2525	S1M10000027B11	*Staphylococcus aureus*
2526	S1M10000027C02	*Staphylococcus aureus*
2527	S1M10000027C04	*Staphylococcus aureus*
2528	S1M10000027C05	*Staphylococcus aureus*
2529	S1M10000027C06	*Staphylococcus aureus*
2530	S1M10000027C08	*Staphylococcus aureus*
2531	S1M10000027C09	*Staphylococcus aureus*
2532	S1M10000027D02	*Staphylococcus aureus*
2533	S1M10000027D03	*Staphylococcus aureus*
2534	S1M10000027D05	*Staphylococcus aureus*
2535	S1M10000027D06	*Staphylococcus aureus*
2536	S1M10000027D08	*Staphylococcus aureus*
2537	S1M10000027D09	*Staphylococcus aureus*
2538	S1M10000027D10	*Staphylococcus aureus*
2539	S1M10000027D11	*Staphylococcus aureus*
2540	S1M10000027E05	*Staphylococcus aureus*
2541	S1M10000027E06	*Staphylococcus aureus*
2542	S1M10000027E07	*Staphylococcus aureus*
2543	S1M10000027E08	*Staphylococcus aureus*
2544	S1M10000027E09	*Staphylococcus aureus*
2545	S1M10000027E11	*Staphylococcus aureus*
2546	S1M10000027F01	*Staphylococcus aureus*
2547	S1M10000027F02	*Staphylococcus aureus*
2548	S1M10000027F05	*Staphylococcus aureus*
2549	S1M10000027F06	*Staphylococcus aureus*
2550	S1M10000027F08	*Staphylococcus aureus*
2551	S1M10000027F09	*Staphylococcus aureus*
2552	S1M10000027G03	*Staphylococcus aureus*
2553	S1M10000027G04	*Staphylococcus aureus*
2554	S1M10000027G05	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2556	S1M10000027G07	*Staphylococcus aureus*
2557	S1M10000027G09	*Staphylococcus aureus*
2558	S1M10000027G11	*Staphylococcus aureus*
2559	S1M10000027H02	*Staphylococcus aureus*
2560	S1M10000027H04	*Staphylococcus aureus*
2561	S1M10000027H05	*Staphylococcus aureus*
2562	S1M10000027H06	*Staphylococcus aureus*
2563	S1M10000027H07	*Staphylococcus aureus*
2564	S1M10000027H08	*Staphylococcus aureus*
2565	S1M10000027H09	*Staphylococcus aureus*
2566	S1M10000027H10	*Staphylococcus aureus*
2567	S1M10000027H11	*Staphylococcus aureus*
2568	S1M10000028A02	*Staphylococcus aureus*
2569	S1M10000028A04	*Staphylococcus aureus*
2570	S1M10000028A06	*Staphylococcus aureus*
2571	S1M10000028A08	*Staphylococcus aureus*
2572	S1M10000028B01	*Staphylococcus aureus*
2573	S1M10000028B02	*Staphylococcus aureus*
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2575	S1M10000028B04	*Staphylococcus aureus*
2576	S1M10000028B05	*Staphylococcus aureus*
2577	S1M10000028B06	*Staphylococcus aureus*
2578	S1M10000028B08	*Staphylococcus aureus*
2579	S1M10000028B09	*Staphylococcus aureus*
2580	S1M10000028C02	*Staphylococcus aureus*
2581	S1M10000028C04	*Staphylococcus aureus*
2582	S1M10000028C05	*Staphylococcus aureus*
2583	S1M10000028C06	*Staphylococcus aureus*
2584	S1M10000028C08	*Staphylococcus aureus*
2585	S1M10000028D03	*Staphylococcus aureus*
2586	S1M10000028D04	*Staphylococcus aureus*
2587	S1M10000028D06	*Staphylococcus aureus*
2588	S1M10000028D07	*Staphylococcus aureus*
2589	S1M10000028D08	*Staphylococcus aureus*
2590	S1M10000028D09	*Staphylococcus aureus*
2591	S1M10000028E01	*Staphylococcus aureus*
2592	S1M10000028E03	*Staphylococcus aureus*
2593	S1M10000028E08	*Staphylococcus aureus*
2594	S1M10000028F01	*Staphylococcus aureus*
2595	S1M10000028F03	*Staphylococcus aureus*
2596	S1M10000028F04	*Staphylococcus aureus*
2597	S1M10000028F05	*Staphylococcus aureus*
2598	S1M10000028F06	*Staphylococcus aureus*
2599	S1M10000028F07	*Staphylococcus aureus*
2600	S1M10000028G01	*Staphylococcus aureus*
2601	S1M10000028G02	*Staphylococcus aureus*
2602	S1M10000028G03	*Staphylococcus aureus*
2603	S1M10000028G04	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2605	S1M10000028G06	*Staphylococcus aureus*
2606	S1M10000028G08	*Staphylococcus aureus*
2607	S1M10000028H03	*Staphylococcus aureus*
2608	S1M10000028H04	*Staphylococcus aureus*
2609	S1M10000028H05	*Staphylococcus aureus*
2610	S1M10000029A02	*Staphylococcus aureus*
2611	S1M10000029A04	*Staphylococcus aureus*
2612	S1M10000029A09	*Staphylococcus aureus*
2613	S1M10000029A10	*Staphylococcus aureus*
2614	S1M10000029A11	*Staphylococcus aureus*
2615	S1M10000029A12	*Staphylococcus aureus*
2616	S1M10000029B02	*Staphylococcus aureus*
2617	S1M10000029B03	*Staphylococcus aureus*
2618	S1M10000029B04	*Staphylococcus aureus*
2619	S1M10000029B05	*Staphylococcus aureus*
2620	S1M10000029B06	*Staphylococcus aureus*
2621	S1M10000029B08	*Staphylococcus aureus*
2622	S1M10000029B10	*Staphylococcus aureus*
2623	S1M10000029C02	*Staphylococcus aureus*
2624	S1M10000029C03	*Staphylococcus aureus*
2625	S1M10000029C05	*Staphylococcus aureus*
2626	S1M10000029C07	*Staphylococcus aureus*
2627	S1M10000029C09	*Staphylococcus aureus*
2628	S1M10000029C10	*Staphylococcus aureus*
2629	S1M10000029C12	*Staphylococcus aureus*
2630	S1M10000029D02	*Staphylococcus aureus*
2631	S1M10000029D05	*Staphylococcus aureus*
2632	S1M10000029D09	*Staphylococcus aureus*
2633	S1M10000029D10	*Staphylococcus aureus*
2634	S1M10000029D12	*Staphylococcus aureus*
2635	S1M10000029E02	*Staphylococcus aureus*
2636	S1M10000029E05	*Staphylococcus aureus*
2637	S1M10000029E10	*Staphylococcus aureus*
2638	S1M10000029E11	*Staphylococcus aureus*
2639	S1M10000029F01	*Staphylococcus aureus*
2640	S1M10000029F02	*Staphylococcus aureus*
2641	S1M10000029F04	*Staphylococcus aureus*
2642	S1M10000029F09	*Staphylococcus aureus*
2643	S1M10000029F10	*Staphylococcus aureus*
2644	S1M10000029F11	*Staphylococcus aureus*
2645	S1M10000029F12	*Staphylococcus aureus*
2646	S1M10000029G01	*Staphylococcus aureus*
2647	S1M10000029G02	*Staphylococcus aureus*
2648	S1M10000029G03	*Staphylococcus aureus*
2649	S1M10000029G05	*Staphylococcus aureus*
2650	S1M10000029G07	*Staphylococcus aureus*
2651	S1M10000029G08	*Staphylococcus aureus*
2652	S1M10000029G12	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2654	S1M10000029H05	*Staphylococcus aureus*
2655	S1M10000029H06	*Staphylococcus aureus*
2656	S1M10000029H08	*Staphylococcus aureus*
2657	S1M10000029H09	*Staphylococcus aureus*
2658	S1M10000029H10	*Staphylococcus aureus*
2659	S1M10000030A02	*Staphylococcus aureus*
2660	S1M10000030A05	*Staphylococcus aureus*
2661	S1M10000030A09	*Staphylococcus aureus*
2662	S1M10000030A10	*Staphylococcus aureus*
2663	S1M10000030A11	*Staphylococcus aureus*
2664	S1M10000030B02	*Staphylococcus aureus*
2665	S1M10000030B05	*Staphylococcus aureus*
2666	S1M10000030B07	*Staphylococcus aureus*
2667	S1M10000030B09	*Staphylococcus aureus*
2668	S1M10000030C02	*Staphylococcus aureus*
2669	S1M10000030C03	*Staphylococcus aureus*
2670	S1M10000030C04	*Staphylococcus aureus*
2671	S1M10000030C05	*Staphylococcus aureus*
2672	S1M10000030C08	*Staphylococcus aureus*
2673	S1M10000030C09	*Staphylococcus aureus*
2674	S1M10000030C10	*Staphylococcus aureus*
2675	S1M10000030C12	*Staphylococcus aureus*
2676	S1M10000030D01	*Staphylococcus aureus*
2677	S1M10000030D02	*Staphylococcus aureus*
2678	S1M10000030D03	*Staphylococcus aureus*
2679	S1M10000030D05	*Staphylococcus aureus*
2680	S1M10000030D06	*Staphylococcus aureus*
2681	S1M10000030D07	*Staphylococcus aureus*
2682	S1M10000030D09	*Staphylococcus aureus*
2683	S1M10000030D10	*Staphylococcus aureus*
2684	S1M10000030D11	*Staphylococcus aureus*
2685	S1M10000030E02	*Staphylococcus aureus*
2686	S1M10000030E06	*Staphylococcus aureus*
2687	S1M10000030E07	*Staphylococcus aureus*
2688	S1M10000030E11	*Staphylococcus aureus*
2689	S1M10000030E12	*Staphylococcus aureus*
2690	S1M10000030F01	*Staphylococcus aureus*
2691	S1M10000030F07	*Staphylococcus aureus*
2692	S1M10000030F08	*Staphylococcus aureus*
2693	S1M10000030F09	*Staphylococcus aureus*
2694	S1M10000030F10	*Staphylococcus aureus*
2695	S1M10000030G03	*Staphylococcus aureus*
2696	S1M10000030G05	*Staphylococcus aureus*
2697	S1M10000030G07	*Staphylococcus aureus*
2698	S1M10000030G08	*Staphylococcus aureus*
2699	S1M10000030G09	*Staphylococcus aureus*
2700	S1M10000030G10	*Staphylococcus aureus*
2701	S1M10000030G11	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2703	S1M10000030H01	*Staphylococcus aureus*
2704	S1M10000030H02	*Staphylococcus aureus*
2705	S1M10000030H03	*Staphylococcus aureus*
2706	S1M10000030H05	*Staphylococcus aureus*
2707	S1M10000030H07	*Staphylococcus aureus*
2708	S1M10000030H09	*Staphylococcus aureus*
2709	S1M10000031A03	*Staphylococcus aureus*
2710	S1M10000031A08	*Staphylococcus aureus*
2711	S1M10000031A10	*Staphylococcus aureus*
2712	S1M10000031B01	*Staphylococcus aureus*
2713	S1M10000031B02	*Staphylococcus aureus*
2714	S1M10000031B04	*Staphylococcus aureus*
2715	S1M10000031B11	*Staphylococcus aureus*
2716	S1M10000031B12	*Staphylococcus aureus*
2717	S1M10000031C04	*Staphylococcus aureus*
2718	S1M10000031C07	*Staphylococcus aureus*
2719	S1M10000031C09	*Staphylococcus aureus*
2720	S1M10000031C11	*Staphylococcus aureus*
2721	S1M10000031D06	*Staphylococcus aureus*
2722	S1M10000031D07	*Staphylococcus aureus*
2723	S1M10000031D08	*Staphylococcus aureus*
2724	S1M10000031D09	*Staphylococcus aureus*
2725	S1M10000031E02	*Staphylococcus aureus*
2726	S1M10000031E03	*Staphylococcus aureus*
2727	S1M10000031E04	*Staphylococcus aureus*
2728	S1M10000031E07	*Staphylococcus aureus*
2729	S1M10000031E08	*Staphylococcus aureus*
2730	S1M10000031E10	*Staphylococcus aureus*
2731	S1M10000031E12	*Staphylococcus aureus*
2732	S1M10000031F02	*Staphylococcus aureus*
2733	S1M10000031F03	*Staphylococcus aureus*
2734	S1M10000031F04	*Staphylococcus aureus*
2735	S1M10000031F05	*Staphylococcus aureus*
2736	S1M10000031F08	*Staphylococcus aureus*
2737	S1M10000031F10	*Staphylococcus aureus*
2738	S1M10000031F11	*Staphylococcus aureus*
2739	S1M10000031F12	*Staphylococcus aureus*
2740	S1M10000031G02	*Staphylococcus aureus*
2741	S1M10000031G03	*Staphylococcus aureus*
2742	S1M10000031G04	*Staphylococcus aureus*
2743	S1M10000031G06	*Staphylococcus aureus*
2744	S1M10000031G09	*Staphylococcus aureus*
2745	S1M10000031G10	*Staphylococcus aureus*
2746	S1M10000031G11	*Staphylococcus aureus*
2747	S1M10000031H01	*Staphylococcus aureus*
2748	S1M10000031H02	*Staphylococcus aureus*
2749	S1M10000031H06	*Staphylococcus aureus*
2750	S1M10000031H09	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2752	S1M10000032A03	*Staphylococcus aureus*
2753	S1M10000032A05	*Staphylococcus aureus*
2754	S1M10000032A06	*Staphylococcus aureus*
2755	S1M10000032A07	*Staphylococcus aureus*
2756	S1M10000032A08	*Staphylococcus aureus*
2757	S1M10000032A10	*Staphylococcus aureus*
2758	S1M10000032B01	*Staphylococcus aureus*
2759	S1M10000032B05	*Staphylococcus aureus*
2760	S1M10000032B07	*Staphylococcus aureus*
2761	S1M10000032B08	*Staphylococcus aureus*
2762	S1M10000032B11	*Staphylococcus aureus*
2763	S1M10000032B12	*Staphylococcus aureus*
2764	S1M10000032C01	*Staphylococcus aureus*
2765	S1M10000032C03	*Staphylococcus aureus*
2766	S1M10000032C04	*Staphylococcus aureus*
2767	S1M10000032C05	*Staphylococcus aureus*
2768	S1M10000032C09	*Staphylococcus aureus*
2769	S1M10000032C10	*Staphylococcus aureus*
2770	S1M10000032C11	*Staphylococcus aureus*
2771	S1M10000032C12	*Staphylococcus aureus*
2772	S1M10000032D03	*Staphylococcus aureus*
2773	S1M10000032D06	*Staphylococcus aureus*
2774	S1M10000032D07	*Staphylococcus aureus*
2775	S1M10000032D09	*Staphylococcus aureus*
2776	S1M10000032D11	*Staphylococcus aureus*
2777	S1M10000032E02	*Staphylococcus aureus*
2778	S1M10000032E03	*Staphylococcus aureus*
2779	S1M10000032E04	*Staphylococcus aureus*
2780	S1M10000032E06	*Staphylococcus aureus*
2781	S1M10000032E08	*Staphylococcus aureus*
2782	S1M10000032E09	*Staphylococcus aureus*
2783	S1M10000032E10	*Staphylococcus aureus*
2784	S1M10000032E11	*Staphylococcus aureus*
2785	S1M10000032E12	*Staphylococcus aureus*
2786	S1M10000032F01	*Staphylococcus aureus*
2787	S1M10000032F04	*Staphylococcus aureus*
2788	S1M10000032F05	*Staphylococcus aureus*
2789	S1M10000032F10	*Staphylococcus aureus*
2790	S1M10000032F11	*Staphylococcus aureus*
2791	S1M10000032F12	*Staphylococcus aureus*
2792	S1M10000032G02	*Staphylococcus aureus*
2793	S1M10000032G03	*Staphylococcus aureus*
2794	S1M10000032G04	*Staphylococcus aureus*
2795	S1M10000032G06	*Staphylococcus aureus*
2796	S1M10000032G08	*Staphylococcus aureus*
2797	S1M10000032G10	*Staphylococcus aureus*
2798	S1M10000032G12	*Staphylococcus aureus*
2799	S1M10000032H01	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2801	S1M10000032H07	*Staphylococcus aureus*
2802	S1M10000032H09	*Staphylococcus aureus*
2803	S1M10000032H11	*Staphylococcus aureus*
2804	S1M10000033A02	*Staphylococcus aureus*
2805	S1M10000033A07	*Staphylococcus aureus*
2806	S1M10000033A08	*Staphylococcus aureus*
2807	S1M10000033A10	*Staphylococcus aureus*
2808	S1M10000033B02	*Staphylococcus aureus*
2809	S1M10000033B07	*Staphylococcus aureus*
2810	S1M10000033B08	*Staphylococcus aureus*
2811	S1M10000033B11	*Staphylococcus aureus*
2812	S1M10000033B12	*Staphylococcus aureus*
2813	S1M10000033C04	*Staphylococcus aureus*
2814	S1M10000033D02	*Staphylococcus aureus*
2815	S1M10000033D03	*Staphylococcus aureus*
2816	S1M10000033D04	*Staphylococcus aureus*
2817	S1M10000033D05	*Staphylococcus aureus*
2818	S1M10000033D06	*Staphylococcus aureus*
2819	S1M10000033D10	*Staphylococcus aureus*
2820	S1M10000033D12	*Staphylococcus aureus*
2821	S1M10000033E04	*Staphylococcus aureus*
2822	S1M10000033E10	*Staphylococcus aureus*
2823	S1M10000033E12	*Staphylococcus aureus*
2824	S1M10000033F02	*Staphylococcus aureus*
2825	S1M10000033F03	*Staphylococcus aureus*
2826	S1M10000033F06	*Staphylococcus aureus*
2827	S1M10000033F07	*Staphylococcus aureus*
2828	S1M10000033F09	*Staphylococcus aureus*
2829	S1M10000033F11	*Staphylococcus aureus*
2830	S1M10000033G05	*Staphylococcus aureus*
2831	S1M10000033G07	*Staphylococcus aureus*
2832	S1M10000033G09	*Staphylococcus aureus*
2833	S1M10000033G10	*Staphylococcus aureus*
2834	S1M10000033G11	*Staphylococcus aureus*
2835	S1M10000033G12	*Staphylococcus aureus*
2836	S1M10000033H01	*Staphylococcus aureus*
2837	S1M10000033H02	*Staphylococcus aureus*
2838	S1M10000033H03	*Staphylococcus aureus*
2839	S1M10000033H07	*Staphylococcus aureus*
2840	S1M10000033H08	*Staphylococcus aureus*
2841	S1M10000033H09	*Staphylococcus aureus*
2842	S1M10000033H10	*Staphylococcus aureus*
2843	S1M10000033H11	*Staphylococcus aureus*
2844	S1M10000034A02	*Staphylococcus aureus*
2845	S1M10000034A03	*Staphylococcus aureus*
2846	S1M10000034A04	*Staphylococcus aureus*
2847	S1M10000034A05	*Staphylococcus aureus*
2848	S1M10000034A08	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2850	S1M10000034A11	*Staphylococcus aureus*
2851	S1M10000034A12	*Staphylococcus aureus*
2852	S1M10000034B03	*Staphylococcus aureus*
2853	S1M10000034B05	*Staphylococcus aureus*
2854	S1M10000034B06	*Staphylococcus aureus*
2855	S1M10000034B07	*Staphylococcus aureus*
2856	S1M10000034B08	*Staphylococcus aureus*
2857	S1M10000034B09	*Staphylococcus aureus*
2858	S1M10000034B10	*Staphylococcus aureus*
2859	S1M10000034B12	*Staphylococcus aureus*
2860	S1M10000034C02	*Staphylococcus aureus*
2861	S1M10000034C06	*Staphylococcus aureus*
2862	S1M10000034C07	*Staphylococcus aureus*
2863	S1M10000034C09	*Staphylococcus aureus*
2864	S1M10000034C12	*Staphylococcus aureus*
2865	S1M10000034D01	*Staphylococcus aureus*
2866	S1M10000034D05	*Staphylococcus aureus*
2867	S1M10000034D06	*Staphylococcus aureus*
2868	S1M10000034D07	*Staphylococcus aureus*
2869	S1M10000034D08	*Staphylococcus aureus*
2870	S1M10000034D10	*Staphylococcus aureus*
2871	S1M10000034D11	*Staphylococcus aureus*
2872	S1M10000034D12	*Staphylococcus aureus*
2873	S1M10000034E01	*Staphylococcus aureus*
2874	S1M10000034E02	*Staphylococcus aureus*
2875	S1M10000034E04	*Staphylococcus aureus*
2876	S1M10000034E05	*Staphylococcus aureus*
2877	S1M10000034E06	*Staphylococcus aureus*
2878	S1M10000034E07	*Staphylococcus aureus*
2879	S1M10000034E10	*Staphylococcus aureus*
2880	S1M10000034E11	*Staphylococcus aureus*
2881	S1M10000034E12	*Staphylococcus aureus*
2882	S1M10000034F01	*Staphylococcus aureus*
2883	S1M10000034F02	*Staphylococcus aureus*
2884	S1M10000034F03	*Staphylococcus aureus*
2885	S1M10000034F04	*Staphylococcus aureus*
2886	S1M10000034F05	*Staphylococcus aureus*
2887	S1M10000034F07	*Staphylococcus aureus*
2888	S1M10000034F08	*Staphylococcus aureus*
2889	S1M10000034F09	*Staphylococcus aureus*
2890	S1M10000034F10	*Staphylococcus aureus*
2891	S1M10000034F12	*Staphylococcus aureus*
2892	S1M10000034G02	*Staphylococcus aureus*
2893	S1M10000034G03	*Staphylococcus aureus*
2894	S1M10000034G06	*Staphylococcus aureus*
2895	S1M10000034G07	*Staphylococcus aureus*
2896	S1M10000034G08	*Staphylococcus aureus*
2897	S1M10000034G09	*Staphylococcus aureus*

SeqID	Clone name	Organism
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2899	S1M10000034G12	*Staphylococcus aureus*
2900	S1M10000034H01	*Staphylococcus aureus*
2901	S1M10000034H02	*Staphylococcus aureus*
2902	S1M10000034H03	*Staphylococcus aureus*
2903	S1M10000034H06	*Staphylococcus aureus*
2904	S1M10000034H07	*Staphylococcus aureus*
2905	S1M10000034H08	*Staphylococcus aureus*
2906	S1M10000034H09	*Staphylococcus aureus*
2907	S1M10000034H10	*Staphylococcus aureus*
2908	S1M10000035A03	*Staphylococcus aureus*
2909	S1M10000035A08	*Staphylococcus aureus*
2910	S1M10000035A09	*Staphylococcus aureus*
2911	S1M10000035A10	*Staphylococcus aureus*
2912	S1M10000035A11	*Staphylococcus aureus*
2913	S1M10000035A12	*Staphylococcus aureus*
2914	S1M10000035B01	*Staphylococcus aureus*
2915	S1M10000035B03	*Staphylococcus aureus*
2916	S1M10000035B04	*Staphylococcus aureus*
2917	S1M10000035B08	*Staphylococcus aureus*
2918	S1M10000035B11	*Staphylococcus aureus*
2919	S1M10000035C01	*Staphylococcus aureus*
2920	S1M10000035C02	*Staphylococcus aureus*
2921	S1M10000035C04	*Staphylococcus aureus*
2922	S1M10000035C06	*Staphylococcus aureus*
2923	S1M10000035C11	*Staphylococcus aureus*
2924	S1M10000035D01	*Staphylococcus aureus*
2925	S1M10000035D04	*Staphylococcus aureus*
2926	S1M10000035D06	*Staphylococcus aureus*
2927	S1M10000035D09	*Staphylococcus aureus*
2928	S1M10000035D12	*Staphylococcus aureus*
2929	S1M10000035E02	*Staphylococcus aureus*
2930	S1M10000035E03	*Staphylococcus aureus*
2931	S1M10000035E04	*Staphylococcus aureus*
2932	S1M10000035E08	*Staphylococcus aureus*
2933	S1M10000035E09	*Staphylococcus aureus*
2934	S1M10000035E12	*Staphylococcus aureus*
2935	S1M10000035F03	*Staphylococcus aureus*
2936	S1M10000035F04	*Staphylococcus aureus*
2937	S1M10000035F09	*Staphylococcus aureus*
2938	S1M10000035F12	*Staphylococcus aureus*
2939	S1M10000035G02	*Staphylococcus aureus*
2940	S1M10000035G09	*Staphylococcus aureus*
2941	S1M10000035G11	*Staphylococcus aureus*
2942	S1M10000035G12	*Staphylococcus aureus*
2943	S1M10000035H01	*Staphylococcus aureus*
2944	S1M10000035H07	*Staphylococcus aureus*
2945	S1M10000035H08	*Staphylococcus aureus*
2946	S1M10000035H09	*Staphylococcus aureus*

SeqID	Clone name	Organism
2947	S1M10000035H10	*Staphylococcus aureus*
2948	S1M10000035H11	*Staphylococcus aureus*
2949	S1M10000036A02	*Staphylococcus aureus*
2950	S1M10000036A03	*Staphylococcus aureus*
2951	S1M10000036A04	*Staphylococcus aureus*
2952	S1M10000036A05	*Staphylococcus aureus*
2953	S1M10000036A08	*Staphylococcus aureus*
2954	S1M10000036A11	*Staphylococcus aureus*
2955	S1M10000036A12	*Staphylococcus aureus*
2956	S1M10000036B04	*Staphylococcus aureus*
2957	S1M10000036B06	*Staphylococcus aureus*
2958	S1M10000036B07	*Staphylococcus aureus*
2959	S1M10000036B08	*Staphylococcus aureus*
2960	S1M10000036B11	*Staphylococcus aureus*
2961	S1M10000036B12	*Staphylococcus aureus*
2962	S1M10000036C01	*Staphylococcus aureus*
2963	S1M10000036C03	*Staphylococcus aureus*
2964	S1M10000036C04	*Staphylococcus aureus*
2965	S1M10000036C05	*Staphylococcus aureus*
2966	S1M10000036C06	*Staphylococcus aureus*
2967	S1M10000036C07	*Staphylococcus aureus*
2968	S1M10000036C09	*Staphylococcus aureus*
2969	S1M10000036C10	*Staphylococcus aureus*
2970	S1M10000036D02	*Staphylococcus aureus*
2971	S1M10000036D03	*Staphylococcus aureus*
2972	S1M10000036D06	*Staphylococcus aureus*
2973	S1M10000036D08	*Staphylococcus aureus*
2974	S1M10000036D10	*Staphylococcus aureus*
2975	S1M10000036D11	*Staphylococcus aureus*
2976	S1M10000036D12	*Staphylococcus aureus*
2977	S1M10000036E06	*Staphylococcus aureus*
2978	S1M10000036E08	*Staphylococcus aureus*
2979	S1M10000036E11	*Staphylococcus aureus*
2980	S1M10000036F06	*Staphylococcus aureus*
2981	S1M10000036F07	*Staphylococcus aureus*
2982	S1M10000036F08	*Staphylococcus aureus*
2983	S1M10000036F09	*Staphylococcus aureus*
2984	S1M10000036F10	*Staphylococcus aureus*
2985	S1M10000036F11	*Staphylococcus aureus*
2986	S1M10000036G03	*Staphylococcus aureus*
2987	S1M10000036G07	*Staphylococcus aureus*
2988	S1M10000036G08	*Staphylococcus aureus*
2989	S1M10000036G11	*Staphylococcus aureus*
2990	S1M10000036H01	*Staphylococcus aureus*
2991	S1M10000036H02	*Staphylococcus aureus*
2992	S1M10000036H03	*Staphylococcus aureus*
2993	S1M10000036H04	*Staphylococcus aureus*
2994	S1M10000036H05	*Staphylococcus aureus*
2995	S1M10000036H06	*Staphylococcus aureus*

SeqID	Clone name	Organism
2996	S1M10000036H08	*Staphylococcus aureus*
2997	S1M10000036H11	*Staphylococcus aureus*
2998	S1M10000037A02	*Staphylococcus aureus*
2999	S1M10000037A03	*Staphylococcus aureus*
3000	S1M10000037A06	*Staphylococcus aureus*
3001	S1M10000037A08	*Staphylococcus aureus*
3002	S1M10000037A09	*Staphylococcus aureus*
3003	S1M10000037A11	*Staphylococcus aureus*
3004	S1M10000037A12	*Staphylococcus aureus*
3005	S1M10000037B03	*Staphylococcus aureus*
3006	S1M10000037B04	*Staphylococcus aureus*
3007	S1M10000037B05	*Staphylococcus aureus*
3008	S1M10000037B06	*Staphylococcus aureus*
3009	S1M10000037B07	*Staphylococcus aureus*
3010	S1M10000037B08	*Staphylococcus aureus*
3011	S1M10000037B10	*Staphylococcus aureus*
3012	S1M10000037B11	*Staphylococcus aureus*
3013	S1M10000037B12	*Staphylococcus aureus*
3014	S1M10000037C05	*Staphylococcus aureus*
3015	S1M10000037C06	*Staphylococcus aureus*
3016	S1M10000037C07	*Staphylococcus aureus*
3017	S1M10000037C08	*Staphylococcus aureus*
3018	S1M10000037C09	*Staphylococcus aureus*
3019	S1M10000037C10	*Staphylococcus aureus*
3020	S1M10000037D04	*Staphylococcus aureus*
3021	S1M10000037D05	*Staphylococcus aureus*
3022	S1M10000037D06	*Staphylococcus aureus*
3023	S1M10000037D09	*Staphylococcus aureus*
3024	S1M10000037D12	*Staphylococcus aureus*
3025	S1M10000037E02	*Staphylococcus aureus*
3026	S1M10000037E03	*Staphylococcus aureus*
3027	S1M10000037E06	*Staphylococcus aureus*
3028	S1M10000037E08	*Staphylococcus aureus*
3029	S1M10000037E09	*Staphylococcus aureus*
3030	S1M10000037E10	*Staphylococcus aureus*
3031	S1M10000037E11	*Staphylococcus aureus*
3032	S1M10000037E12	*Staphylococcus aureus*
3033	S1M10000037F02	*Staphylococcus aureus*
3034	S1M10000037F03	*Staphylococcus aureus*
3035	S1M10000037F04	*Staphylococcus aureus*
3036	S1M10000037F05	*Staphylococcus aureus*
3037	S1M10000037F06	*Staphylococcus aureus*
3038	S1M10000037F07	*Staphylococcus aureus*
3039	S1M10000037F08	*Staphylococcus aureus*
3040	S1M10000037F09	*Staphylococcus aureus*
3041	S1M10000037F10	*Staphylococcus aureus*
3042	S1M10000037G01	*Staphylococcus aureus*
3043	S1M10000037G02	*Staphylococcus aureus*
3044	S1M10000037G03	*Staphylococcus aureus*

SeqID	Clone name	Organism
3045	S1M10000037G06	*Staphylococcus aureus*
3046	S1M10000037G07	*Staphylococcus aureus*
3047	S1M10000037G08	*Staphylococcus aureus*
3048	S1M10000037G10	*Staphylococcus aureus*
3049	S1M10000037H02	*Staphylococcus aureus*
3050	S1M10000037H03	*Staphylococcus aureus*
3051	S1M10000037H05	*Staphylococcus aureus*
3052	S1M10000037H07	*Staphylococcus aureus*
3053	S1M10000037H08	*Staphylococcus aureus*
3054	S1M10000037H09	*Staphylococcus aureus*
3055	S1M10000037H11	*Staphylococcus aureus*
3056	S1M10000038A04	*Staphylococcus aureus*
3057	S1M10000038A07	*Staphylococcus aureus*
3058	S1M10000038A08	*Staphylococcus aureus*
3059	S1M10000038A09	*Staphylococcus aureus*
3060	S1M10000038A11	*Staphylococcus aureus*
3061	S1M10000038A12	*Staphylococcus aureus*
3062	S1M10000038B01	*Staphylococcus aureus*
3063	S1M10000038B03	*Staphylococcus aureus*
3064	S1M10000038B07	*Staphylococcus aureus*
3065	S1M10000038B08	*Staphylococcus aureus*
3066	S1M10000038B09	*Staphylococcus aureus*
3067	S1M10000038B12	*Staphylococcus aureus*
3068	S1M10000038C01	*Staphylococcus aureus*
3069	S1M10000038C02	*Staphylococcus aureus*
3070	S1M10000038C06	*Staphylococcus aureus*
3071	S1M10000038C08	*Staphylococcus aureus*
3072	S1M10000038C10	*Staphylococcus aureus*
3073	S1M10000038C11	*Staphylococcus aureus*
3074	S1M10000038C12	*Staphylococcus aureus*
3075	S1M10000038D02	*Staphylococcus aureus*
3076	S1M10000038D05	*Staphylococcus aureus*
3077	S1M10000038D07	*Staphylococcus aureus*
3078	S1M10000038D08	*Staphylococcus aureus*
3079	S1M10000038D09	*Staphylococcus aureus*
3080	S1M10000038D10	*Staphylococcus aureus*
3081	S1M10000038D11	*Staphylococcus aureus*
3082	S1M10000038D12	*Staphylococcus aureus*
3083	S1M10000038E01	*Staphylococcus aureus*
3084	S1M10000038E02	*Staphylococcus aureus*
3085	S1M10000038E03	*Staphylococcus aureus*
3086	S1M10000038E04	*Staphylococcus aureus*
3087	S1M10000038E05	*Staphylococcus aureus*
3088	S1M10000038E06	*Staphylococcus aureus*
3089	S1M10000038E07	*Staphylococcus aureus*
3090	S1M10000038E10	*Staphylococcus aureus*
3091	S1M10000038E12	*Staphylococcus aureus*
3092	S1M10000038F03	*Staphylococcus aureus*
3093	S1M10000038F04	*Staphylococcus aureus*

TABLE IA

SeqID	Clone name	Organism
3094	S1M10000038F05	*Staphylococcus aureus*
3095	S1M10000038F06	*Staphylococcus aureus*
3096	S1M10000038F08	*Staphylococcus aureus*
3097	S1M10000038F09	*Staphylococcus aureus*
3098	S1M10000038F10	*Staphylococcus aureus*
3099	S1M10000038F11	*Staphylococcus aureus*
3100	S1M10000038F12	*Staphylococcus aureus*
3101	S1M10000038G01	*Staphylococcus aureus*
3102	S1M10000038G03	*Staphylococcus aureus*
3103	S1M10000038G04	*Staphylococcus aureus*
3104	S1M10000038G06	*Staphylococcus aureus*
3105	S1M10000038G08	*Staphylococcus aureus*
3106	S1M10000038G10	*Staphylococcus aureus*
3107	S1M10000038G11	*Staphylococcus aureus*
3108	S1M10000038G12	*Staphylococcus aureus*
3109	S1M10000038H03	*Staphylococcus aureus*
3110	S1M10000038H07	*Staphylococcus aureus*
3111	S1M10000038H09	*Staphylococcus aureus*
3112	S1M10000038H11	*Staphylococcus aureus*
3113	S1M10000039A02	*Staphylococcus aureus*
3114	S1M10000039A05	*Staphylococcus aureus*
3115	S1M10000039A07	*Staphylococcus aureus*
3116	S1M10000039A08	*Staphylococcus aureus*
3117	S1M10000039A11	*Staphylococcus aureus*
3118	S1M10000039A12	*Staphylococcus aureus*
3119	S1M10000039B02	*Staphylococcus aureus*
3120	S1M10000039B06	*Staphylococcus aureus*
3121	S1M10000039B07	*Staphylococcus aureus*
3122	S1M10000039B10	*Staphylococcus aureus*
3123	S1M10000039B12	*Staphylococcus aureus*
3124	S1M10000039C04	*Staphylococcus aureus*
3125	S1M10000039C06	*Staphylococcus aureus*
3126	S1M10000039C07	*Staphylococcus aureus*
3127	S1M10000039C08	*Staphylococcus aureus*
3128	S1M10000039C09	*Staphylococcus aureus*
3129	S1M10000039C10	*Staphylococcus aureus*
3130	S1M10000039C11	*Staphylococcus aureus*
3131	S1M10000039D02	*Staphylococcus aureus*
3132	S1M10000039D09	*Staphylococcus aureus*
3133	S1M10000039D10	*Staphylococcus aureus*
3134	S1M10000039E01	*Staphylococcus aureus*
3135	S1M10000039E08	*Staphylococcus aureus*
3136	S1M10000039E09	*Staphylococcus aureus*
3137	S1M10000039E10	*Staphylococcus aureus*
3138	S1M10000039E11	*Staphylococcus aureus*
3139	S1M10000039F02	*Staphylococcus aureus*
3140	S1M10000039F03	*Staphylococcus aureus*
3141	S1M10000039F05	*Staphylococcus aureus*
3142	S1M10000039F07	*Staphylococcus aureus*

SeqID	Clone name	Organism
3143	S1M10000039F08	*Staphylococcus aureus*
3144	S1M10000039F09	*Staphylococcus aureus*
3145	S1M10000039F10	*Staphylococcus aureus*
3146	S1M10000039F12	*Staphylococcus aureus*
3147	S1M10000039G03	*Staphylococcus aureus*
3148	S1M10000039G04	*Staphylococcus aureus*
3149	S1M10000039G07	*Staphylococcus aureus*
3150	S1M10000039G10	*Staphylococcus aureus*
3151	S1M10000039H02	*Staphylococcus aureus*
3152	S1M10000039H03	*Staphylococcus aureus*
3153	S1M10000039H04	*Staphylococcus aureus*
3154	S1M10000039H06	*Staphylococcus aureus*
3155	S1M10000039H07	*Staphylococcus aureus*
3156	S1M10000039H08	*Staphylococcus aureus*
3157	S1M10000040A04	*Staphylococcus aureus*
3158	S1M10000040A05	*Staphylococcus aureus*
3159	S1M10000040A07	*Staphylococcus aureus*
3160	S1M10000040A08	*Staphylococcus aureus*
3161	S1M10000040A10	*Staphylococcus aureus*
3162	S1M10000040A11	*Staphylococcus aureus*
3163	S1M10000040B01	*Staphylococcus aureus*
3164	S1M10000040B03	*Staphylococcus aureus*
3165	S1M10000040B07	*Staphylococcus aureus*
3166	S1M10000040B11	*Staphylococcus aureus*
3167	S1M10000040C03	*Staphylococcus aureus*
3168	S1M10000040C04	*Staphylococcus aureus*
3169	S1M10000040C05	*Staphylococcus aureus*
3170	S1M10000040C06	*Staphylococcus aureus*
3171	S1M10000040C07	*Staphylococcus aureus*
3172	S1M10000040C08	*Staphylococcus aureus*
3173	S1M10000040C10	*Staphylococcus aureus*
3174	S1M10000040C11	*Staphylococcus aureus*
3175	S1M10000040D01	*Staphylococcus aureus*
3176	S1M10000040D03	*Staphylococcus aureus*
3177	S1M10000040D08	*Staphylococcus aureus*
3178	S1M10000040D09	*Staphylococcus aureus*
3179	S1M10000040D11	*Staphylococcus aureus*
3180	S1M10000040E01	*Staphylococcus aureus*
3181	S1M10000040E02	*Staphylococcus aureus*
3182	S1M10000040E04	*Staphylococcus aureus*
3183	S1M10000040E05	*Staphylococcus aureus*
3184	S1M10000040E06	*Staphylococcus aureus*
3185	S1M10000040E07	*Staphylococcus aureus*
3186	S1M10000040E09	*Staphylococcus aureus*
3187	S1M10000040E10	*Staphylococcus aureus*
3188	S1M10000040E11	*Staphylococcus aureus*
3189	S1M10000040E12	*Staphylococcus aureus*
3190	S1M10000040F01	*Staphylococcus aureus*
3191	S1M10000040F02	*Staphylococcus aureus*

SeqID	Clone name	Organism
3192	S1M10000040F03	*Staphylococcus aureus*
3193	S1M10000040F04	*Staphylococcus aureus*
3194	S1M10000040F05	*Staphylococcus aureus*
3195	S1M10000040F06	*Staphylococcus aureus*
3196	S1M10000040F08	*Staphylococcus aureus*
3197	S1M10000040F09	*Staphylococcus aureus*
3198	S1M10000040F12	*Staphylococcus aureus*
3199	S1M10000040G01	*Staphylococcus aureus*
3200	S1M10000040G02	*Staphylococcus aureus*
3201	S1M10000040G04	*Staphylococcus aureus*
3202	S1M10000040G07	*Staphylococcus aureus*
3203	S1M10000040G08	*Staphylococcus aureus*
3204	S1M10000040G12	*Staphylococcus aureus*
3205	S1M10000040H02	*Staphylococcus aureus*
3206	S1M10000040H03	*Staphylococcus aureus*
3207	S1M10000040H04	*Staphylococcus aureus*
3208	S1M10000040H05	*Staphylococcus aureus*
3209	S1M10000040H07	*Staphylococcus aureus*
3210	S1M10000040H10	*Staphylococcus aureus*
3211	S1M10000041A03	*Staphylococcus aureus*
3212	S1M10000041B02	*Staphylococcus aureus*
3213	S1M10000041B03	*Staphylococcus aureus*
3214	S1M10000041B05	*Staphylococcus aureus*
3215	S1M10000041B06	*Staphylococcus aureus*
3216	S1M10000041B07	*Staphylococcus aureus*
3217	S1M10000041B12	*Staphylococcus aureus*
3218	S1M10000041C08	*Staphylococcus aureus*
3219	S1M10000041C10	*Staphylococcus aureus*
3220	S1M10000041C11	*Staphylococcus aureus*
3221	S1M10000041D06	*Staphylococcus aureus*
3222	S1M10000041D07	*Staphylococcus aureus*
3223	S1M10000041D08	*Staphylococcus aureus*
3224	S1M10000041D10	*Staphylococcus aureus*
3225	S1M10000041D12	*Staphylococcus aureus*
3226	S1M10000041E03	*Staphylococcus aureus*
3227	S1M10000041E06	*Staphylococcus aureus*
3228	S1M10000041E09	*Staphylococcus aureus*
3229	S1M10000041E12	*Staphylococcus aureus*
3230	S1M10000041F03	*Staphylococcus aureus*
3231	S1M10000041F11	*Staphylococcus aureus*
3232	S1M10000041F12	*Staphylococcus aureus*
3233	S1M10000041G01	*Staphylococcus aureus*
3234	S1M10000041G06	*Staphylococcus aureus*
3235	S1M10000041G08	*Staphylococcus aureus*
3236	S1M10000041G10	*Staphylococcus aureus*
3237	S1M10000041G11	*Staphylococcus aureus*
3238	S1M10000041H01	*Staphylococcus aureus*
3239	S1M10000041H04	*Staphylococcus aureus*
3240	S1M10000041H05	*Staphylococcus aureus*

SeqID	Clone name	Organism
3241	S1M10000041H07	*Staphylococcus aureus*
3242	S1M10000041H08	*Staphylococcus aureus*
3243	S1M10000041H09	*Staphylococcus aureus*
3244	S1M10000042A04	*Staphylococcus aureus*
3245	S1M10000042A05	*Staphylococcus aureus*
3246	S1M10000042A06	*Staphylococcus aureus*
3247	S1M10000042A07	*Staphylococcus aureus*
3248	S1M10000042A09	*Staphylococcus aureus*
3249	S1M10000042A11	*Staphylococcus aureus*
3250	S1M10000042A12	*Staphylococcus aureus*
3251	S1M10000042B02	*Staphylococcus aureus*
3252	S1M10000042B03	*Staphylococcus aureus*
3253	S1M10000042B06	*Staphylococcus aureus*
3254	S1M10000042B07	*Staphylococcus aureus*
3255	S1M10000042B08	*Staphylococcus aureus*
3256	S1M10000042B09	*Staphylococcus aureus*
3257	S1M10000042B10	*Staphylococcus aureus*
3258	S1M10000042B11	*Staphylococcus aureus*
3259	S1M10000042B12	*Staphylococcus aureus*
3260	S1M10000042C02	*Staphylococcus aureus*
3261	S1M10000042C06	*Staphylococcus aureus*
3262	S1M10000042C10	*Staphylococcus aureus*
3263	S1M10000042C11	*Staphylococcus aureus*
3264	S1M10000042D04	*Staphylococcus aureus*
3265	S1M10000042D07	*Staphylococcus aureus*
3266	S1M10000042D10	*Staphylococcus aureus*
3267	S1M10000042D11	*Staphylococcus aureus*
3268	S1M10000042E03	*Staphylococcus aureus*
3269	S1M10000042E06	*Staphylococcus aureus*
3270	S1M10000042E08	*Staphylococcus aureus*
3271	S1M10000042F01	*Staphylococcus aureus*
3272	S1M10000042F02	*Staphylococcus aureus*
3273	S1M10000042F05	*Staphylococcus aureus*
3274	S1M10000042F06	*Staphylococcus aureus*
3275	S1M10000042F08	*Staphylococcus aureus*
3276	S1M10000042F09	*Staphylococcus aureus*
3277	S1M10000042F10	*Staphylococcus aureus*
3278	S1M10000042F11	*Staphylococcus aureus*
3279	S1M10000042G01	*Staphylococcus aureus*
3280	S1M10000042G03	*Staphylococcus aureus*
3281	S1M10000042G08	*Staphylococcus aureus*
3282	S1M10000042G09	*Staphylococcus aureus*
3283	S1M10000042G12	*Staphylococcus aureus*
3284	S1M10000042H05	*Staphylococcus aureus*
3285	S1M10000042H07	*Staphylococcus aureus*
3286	S1M10000042H11	*Staphylococcus aureus*
3287	S1M10000043A02	*Staphylococcus aureus*
3288	S1M10000043A03	*Staphylococcus aureus*
3289	S1M10000043A04	*Staphylococcus aureus*

SeqID	Clone name	Organism
3290	S1M10000043A06	*Staphylococcus aureus*
3291	S1M10000043A07	*Staphylococcus aureus*
3292	S1M10000043A08	*Staphylococcus aureus*
3293	S1M10000043A10	*Staphylococcus aureus*
3294	S1M10000043A11	*Staphylococcus aureus*
3295	S1M10000043A12	*Staphylococcus aureus*
3296	S1M10000043B01	*Staphylococcus aureus*
3297	S1M10000043B02	*Staphylococcus aureus*
3298	S1M10000043B07	*Staphylococcus aureus*
3299	S1M10000043B08	*Staphylococcus aureus*
3300	S1M10000043B09	*Staphylococcus aureus*
3301	S1M10000043B10	*Staphylococcus aureus*
3302	S1M10000043B12	*Staphylococcus aureus*
3303	S1M10000043C02	*Staphylococcus aureus*
3304	S1M10000043C07	*Staphylococcus aureus*
3305	S1M10000043C11	*Staphylococcus aureus*
3306	S1M10000043C12	*Staphylococcus aureus*
3307	S1M10000043D01	*Staphylococcus aureus*
3308	S1M10000043D02	*Staphylococcus aureus*
3309	S1M10000043D04	*Staphylococcus aureus*
3310	S1M10000043D10	*Staphylococcus aureus*
3311	S1M10000043D12	*Staphylococcus aureus*
3312	S1M10000043E02	*Staphylococcus aureus*
3313	S1M10000043E03	*Staphylococcus aureus*
3314	S1M10000043E05	*Staphylococcus aureus*
3315	S1M10000043E07	*Staphylococcus aureus*
3316	S1M10000043E08	*Staphylococcus aureus*
3317	S1M10000043E10	*Staphylococcus aureus*
3318	S1M10000043E11	*Staphylococcus aureus*
3319	S1M10000043E12	*Staphylococcus aureus*
3320	S1M10000043F01	*Staphylococcus aureus*
3321	S1M10000043F05	*Staphylococcus aureus*
3322	S1M10000043F07	*Staphylococcus aureus*
3323	S1M10000043F08	*Staphylococcus aureus*
3324	S1M10000043F09	*Staphylococcus aureus*
3325	S1M10000043G01	*Staphylococcus aureus*
3326	S1M10000043G04	*Staphylococcus aureus*
3327	S1M10000043G05	*Staphylococcus aureus*
3328	S1M10000043G09	*Staphylococcus aureus*
3329	S1M10000043G10	*Staphylococcus aureus*
3330	S1M10000043H01	*Staphylococcus aureus*
3331	S1M10000043H03	*Staphylococcus aureus*
3332	S1M10000043H04	*Staphylococcus aureus*
3333	S1M10000043H05	*Staphylococcus aureus*
3334	S1M10000043H06	*Staphylococcus aureus*
3335	S1M10000043H09	*Staphylococcus aureus*
3336	S1M10000043H10	*Staphylococcus aureus*
3337	S1M10000043H11	*Staphylococcus aureus*
3338	S1M10000044A02	*Staphylococcus aureus*

SeqID	Clone name	Organism
3339	S1M10000044A06	*Staphylococcus aureus*
3340	S1M10000044A08	*Staphylococcus aureus*
3341	S1M10000044A09	*Staphylococcus aureus*
3342	S1M10000044A11	*Staphylococcus aureus*
3343	S1M10000044A12	*Staphylococcus aureus*
3344	S1M10000044B01	*Staphylococcus aureus*
3345	S1M10000044B02	*Staphylococcus aureus*
3346	S1M10000044B05	*Staphylococcus aureus*
3347	S1M10000044B06	*Staphylococcus aureus*
3348	S1M10000044B08	*Staphylococcus aureus*
3349	S1M10000044B11	*Staphylococcus aureus*
3350	S1M10000044B12	*Staphylococcus aureus*
3351	S1M10000044C04	*Staphylococcus aureus*
3352	S1M10000044C06	*Staphylococcus aureus*
3353	S1M10000044C07	*Staphylococcus aureus*
3354	S1M10000044C08	*Staphylococcus aureus*
3355	S1M10000044C11	*Staphylococcus aureus*
3356	S1M10000044C12	*Staphylococcus aureus*
3357	S1M10000044D01	*Staphylococcus aureus*
3358	S1M10000044D04	*Staphylococcus aureus*
3359	S1M10000044D06	*Staphylococcus aureus*
3360	S1M10000044D08	*Staphylococcus aureus*
3361	S1M10000044D09	*Staphylococcus aureus*
3362	S1M10000044D10	*Staphylococcus aureus*
3363	S1M10000044D11	*Staphylococcus aureus*
3364	S1M10000044D12	*Staphylococcus aureus*
3365	S1M10000044E01	*Staphylococcus aureus*
3366	S1M10000044E02	*Staphylococcus aureus*
3367	S1M10000044E06	*Staphylococcus aureus*
3368	S1M10000044E07	*Staphylococcus aureus*
3369	S1M10000044E09	*Staphylococcus aureus*
3370	S1M10000044E10	*Staphylococcus aureus*
3371	S1M10000044E11	*Staphylococcus aureus*
3372	S1M10000044F02	*Staphylococcus aureus*
3373	S1M10000044F06	*Staphylococcus aureus*
3374	S1M10000044F08	*Staphylococcus aureus*
3375	S1M10000044F10	*Staphylococcus aureus*
3376	S1M10000044G02	*Staphylococcus aureus*
3377	S1M10000044G05	*Staphylococcus aureus*
3378	S1M10000044G08	*Staphylococcus aureus*
3379	S1M10000044G10	*Staphylococcus aureus*
3380	S1M10000044G11	*Staphylococcus aureus*
3381	S1M10000044H06	*Staphylococcus aureus*
3382	S1M10000044H07	*Staphylococcus aureus*
3383	S1M10000044H08	*Staphylococcus aureus*
3384	S1M10000044H09	*Staphylococcus aureus*
3385	S1M10000044H10	*Staphylococcus aureus*
3386	S1M10000044H11	*Staphylococcus aureus*
3387	S1M10000045A02	*Staphylococcus aureus*

SeqID	Clone name	Organism
3388	S1M10000045A06	*Staphylococcus aureus*
3389	S1M10000045A07	*Staphylococcus aureus*
3390	S1M10000045A08	*Staphylococcus aureus*
3391	S1M10000045A12	*Staphylococcus aureus*
3392	S1M10000045B01	*Staphylococcus aureus*
3393	S1M10000045B02	*Staphylococcus aureus*
3394	S1M10000045B03	*Staphylococcus aureus*
3395	S1M10000045B07	*Staphylococcus aureus*
3396	S1M10000045B10	*Staphylococcus aureus*
3397	S1M10000045B11	*Staphylococcus aureus*
3398	S1M10000045B12	*Staphylococcus aureus*
3399	S1M10000045C02	*Staphylococcus aureus*
3400	S1M10000045C03	*Staphylococcus aureus*
3401	S1M10000045C04	*Staphylococcus aureus*
3402	S1M10000045C05	*Staphylococcus aureus*
3403	S1M10000045C07	*Staphylococcus aureus*
3404	S1M10000045C09	*Staphylococcus aureus*
3405	S1M10000045D01	*Staphylococcus aureus*
3406	S1M10000045D03	*Staphylococcus aureus*
3407	S1M10000045D07	*Staphylococcus aureus*
3408	S1M10000045D08	*Staphylococcus aureus*
3409	S1M10000045D09	*Staphylococcus aureus*
3410	S1M10000045D10	*Staphylococcus aureus*
3411	S1M10000045D11	*Staphylococcus aureus*
3412	S1M10000045D12	*Staphylococcus aureus*
3413	S1M10000045E04	*Staphylococcus aureus*
3414	S1M10000045E05	*Staphylococcus aureus*
3415	S1M10000045E08	*Staphylococcus aureus*
3416	S1M10000045E09	*Staphylococcus aureus*
3417	S1M10000045E10	*Staphylococcus aureus*
3418	S1M10000045E11	*Staphylococcus aureus*
3419	S1M10000045E12	*Staphylococcus aureus*
3420	S1M10000045F04	*Staphylococcus aureus*
3421	S1M10000045F05	*Staphylococcus aureus*
3422	S1M10000045F08	*Staphylococcus aureus*
3423	S1M10000045F11	*Staphylococcus aureus*
3424	S1M10000045F12	*Staphylococcus aureus*
3425	S1M10000045G03	*Staphylococcus aureus*
3426	S1M10000045G06	*Staphylococcus aureus*
3427	S1M10000045G07	*Staphylococcus aureus*
3428	S1M10000045G08	*Staphylococcus aureus*
3429	S1M10000045G10	*Staphylococcus aureus*
3430	S1M10000045G12	*Staphylococcus aureus*
3431	S1M10000045H06	*Staphylococcus aureus*
3432	S1M10000045H10	*Staphylococcus aureus*
3433	S1M10000045H11	*Staphylococcus aureus*
3434	S1M10000046A03	*Staphylococcus aureus*
3435	S1M10000046A04	*Staphylococcus aureus*
3436	S1M10000046A06	*Staphylococcus aureus*

SeqID	Clone name	Organism
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3438	S1M10000046A09	*Staphylococcus aureus*
3439	S1M10000046A11	*Staphylococcus aureus*
3440	S1M10000046A12	*Staphylococcus aureus*
3441	S1M10000046B01	*Staphylococcus aureus*
3442	S1M10000046B03	*Staphylococcus aureus*
3443	S1M10000046B04	*Staphylococcus aureus*
3444	S1M10000046B05	*Staphylococcus aureus*
3445	S1M10000046B07	*Staphylococcus aureus*
3446	S1M10000046B08	*Staphylococcus aureus*
3447	S1M10000046B09	*Staphylococcus aureus*
3448	S1M10000046B11	*Staphylococcus aureus*
3449	S1M10000046B12	*Staphylococcus aureus*
3450	S1M10000046C02	*Staphylococcus aureus*
3451	S1M10000046C04	*Staphylococcus aureus*
3452	S1M10000046C05	*Staphylococcus aureus*
3453	S1M10000046C06	*Staphylococcus aureus*
3454	S1M10000046C07	*Staphylococcus aureus*
3455	S1M10000046C08	*Staphylococcus aureus*
3456	S1M10000046C11	*Staphylococcus aureus*
3457	S1M10000046C12	*Staphylococcus aureus*
3458	S1M10000046D01	*Staphylococcus aureus*
3459	S1M10000046D02	*Staphylococcus aureus*
3460	S1M10000046D03	*Staphylococcus aureus*
3461	S1M10000046D04	*Staphylococcus aureus*
3462	S1M10000046D05	*Staphylococcus aureus*
3463	S1M10000046D08	*Staphylococcus aureus*
3464	S1M10000046D09	*Staphylococcus aureus*
3465	S1M10000046D10	*Staphylococcus aureus*
3466	S1M10000046D11	*Staphylococcus aureus*
3467	S1M10000046D12	*Staphylococcus aureus*
3468	S1M10000046E01	*Staphylococcus aureus*
3469	S1M10000046E02	*Staphylococcus aureus*
3470	S1M10000046E04	*Staphylococcus aureus*
3471	S1M10000046E07	*Staphylococcus aureus*
3472	S1M10000046E08	*Staphylococcus aureus*
3473	S1M10000046E10	*Staphylococcus aureus*
3474	S1M10000046F01	*Staphylococcus aureus*
3475	S1M10000046F02	*Staphylococcus aureus*
3476	S1M10000046F05	*Staphylococcus aureus*
3477	S1M10000046F06	*Staphylococcus aureus*
3478	S1M10000046F08	*Staphylococcus aureus*
3479	S1M10000046F09	*Staphylococcus aureus*
3480	S1M10000046F10	*Staphylococcus aureus*
3481	S1M10000046F12	*Staphylococcus aureus*
3482	S1M10000046G01	*Staphylococcus aureus*
3483	S1M10000046G02	*Staphylococcus aureus*
3484	S1M10000046G03	*Staphylococcus aureus*
3485	S1M10000046G04	*Staphylococcus aureus*

SeqID	Clone name	Organism
3486	S1M10000046G07	*Staphylococcus aureus*
3487	S1M10000046G09	*Staphylococcus aureus*
3488	S1M10000046G10	*Staphylococcus aureus*
3489	S1M10000046H01	*Staphylococcus aureus*
3490	S1M10000046H10	*Staphylococcus aureus*
3491	S1M10000047A03	*Staphylococcus aureus*
3492	S1M10000047A04	*Staphylococcus aureus*
3493	S1M10000047A05	*Staphylococcus aureus*
3494	S1M10000047A06	*Staphylococcus aureus*
3495	S1M10000047A07	*Staphylococcus aureus*
3496	S1M10000047A08	*Staphylococcus aureus*
3497	S1M10000047A09	*Staphylococcus aureus*
3498	S1M10000047A10	*Staphylococcus aureus*
3499	S1M10000047A11	*Staphylococcus aureus*
3500	S1M10000047A12	*Staphylococcus aureus*
3501	S1M10000047B02	*Staphylococcus aureus*
3502	S1M10000047B04	*Staphylococcus aureus*
3503	S1M10000047B05	*Staphylococcus aureus*
3504	S1M10000047B06	*Staphylococcus aureus*
3505	S1M10000047B08	*Staphylococcus aureus*
3506	S1M10000047B09	*Staphylococcus aureus*
3507	S1M10000047B10	*Staphylococcus aureus*
3508	S1M10000047B12	*Staphylococcus aureus*
3509	S1M10000047C01	*Staphylococcus aureus*
3510	S1M10000047C02	*Staphylococcus aureus*
3511	S1M10000047C03	*Staphylococcus aureus*
3512	S1M10000047C04	*Staphylococcus aureus*
3513	S1M10000047C06	*Staphylococcus aureus*
3514	S1M10000047C08	*Staphylococcus aureus*
3515	S1M10000047C09	*Staphylococcus aureus*
3516	S1M10000047C11	*Staphylococcus aureus*
3517	S1M10000047C12	*Staphylococcus aureus*
3518	S1M10000047D02	*Staphylococcus aureus*
3519	S1M10000047D03	*Staphylococcus aureus*
3520	S1M10000047D04	*Staphylococcus aureus*
3521	S1M10000047D05	*Staphylococcus aureus*
3522	S1M10000047D09	*Staphylococcus aureus*
3523	S1M10000047D10	*Staphylococcus aureus*
3524	S1M10000047D11	*Staphylococcus aureus*
3525	S1M10000047D12	*Staphylococcus aureus*
3526	S1M10000047E01	*Staphylococcus aureus*
3527	S1M10000047E02	*Staphylococcus aureus*
3528	S1M10000047E03	*Staphylococcus aureus*
3529	S1M10000047E04	*Staphylococcus aureus*
3530	S1M10000047E05	*Staphylococcus aureus*
3531	S1M10000047E06	*Staphylococcus aureus*
3532	S1M10000047E08	*Staphylococcus aureus*
3533	S1M10000047E09	*Staphylococcus aureus*
3534	S1M10000047E10	*Staphylococcus aureus*

SeqID	Clone name	Organism
3535	S1M10000047E11	*Staphylococcus aureus*
3536	S1M10000047E12	*Staphylococcus aureus*
3537	S1M10000047F02	*Staphylococcus aureus*
3538	S1M10000047F03	*Staphylococcus aureus*
3539	S1M10000047F04	*Staphylococcus aureus*
3540	S1M10000047F05	*Staphylococcus aureus*
3541	S1M10000047F06	*Staphylococcus aureus*
3542	S1M10000047F07	*Staphylococcus aureus*
3543	S1M10000047F08	*Staphylococcus aureus*
3544	S1M10000047F09	*Staphylococcus aureus*
3545	S1M10000047F10	*Staphylococcus aureus*
3546	S1M10000047F11	*Staphylococcus aureus*
3547	S1M10000047F12	*Staphylococcus aureus*
3548	S1M10000047G01	*Staphylococcus aureus*
3549	S1M10000047G02	*Staphylococcus aureus*
3550	S1M10000047G04	*Staphylococcus aureus*
3551	S1M10000047G05	*Staphylococcus aureus*
3552	S1M10000047G06	*Staphylococcus aureus*
3553	S1M10000047G07	*Staphylococcus aureus*
3554	S1M10000047G08	*Staphylococcus aureus*
3555	S1M10000047G09	*Staphylococcus aureus*
3556	S1M10000047G10	*Staphylococcus aureus*
3557	S1M10000047H03	*Staphylococcus aureus*
3558	S1M10000047H04	*Staphylococcus aureus*
3559	S1M10000047H05	*Staphylococcus aureus*
3560	S1M10000047H06	*Staphylococcus aureus*
3561	S1M10000047H07	*Staphylococcus aureus*
3562	S1M10000047H08	*Staphylococcus aureus*
3563	S1M10000047H09	*Staphylococcus aureus*
3564	S1M10000047H11	*Staphylococcus aureus*
3565	S1M10000048A02	*Staphylococcus aureus*
3566	S1M10000048A03	*Staphylococcus aureus*
3567	S1M10000048A04	*Staphylococcus aureus*
3568	S1M10000048A05	*Staphylococcus aureus*
3569	S1M10000048A06	*Staphylococcus aureus*
3570	S1M10000048A07	*Staphylococcus aureus*
3571	S1M10000048A09	*Staphylococcus aureus*
3572	S1M10000048A10	*Staphylococcus aureus*
3573	S1M10000048A11	*Staphylococcus aureus*
3574	S1M10000048A12	*Staphylococcus aureus*
3575	S1M10000048B02	*Staphylococcus aureus*
3576	S1M10000048B05	*Staphylococcus aureus*
3577	S1M10000048B08	*Staphylococcus aureus*
3578	S1M10000048B10	*Staphylococcus aureus*
3579	S1M10000048B11	*Staphylococcus aureus*
3580	S1M10000048B12	*Staphylococcus aureus*
3581	S1M10000048C01	*Staphylococcus aureus*
3582	S1M10000048C02	*Staphylococcus aureus*
3583	S1M10000048C03	*Staphylococcus aureus*

SeqID	Clone name	Organism
3584	S1M10000048C05	*Staphylococcus aureus*
3585	S1M10000048C06	*Staphylococcus aureus*
3586	S1M10000048C07	*Staphylococcus aureus*
3587	S1M10000048C08	*Staphylococcus aureus*
3588	S1M10000048C09	*Staphylococcus aureus*
3589	S1M10000048C11	*Staphylococcus aureus*
3590	S1M10000048D02	*Staphylococcus aureus*
3591	S1M10000048D08	*Staphylococcus aureus*
3592	S1M10000048D09	*Staphylococcus aureus*
3593	S1M10000048D10	*Staphylococcus aureus*
3594	S1M10000048D12	*Staphylococcus aureus*
3595	S1M10000048E02	*Staphylococcus aureus*
3596	S1M10000048E03	*Staphylococcus aureus*
3597	S1M10000048E04	*Staphylococcus aureus*
3598	S1M10000048E06	*Staphylococcus aureus*
3599	S1M10000048E07	*Staphylococcus aureus*
3600	S1M10000048E08	*Staphylococcus aureus*
3601	S1M10000048E10	*Staphylococcus aureus*
3602	S1M10000048F02	*Staphylococcus aureus*
3603	S1M10000048F07	*Staphylococcus aureus*
3604	S1M10000048F08	*Staphylococcus aureus*
3605	S1M10000048F09	*Staphylococcus aureus*
3606	S1M10000048F11	*Staphylococcus aureus*
3607	S1M10000048F12	*Staphylococcus aureus*
3608	S1M10000048G02	*Staphylococcus aureus*
3609	S1M10000048G03	*Staphylococcus aureus*
3610	S1M10000048G04	*Staphylococcus aureus*
3611	S1M10000048G05	*Staphylococcus aureus*
3612	S1M10000048G07	*Staphylococcus aureus*
3613	S1M10000048G10	*Staphylococcus aureus*
3614	S1M10000048G11	*Staphylococcus aureus*
3615	S1M10000048H01	*Staphylococcus aureus*
3616	S1M10000048H02	*Staphylococcus aureus*
3617	S1M10000048H03	*Staphylococcus aureus*
3618	S1M10000048H04	*Staphylococcus aureus*
3619	S1M10000048H05	*Staphylococcus aureus*
3620	S1M10000048H07	*Staphylococcus aureus*
3621	S1M10000048H08	*Staphylococcus aureus*
3622	S1M10000048H09	*Staphylococcus aureus*
3623	S1M10000048H10	*Staphylococcus aureus*
3624	S1M10000048H11	*Staphylococcus aureus*
3625	S1M10000009E10	*Staphylococcus aureus*
3626	S1M10000001F01	*Staphylococcus aureus*
3627	S1M10000006B12	*Staphylococcus aureus*
3628	S1M10000003D09	*Staphylococcus aureus*
3629	S1M10000001D11	*Staphylococcus aureus*
3630	S1M10000003B07	*Staphylococcus aureus*
3631	S1M10000002A07	*Staphylococcus aureus*
3632	S1M10000003F11	*Staphylococcus aureus*

SeqID	Clone name	Organism
3633	S1M10000047C07	*Staphylococcus aureus*
3634	S1M10000013F10	*Staphylococcus aureus*
3635	S1M10000014D11	*Staphylococcus aureus*
3636	S1M10000015F05	*Staphylococcus aureus*
3637	S1M10000048D01	*Staphylococcus aureus*
3638	S1M10000011C03	*Staphylococcus aureus*
3639	S1M10000012F03	*Staphylococcus aureus*
3640	S1M10000002F07	*Staphylococcus aureus*
3641	S1M10000048G01	*Staphylococcus aureus*
3642	S1M10000009G12	*Staphylococcus aureus*
3643	S1M10000012D05	*Staphylococcus aureus*
3644	S1M10000014D07	*Staphylococcus aureus*
3645	S1M10000047C05	*Staphylococcus aureus*
3646	S1M10000018D08*	*Staphylococcus aureus*
3647	S1M10000047B01	*Staphylococcus aureus*
3648	S1M10000047H10	*Staphylococcus aureus*
3649	S1M10000001A04	*Staphylococcus aureus*
3650	S1M10000016E01	*Staphylococcus aureus*
3651	S1M10000017E12	*Staphylococcus aureus*
3652	S1M10000019B01	*Staphylococcus aureus*
3653	S1M10000048F03	*Staphylococcus aureus*
3654	S1M10000034A07	*Staphylococcus aureus*
3655	S1M10000023G01	*Staphylococcus aureus*
3656	S1M10000021G12	*Staphylococcus aureus*
3657	S1M10000024E04	*Staphylococcus aureus*
3658	S1M10000028H08	*Staphylococcus aureus*
3659	S1M10000022B07	*Staphylococcus aureus*
3660	S1M10000003A05	*Staphylococcus aureus*
3661	S1M10000003A09	*Staphylococcus aureus*
3662	S1M10000003E01	*Staphylococcus aureus*
3663	S1M10000004C11	*Staphylococcus aureus*
3664	S1M10000007E08	*Staphylococcus aureus*
3665	S1M10000021G06	*Staphylococcus aureus*
3666	S1M10000024C06	*Staphylococcus aureus*
3667	S1M10000024D01	*Staphylococcus aureus*
3668	S1M10000027D07	*Staphylococcus aureus*
3669	S1M10000027E03	*Staphylococcus aureus*
3670	S1M10000027G01	*Staphylococcus aureus*
3671	S1M10000029A03	*Staphylococcus aureus*
3672	S1M10000032B10	*Staphylococcus aureus*
3673	S1M10000032C07	*Staphylococcus aureus*
3674	S1M10000038D04	*Staphylococcus aureus*
3675	S1M10000047D07	*Staphylococcus aureus*
3676	S1M10000048B03	*Staphylococcus aureus*
3677	S1M10000048B06	*Staphylococcus aureus*
3678	S1M10000048C10	*Staphylococcus aureus*
3679	S1M10000048F05	*Staphylococcus aureus*
3680	S4M10000001C01	*Salmonella typhimurium*
3681	S4M10000002B06	*Salmonella typhimurium*

SeqID	Clone name	Organism
3682	S4M10000002B09	*Salmonella typhimurium*
3683	S4M10000002G04	*Salmonella typhimurium*
3684	S4M10000002G08	*Salmonella typhimurium*
3685	S4M10000005G05	*Salmonella typhimurium*
3686	S4M10000005H02	*Salmonella typhimurium*
3687	S4M10000006A06	*Salmonella typhimurium*
3688	S4M10000006A08	*Salmonella typhimurium*
3689	S4M10000006C05	*Salmonella typhimurium*
3690	S4M10000006F08	*Salmonella typhimurium*
3691	S4M10000007G01	*Salmonella typhimurium*
3692	S4M10000008C08	*Salmonella typhimurium*
3693	S4M10000008H10	*Salmonella typhimurium*
3694	S4M10000009A05	*Salmonella typhimurium*
3695	S4M10000010B05	*Salmonella typhimurium*
3696	S4M10000010D04	*Salmonella typhimurium*
3697	S4M10000010H04	*Salmonella typhimurium*
3698	S4M10000011D08	*Salmonella typhimurium*
3699	S4M10000011E08	*Salmonella typhimurium*
3700	S4M10000012B06	*Salmonella typhimurium*
3701	S4M10000012B12	*Salmonella typhimurium*
3702	S4M10000012D02	*Salmonella typhimurium*
3703	S4M10000013H02	*Salmonella typhimurium*
3704	S4M10000014B05	*Salmonella typhimurium*
3705	S4M10000014D04	*Salmonella typhimurium*
3706	S4M10000014D07	*Salmonella typhimurium*
3707	S4M10000014H02	*Salmonella typhimurium*
3708	S4M10000015B11	*Salmonella typhimurium*
3709	S4M10000015E09	*Salmonella typhimurium*
3710	S4M10000016A02	*Salmonella typhimurium*
3711	S4M10000018D09	*Salmonella typhimurium*
3712	S4M10000018E10	*Salmonella typhimurium*
3713	S4M10000018F10	*Salmonella typhimurium*
3714	S4M10000018G03	*Salmonella typhimurium*
3715	S4M10000018H04	*Salmonella typhimurium*
3716	S4M10000019F05	*Salmonella typhimurium*
3717	S4M10000019G04	*Salmonella typhimurium*
3718	S4M10000019G05	*Salmonella typhimurium*
3719	S4M10000019H06	*Salmonella typhimurium*
3720	S4M10000020A04	*Salmonella typhimurium*
3721	S4M10000020F05	*Salmonella typhimurium*
3722	S4M10000020G10	*Salmonella typhimurium*
3723	S4M10000022D04	*Salmonella typhimurium*
3724	S4M10000022D12	*Salmonella typhimurium*
3725	S4M10000022E12	*Salmonella typhimurium*
3726	S4M10000022G07	*Salmonella typhimurium*
3727	S4M10000022H06	*Salmonella typhimurium*
3728	S4M10000023F01	*Salmonella typhimurium*
3729	S4M10000024B02	*Salmonella typhimurium*
3730	S4M10000024C06	*Salmonella typhimurium*

SeqID	Clone name	Organism
3731	S4M10000024C11	*Salmonella typhimurium*
3732	S4M10000024F08	*Salmonella typhimurium*
3733	S4M10000024G01	*Salmonella typhimurium*
3734	S4M10000024G04	*Salmonella typhimurium*
3735	S4M10000024G09	*Salmonella typhimurium*
3736	S4M10000024H02	*Salmonella typhimurium*
3737	S4M10000025A11	*Salmonella typhimurium*
3738	S4M10000025E02	*Salmonella typhimurium*
3739	S4M10000025E05	*Salmonella typhimurium*
3740	S4M10000025H07	*Salmonella typhimurium*
3741	S4M10000026C10	*Salmonella typhimurium*
3742	S4M10000026D04	*Salmonella typhimurium*
3743	S4M10000026E06	*Salmonella typhimurium*
3744	S4M10000026E12	*Salmonella typhimurium*
3745	S4M10000027C10	*Salmonella typhimurium*
3746	S4M10000027E02	*Salmonella typhimurium*
3747	S4M10000029B12	*Salmonella typhimurium*
3748	S4M10000029D12	*Salmonella typhimurium*
3749	S4M10000030D03	*Salmonella typhimurium*
3750	S4M10000030F07	*Salmonella typhimurium*
3751	S4M10000030G11	*Salmonella typhimurium*
3752	S4M10000032B12	*Salmonella typhimurium*
3753	S4M10000033F08	*Salmonella typhimurium*
3754	S4M10000033G05	*Salmonella typhimurium*
3755	S4M10000033G09	*Salmonella typhimurium*
3756	S4M10000034A02	*Salmonella typhimurium*
3757	S4M10000034A09	*Salmonella typhimurium*
3758	S4M10000034D06	*Salmonella typhimurium*
3759	S4M10000034H05	*Salmonella typhimurium*
3760	S4M10000034H09	*Salmonella typhimurium*
3761	S4M10000035B01	*Salmonella typhimurium*
3762	S4M10000035D01	*Salmonella typhimurium*
3763	S4M10000035D02	*Salmonella typhimurium*
3764	S4M10000035E03	*Salmonella typhimurium*
3765	S4M10000035F02	*Salmonella typhimurium*
3766	S4M10000035F09	*Salmonella typhimurium*
3767	S4M10000036D07	*Salmonella typhimurium*
3768	S4M10000036F07	*Salmonella typhimurium*
3769	S4M10000037A04	*Salmonella typhimurium*
3770	S4M10000037A10	*Salmonella typhimurium*
3771	S4M10000037E10	*Salmonella typhimurium*
3772	S4M10000037H09	*Salmonella typhimurium*
3773	S4M10000001H01	*Salmonella typhimurium*
3774	S4M10000002F06	*Salmonella typhimurium*
3775	S4M10000008D01	*Salmonella typhimurium*
3776	S4M10000009G11	*Salmonella typhimurium*
3777	S4M10000011F09	*Salmonella typhimurium*
3778	S4M10000020F08	*Salmonella typhimurium*
3779	S4M10000021E07	*Salmonella typhimurium*

SeqID	Clone name	Organism
3780	S4M10000022B05	*Salmonella typhimurium*
3781	S4M10000025H11	*Salmonella typhimurium*
3782	S4M10000026B10	*Salmonella typhimurium*
3783	S4M10000026E03	*Salmonella typhimurium*
3784	S4M10000029A03	*Salmonella typhimurium*
3785	S4M10000029C11	*Salmonella typhimurium*
3786	S4M10000030F06	*Salmonella typhimurium*
3787	S4M10000032F03	*Salmonella typhimurium*
3788	S4M10000032G01	*Salmonella typhimurium*
3789	S4M10000034C05	*Salmonella typhimurium*
3790	S4M10000034H04	*Salmonella typhimurium*
3791	S4M10000035A09	*Salmonella typhimurium*
3792	S4M10000035B06	*Salmonella typhimurium*
3793	S4M10000035F01	*Salmonella typhimurium*
3794	S4M10000037A08	*Salmonella typhimurium*
3795	S4M10000037E03	*Salmonella typhimurium*

TABLE IB

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
E3M10000001A02	8	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000001A06	9	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000001B01	10	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000001B02	11	EFA100739	4888	EFA1c0022_orf_23p	10537
E3M10000001B02	11	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000001B02	11	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000001B05	12	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000001B06	13	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000001B08	14	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000001B10	15	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000001C02	16	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000001C09	17	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000001D02	18	EFA101159	4916	EFA1c0022_orf_2p	10543
E3M10000001D04	19	EFA100742	4891	EFA1c0022_orf_20p	10534
E3M10000001D04	19	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000001D04	19	EFA102554	5002	EFA1c0022_orf_19p	10532
E3M10000001D05	20	EFA100955	4902	EFA1c0022_orf_28p	10542
E3M10000001D05	20	EFA100978	4904	EFA1c0022_orf_27p	10541
E3M10000001D09	21	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000001D09	21	EFA100211	4871	EFA1c0022_orf_10p	10523
E3M10000001E01	22	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000001E01	22	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000001E02	23	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000001E03	24	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000001E03	24	EFA100211	4871	EFA1c0022_orf_10p	10523
E3M10000001E04	25	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000001E08	26	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000001E09	27	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000001E09	27	EFA100211	4871	EFA1c0022_orf_10p	10523
E3M10000001F02	28	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000001F04	29	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000001F06	30	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000001F07	31	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000001G02	32	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000001G03	33	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000001G03	33	EFA100211	4871	EFA1c0022_orf_10p	10523
E3M10000001G04	34	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000001G05	35	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000001H02	36	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000001H03	37	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000001H03	37	EFA100211	4871	EFA1c0022_orf_10p	10523
E3M10000001H04	38	EFA100742	4891	EFA1c0022_orf_20p	10534
E3M10000001H04	38	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000001H04	38	EFA102554	5002	EFA1c0022_orf_19p	10532
E3M10000004A04	39	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000004A04	39	EFA102554	5002	EFA1c0022_orf_19p	10532

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
E3M10000004C03	40	EFA100478	4880	EFA1c0012_orf_2p	10486
E3M10000004D01	41	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000004D01	41	EFA101413	4938	#N/A	#N/A
E3M10000004D01	41	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000004D02	42	EFA102022	4974	EFA1c0044_orf_106p	10881
E3M10000004D02	42	EFA102023	4975	EFA1c0044_orf_107p	10882
E3M10000004D10	43	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000004D10	43	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000004E11	44	EFA101086	4910	EFA1c0040_orf_90p	10763
E3M10000004F08	45	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000004F08	45	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000004F10	46	EFA101086	4910	EFA1c0040_orf_90p	10763
E3M10000004G01	47	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000004H11	48	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000004H11	48	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000005A07	49	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000005B01	50	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000005B01	50	EFA101415	4940	EFA1c0022_orf_16p	10529
E3M10000005B08	51	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000005B08	51	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000005C01	52	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000005C03	53	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000005C04	54	EFA102186	4981	EFA1c0045_orf_94p	10949
E3M10000005C04	54	EFA102453	4993	EFA1c0045_orf_203p	10931
E3M10000005C04	54	EFA102728	5006	EFA1c0045_orf_93p	10948
E3M10000005D03	55	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000005D04	56	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000005D10	57	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000005D10	57	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000005E01	58	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000005E01	58	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000005E02	59	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000005E02	59	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000005E03	60	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000005E08	61	EFA101403	4932	EFA1c0033_orf_54p	10662
E3M10000005F07	62	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000005F10	63	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000005F10	63	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000005G05	64	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000005G05	64	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000005H04	65	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000006B03	66	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000006B03	66	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000006C01	67	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000006C01	67	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000006C12	68	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000006C12	68	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000006D03	69	EFA101416	4941	EFA1c0022_orf_17p	10530

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
E3M10000006D03	69	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000006E11	70	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000006E11	70	EFA102542	4999	EFA1c0028_orf_4p	10603
E3M10000006F04	71	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000006F04	71	EFA102542	4999	EFA1c0028_orf_4p	10603
E3M10000006G04	72	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000006G04	72	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000006G12	73	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000006G12	73	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000006H09	74	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000007A02	75	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000007A02	75	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000007B02	76	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000007B02	76	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000007B03	77	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000007B03	77	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000007C03	78	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000007C03	78	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000007C04	79	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000007D03	80	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000007D03	80	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000007E05	81	EFA100742	4891	EFA1c0022_orf_20p	10534
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E3M10000007E05	81	EFA102554	5002	EFA1c0022_orf_19p	10532
E3M10000007F01	82	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000007F01	82	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000007F06	83	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000007F06	83	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000007G01	84	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000007G01	84	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000008C03	85	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000008C08	86	EFA101536	4946	EFA1c0042_orf_46p	10823
E3M10000008C09	87	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000008D08	88	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000008E02	89	EFA100783	4895	EFA1c0042_orf_141p	10811
E3M10000008G05	90	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000008G05	90	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000008G09	91	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000008G09	91	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000008H02	92	EFA101695	4954	EFA1c0031_orf_6p	10629
E3M10000009C07	93	EFA103508	5029	EFA1c0033_orf_95p	10672
E3M10000009C09	94	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000009D01	95	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000009E02	96	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000009E02	96	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000009E03	97	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000009E05	98	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000009G02	99	EFA102501	4994	EFA1c0031_orf_35p	10626

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
E3M10000010C08	100	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000010D05	101	EFA100757	4894	EFA1c0044_orf_27p	10897
E3M10000010F01	102	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000010G05	103	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000010G07	104	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000010G09	105	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000010G10	106	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000010H02	107	EFA100194	4868	EFA1c0022_orf_26p	10540
E3M10000011A09	108	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000011B03	109	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000011B09	110	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000011C07	111	EFA101790	4959	EFA1c0042_orf_111p	10803
E3M10000011D03	112	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000011D03	112	EFA100211	4871	EFA1c0022_orf_10p	10523
E3M10000011H02	113	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000011H05	114	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000012B01	115	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000012B02	116	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000012B07	117	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000012B07	117	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000012B07	117	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000012B08	118	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000012C01	119	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000012D10	120	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000012E08	121	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000012F05	122	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000012F06	123	EFA101409	4934	EFA1c0022_orf_11p	10524
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E3M10000012F10	125	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000012F10	125	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000012G02	126	EFA101165	4922	EFA1c0022_orf_8p	10559
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E3M10000013A06	128	EFA101159	4916	EFA1c0022_orf_2p	10543
E3M10000013A07	129	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000013C05	130	EFA101160	4917	EFA1c0022_orf_3p	10549
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E3M10000013D02	131	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000013D08	132	EFA101415	4940	EFA1c0022_orf_16p	10529
E3M10000013D10	133	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000013D10	133	EFA100211	4871	EFA1c0022_orf_10p	10523
E3M10000013E02	134	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000013E08	135	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000013F05	136	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000013F12	137	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000013F12	137	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000013G10	138	EFA103062	5019	EFA1c0030_orf_19p	10615

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
E3M10000013H03	139	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000013H05	140	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000013H10	141	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000014B12	142	EFA100739	4888	EFA1c0022_orf_23p	10537
E3M10000014B12	142	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000014B12	142	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000014E12	143	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000014E12	143	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000014G09	144	EFA100991	4905	EFA1c0035_orf_60p	10681
E3M10000014G09	144	EFA103033	5016	EFA1c0035_orf_60p	10681
E3M10000015B04	145	EFA100065	4863	EFA1c0042_orf_14p	10813
E3M10000015B12	146	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000015E12	147	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000015E12	147	EFA100211	4871	EFA1c0022_orf_10p	10523
E3M10000016A03	148	EFA101753	4957	EFA1c0022_orf_50p	10552
E3M10000016A04	149	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000016C11	150	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000016C11	150	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000016D03	151	EFA102774	5009	EFA1c0044_orf_25p	10896
E3M10000016F06	152	EFA102205	4983	EFA1c0041_orf_115p	10769
E3M10000016F10	153	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000016F10	153	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000016H05	154	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000016H10	155	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000017A09	156	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000017A09	156	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000017D09	157	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000018A07	158	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000018C02	159	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000018E01	160	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000018G09	161	EFA101583	4949	EFA1c0026_orf_23p	10593
E3M10000018H06	162	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000019B06	163	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000019D02	164	EFA102022	4974	EFA1c0044_orf_106p	10881
E3M10000019E03	165	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000019E03	165	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000019E04	166	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000020G04	167	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000020G04	167	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000020H05	168	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000021A08	169	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000021A08	169	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000021A11	170	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000021B10	171	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000021C03	172	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000021C04	173	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000021C08	174	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000021D04	175	EFA100870	4899	EFA1c0031_orf_36p	10627

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000021E10	176	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000021G04	177	EFA100955	4902	EFA1c0022_orf_28p	10542
E3M10000021G10	178	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000021G11	179	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000021H11	180	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000022A04	181	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000022A11	182	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000022B04	183	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000022B05	184	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000022B05	184	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000022B07	185	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000022C05	186	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000022C05	186	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000022C06	187	EFA100978	4904	EFA1c0022_orf_27p	10541
E3M10000022C09	188	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000022D04	189	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000022F05	190	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000022F06	191	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000022F06	191	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000022F08	192	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000022G02	193	EFA101022	4906	EFA1c0043_orf_69p	10875
E3M10000022G12	194	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000023A03	195	EFA101413	4938	#N/A	#N/A
E3M10000023A06	196	EFA100978	4904	EFA1c0022_orf_27p	10541
E3M10000023A07	197	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000023A09	198	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000023B02	199	EFA101159	4916	EFA1c0022_orf_2p	10543
E3M10000023B02	199	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000023B06	200	EFA102541	4998	EFA1c0028_orf_3p	10602
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E3M10000023C03	201	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000023C04	202	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000023C06	203	EFA101413	4938	#N/A	#N/A
E3M10000023C08	204	EFA100955	4902	EFA1c0022_orf_28p	10542
E3M10000023C09	205	EFA101159	4916	EFA1c0022_orf_2p	10543
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E3M10000023D10	208	EFA101413	4938	#N/A	#N/A
E3M10000023E04	209	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000023E07	210	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000023E09	211	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000023F02	212	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000023F10	213	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000023G02	214	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000023G04	215	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000023G10	216	EFA101411	4936	EFA1c0022_orf_13p	10526

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
E3M10000023H08	217	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000024A03	218	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000024A04	219	EFA102006	4973	EFA1c0025_orf_17p	10580
E3M10000024A08	220	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000024A08	220	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000024C06	221	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000025A06	222	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000025B01	223	EFA100194	4868	EFA1c0022_orf_26p	10540
E3M10000025B01	223	EFA100978	4904	EFA1c0022_orf_27p	10541
E3M10000025B03	224	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000025B03	224	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000025B05	225	EFA100978	4904	EFA1c0022_orf_27p	10541
E3M10000025B10	226	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000025C01	227	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000025C04	228	EFA101159	4916	EFA1c0022_orf_2p	10543
E3M10000025C05	229	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000025C05	229	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000025C07	230	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000025C08	231	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000025C08	231	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000025C09	232	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000025C11	233	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000025D01	234	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000025D01	234	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000025D10	235	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000025E07	236	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000025E08	237	EFA100955	4902	EFA1c0022_orf_28p	10542
E3M10000025E12	238	EFA102728	5006	EFA1c0045_orf_93p	10948
E3M10000025F04	239	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000025F04	239	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000025F06	240	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000025F06	240	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000025F06	240	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000025F08	241	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000025F09	242	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000025F10	243	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000025F11	244	EFA100955	4902	EFA1c0022_orf_28p	10542
E3M10000025F12	245	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000025G02	246	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000025G07	247	EFA101159	4916	EFA1c0022_orf_2p	10543
E3M10000025G09	248	EFA102185	4980	EFA1c0045_orf_95p	10950
E3M10000027A02	249	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000027A07	250	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000027A09	251	EFA101413	4938	#N/A	#N/A
E3M10000027A09	251	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000027B07	252	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000027B08	253	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000027B09	254	EFA100870	4899	EFA1c0031_orf_36p	10627

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000027C02	255	EFA103062	5019	EFA1c0030_orf_19p	10615
E3M10000027C03	256	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000027C08	257	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000027D03	258	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000027D03	258	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000027D05	259	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000027D08	260	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000027D10	261	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000027G01	262	EFA102186	4981	EFA1c0045_orf_94p	10949
E3M10000027G08	263	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000027H04	264	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000027H07	265	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000027H07	265	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000028A02	266	EFA102554	5002	EFA1c0022_orf_19p	10532
E3M10000028A03	267	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000028A04	268	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000028A04	268	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000028A05	269	EFA101080	4909	#N/A	#N/A
E3M10000028A05	269	EFA102915	5014	EFA1c0032_orf_27p	10640
E3M10000028A06	270	EFA103210	5022	EFA1c0036_orf_119p	10688
E3M10000028A08	271	EFA101424	4943	EFA1c0041_orf_39p	10784
E3M10000028A08	271	EFA101425	4944	EFA1c0041_orf_40p	10785
E3M10000028B01	272	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000028B02	273	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000028B02	273	EFA102542	4999	EFA1c0028_orf_4p	10603
E3M10000028B03	274	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000028B04	275	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000028B05	276	EFA101424	4943	EFA1c0041_orf_39p	10784
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E3M10000028B06	277	EFA103038	5017	EFA1c0030_orf_17p	10613
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E3M10000028B08	279	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000028C01	280	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000028C01	280	EFA102542	4999	EFA1c0028_orf_4p	10603
E3M10000028C02	281	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000028C02	281	EFA102542	4999	EFA1c0028_orf_4p	10603
E3M10000028C04	282	EFA101322	4927	EFA1c0030_orf_57p	10620
E3M10000028C05	283	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000028C06	284	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000028C07	285	EFA101022	4906	EFA1c0043_orf_69p	10875
E3M10000028C08	286	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000028C08	286	EFA102542	4999	EFA1c0028_orf_4p	10603
E3M10000028D01	287	EFA100194	4868	EFA1c0022_orf_26p	10540
E3M10000028D01	287	EFA100978	4904	EFA1c0022_orf_27p	10541
E3M10000028D02	288	EFA101022	4906	EFA1c0043_orf_69p	10875
E3M10000028D05	289	EFA101080	4909	#N/A	#N/A
E3M10000028D06	290	EFA103021	5015	EFA1c0030_orf_16p	10612

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000028E01	292	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000028E04	293	EFA101370	4931	EFA1c0040_orf_103p	10738
E3M10000028E07	294	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000028F02	295	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000028F03	296	EFA100742	4891	EFA1c0022_orf_20p	10534
E3M10000028F03	296	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000028F03	296	EFA102554	5002	EFA1c0022_orf_19p	10532
E3M10000028F04	297	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000028F04	297	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000028F05	298	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000028F06	299	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000028F07	300	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000028G05	301	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000028G06	302	EFA100748	4892	EFA1c0011_orf_10p	10483
E3M10000028G07	303	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000028G07	303	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000028H04	304	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000028H07	305	EFA103062	5019	EFA1c0030_orf_19p	10615
E3M10000029A02	306	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000029A04	307	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000029A05	308	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000029A10	309	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000029A11	310	EFA101413	4938	#N/A	#N/A
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E3M10000029B02	312	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000029B05	313	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000029B06	314	EFA100914	4900	EFA1c0024_orf_9p	10579
E3M10000029B08	315	EFA102338	4987	EFA1c0032_orf_8p	10651
E3M10000029B11	316	EFA100397	4877	EFA1c0041_orf_148p	10773
E3M10000029B12	317	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000029C01	318	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000029C02	319	EFA102788	5011	EFA1c0033_orf_41p	10661
E3M10000029C03	320	EFA102253	4984	EFA1c0038_orf_85p	10727
E3M10000029C04	321	EFA102503	4996	EFA1c0032_orf_32p	10643
E3M10000029C05	322	EFA100399	4878	EFA1c0041_orf_104p	10766
E3M10000029C06	323	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000029C06	323	EFA101415	4940	EFA1c0022_orf_16p	10529
E3M10000029C07	324	EFA102352	4990	EFA1c0032_orf_21p	10635
E3M10000029C07	324	EFA102353	4991	EFA1c0032_orf_22p	10636
E3M10000029C08	325	EFA101868	4966	EFA1c0042_orf_69p	10829
E3M10000029C09	326	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000029C10	327	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000029C12	328	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000029D01	329	EFA101080	4909	#N/A	#N/A
E3M10000029D03	330	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000029D04	331	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000029D05	332	EFA100210	4870	EFA1c0022_orf_9p	10560

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E3M10000029D08	334	EFA102736	5007	EFA1c0022_orf_60p	10556
E3M10000029D12	335	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000029E01	336	EFA101404	4933	EFA1c0033_orf_55p	10663
E3M10000029E02	337	EFA102051	4976	#N/A	#N/A
E3M10000029E03	338	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000029E05	339	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000029E07	340	EFA100919	4901	EFA1c0013_orf_12p	10491
E3M10000029E08	341	EFA101022	4906	EFA1c0043_orf_69p	10875
E3M10000029E09	342	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000029E12	343	EFA100397	4877	EFA1c0041_orf_148p	10773
E3M10000029F01	344	EFA100023	4862	EFA1c0017_orf_1p	10505
E3M10000029F05	345	EFA102503	4996	EFA1c0032_orf_32p	10643
E3M10000029F06	346	EFA101795	4962	EFA1c0045_orf_165p	10922
E3M10000029F09	347	EFA100689	4886	EFA1c0038_orf_54p	10717
E3M10000029F10	348	EFA100919	4901	EFA1c0013_orf_12p	10491
E3M10000029F11	349	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000029F12	350	EFA102282	4985	EFA1c0038_orf_89p	10729
E3M10000029G01	351	EFA100394	4876	EFA1c0034_orf_6p	10675
E3M10000029G04	352	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000029G05	353	EFA102351	4989	EFA1c0032_orf_20p	10634
E3M10000029G07	354	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000029G08	355	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000029G09	356	EFA102201	4982	#N/A	#N/A
E3M10000029G10	357	EFA101797	4963	EFA1c0045_orf_167p	10924
E3M10000029G11	358	EFA102006	4973	EFA1c0025_orf_17p	10580
E3M10000029G12	359	EFA101541	4948	EFA1c0012_orf_5p	10488
E3M10000029H02	360	EFA101339	4928	EFA1c0040_orf_13p	10743
E3M10000029H02	360	EFA101340	4929	EFA1c0040_orf_15p	10745
E3M10000029H04	361	EFA102352	4990	EFA1c0032_orf_21p	10635
E3M10000029H04	361	EFA102353	4991	EFA1c0032_orf_22p	10636
E3M10000029H05	362	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000029H07	363	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000029H08	364	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000029H11	365	EFA101159	4916	EFA1c0022_orf_2p	10543
E3M10000030A05	366	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000030A08	367	EFA102351	4989	EFA1c0032_orf_20p	10634
E3M10000030A09	368	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000030A11	369	EFA102736	5007	EFA1c0022_orf_60p	10556
E3M10000030B03	370	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000030B04	371	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000030B05	372	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000030B06	373	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000030B07	374	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000030B08	375	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000030B10	376	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000030B11	377	EFA101121	4912	EFA1c0036_orf_112p	10686

TABLE IA

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
E3M10000030B12	378	EFA102352	4990	EFA1c0032_orf_21p	10635
E3M10000030B12	378	EFA102353	4991	EFA1c0032_orf_22p	10636
E3M10000030C03	379	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000030C04	380	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000030C12	381	EFA102351	4989	EFA1c0032_orf_20p	10634
E3M10000030D02	382	EFA102350	4988	EFA1c0032_orf_19p	10632
E3M10000030D05	383	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000030D08	384	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000030D09	385	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000030D10	386	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000030D12	387	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000030E01	388	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000030E01	388	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000030E02	389	EFA100329	4875	EFA1c0041_orf_35p	10782
E3M10000030E04	390	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000030E08	391	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000030E09	392	EFA103365	5026	EFA1c0022_orf_1p	10533
E3M10000030E10	393	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000030F01	394	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000030F04	395	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000030F06	396	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000030F07	397	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000030F10	398	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000030F12	399	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000030G01	400	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000030G03	401	EFA100023	4862	EFA1c0017_orf_1p	10505
E3M10000030G06	402	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000030G08	403	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000030G09	404	EFA103210	5022	EFA1c0036_orf_119p	10688
E3M10000030G12	405	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000030H03	406	EFA101258	4926	EFA1c0045_orf_160p	10918
E3M10000030H04	407	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000030H06	408	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000030H07	409	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000030H08	410	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000030H10	411	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000030H11	412	EFA100615	4881	EFA1c0016_orf_29p	10501
E3M10000031A02	413	EFA102006	4973	EFA1c0025_orf_17p	10580
E3M10000031A06	414	EFA100970	4903	EFA1c0044_orf_98p	10906
E3M10000031A07	415	EFA102201	4982	#N/A	#N/A
E3M10000031A08	416	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000031B02	417	EFA100289	4872	EFA1c0042_orf_139p	10810
E3M10000031B03	418	EFA100426	4879	EFA1c0036_orf_59p	10702
E3M10000031B04	419	EFA100394	4876	EFA1c0034_orf_6p	10675
E3M10000031B09	420	EFA102183	4979	EFA1c0045_orf_97p	10952
E3M10000031B10	421	EFA101253	4924	EFA1c0043_orf_178p	10852
E3M10000031B11	422	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000031B12	423	EFA100642	4884	EFA1c0041_orf_56p	10792

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
E3M10000031C01	424	EFA102736	5007	EFA1c0022_orf_60p	10556
E3M10000031C04	425	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000031C06	426	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000031C10	427	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000031C11	428	EFA101120	4911	EFA1c0036_orf_113p	10687
E3M10000031C12	429	EFA100668	4885	EFA1c0035_orf_58p	10679
E3M10000031D03	430	EFA102503	4996	EFA1c0032_orf_32p	10643
E3M10000031D04	431	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000031D08	432	EFA102503	4996	EFA1c0032_orf_32p	10643
E3M10000031E03	433	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000031E09	434	EFA102736	5007	EFA1c0022_orf_60p	10556
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E3M10000031F02	435	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000031F04	436	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000031F07	437	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000031F09	438	EFA102764	5008	EFA1c0008_orf_3p	10478
E3M10000031F11	439	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000031F11	439	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000031G03	440	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000031G04	441	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000031G05	442	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000031G06	443	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000031G07	444	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000031G08	445	EFA100295	4873	EFA1c0021_orf_15p	10517
E3M10000031G11	446	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000031H05	447	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000031H06	448	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000031H07	449	EFA103038	5017	EFA1c0030_orf_17p	10613
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E3M10000031H10	451	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000031H11	452	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000031H11	452	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000032A02	453	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000032A04	454	EFA101670	4950	EFA1c0019_orf_20p	10511
E3M10000032A06	455	EFA101022	4906	EFA1c0043_orf_69p	10875
E3M10000032A07	456	EFA101670	4950	EFA1c0019_orf_20p	10511
E3M10000032A08	457	EFA100329	4875	EFA1c0041_orf_35p	10782
E3M10000032A09	458	EFA100394	4876	EFA1c0034_orf_6p	10675
E3M10000032A10	459	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000032A11	460	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000032A11	460	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000032B03	461	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000032B04	462	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000032B07	463	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000032B08	464	EFA102698	5005	EFA1c0045_orf_115p	10909
E3M10000032B09	465	EFA102051	4976	#N/A	#N/A
E3M10000032B11	466	EFA102091	4977	EFA1c0010_orf_3p	10481
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
E3M10000032C01	468	EFA103062	5019	EFA1c0030_orf_19p	10615
E3M10000032C02	469	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000032C03	470	EFA103348	5025	EFA1c0043_orf_67p	10873
E3M10000032C04	471	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000032C06	472	EFA101150	4915	EFA1c0038_orf_57p	10719
E3M10000032C09	473	EFA100740	4889	EFA1c0022_orf_22p	10536
E3M10000032C11	474	EFA102501	4994	EFA1c0031_orf_35p	10626
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E3M10000032D01	476	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000032D02	477	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000032D03	478	EFA100399	4878	EFA1c0041_orf_104p	10766
E3M10000032D06	479	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000032D09	480	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000032D12	481	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000032E04	482	EFA101792	4961	EFA1c0042_orf_113p	10805
E3M10000032E04	482	EFA103786	5031	EFA1c0042_orf_114p	10806
E3M10000032E05	483	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000032E08	484	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000032E10	485	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000032E10	485	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000032E11	486	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000032E12	487	EFA102326	4986	#N/A	#N/A
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E3M10000032F02	488	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000032F03	489	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000032F05	490	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000032F07	491	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000032F08	492	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000032F11	493	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000032F12	494	EFA102201	4982	#N/A	#N/A
E3M10000032G01	495	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000032G02	496	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000032G04	497	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000032G05	498	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000032G06	499	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000032G07	500	EFA100919	4901	EFA1c0013_orf_12p	10491
E3M10000032H05	501	EFA100200	4869	EFA1c0041_orf_88p	10798
E3M10000032H06	502	EFA101833	4965	EFA1c0038_orf_61p	10720
E3M10000032H08	503	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000032H09	504	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000032H10	505	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000033A03	506	EFA101253	4924	EFA1c0043_orf_178p	10852
E3M10000033A04	507	EFA102503	4996	EFA1c0032_orf_32p	10643
E3M10000033A05	508	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000033A06	509	EFA101415	4940	EFA1c0022_orf_16p	10529
E3M10000033A07	510	EFA102774	5009	EFA1c0044_orf_25p	10896
E3M10000033A08	511	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000033A11	512	EFA100642	4884	EFA1c0041_orf_56p	10792

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000033B02	514	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000033B04	515	EFA101765	4958	EFA1c0025_orf_33p	10587
E3M10000033B05	516	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000033B06	517	EFA102351	4989	EFA1c0032_orf_20p	10634
E3M10000033B08	518	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000033B09	519	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000033C01	520	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000033C02	521	EFA103174	5021	EFA1c0036_orf_120p	10689
E3M10000033C05	522	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000033C05	522	EFA102542	4999	EFA1c0028_orf_4p	10603
E3M10000033C09	523	EFA100811	4898	EFA1c0022_orf_33p	10546
E3M10000033C10	524	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000033C10	524	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000033C11	525	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000033C12	526	EFA102389	4992	EFA1c0044_orf_83p	10904
E3M10000033D01	527	EFA102351	4989	EFA1c0032_orf_20p	10634
E3M10000033D04	528	EFA101682	4951	EFA1c0041_orf_53p	10789
E3M10000033D05	529	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000033D06	530	EFA100641	4883	EFA1c0041_orf_57p	10793
E3M10000033D06	530	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000033D09	531	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000033D10	532	EFA102006	4973	EFA1c0025_orf_17p	10580
E3M10000033D11	533	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000033E02	534	EFA101477	4945	EFA1c0043_orf_224p	10861
E3M10000033E03	535	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000033E03	535	EFA101415	4940	EFA1c0022_orf_16p	10529
E3M10000033E04	536	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000033E05	537	EFA102503	4996	EFA1c0032_orf_32p	10643
E3M10000033E07	538	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000033E08	539	EFA102351	4989	EFA1c0032_orf_20p	10634
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E3M10000033E11	541	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000033F01	542	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000033F03	543	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000033F04	544	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000033F05	545	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000033F07	546	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000033F08	547	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000033F10	548	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000033F12	549	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000033F12	549	EFA102542	4999	EFA1c0028_orf_4p	10603
E3M10000033G01	550	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000033G02	551	EFA102813	5013	EFA1c0043_orf_9p	10878
E3M10000033G03	552	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000033G04	553	EFA102326	4986	#N/A	#N/A
E3M10000033G06	554	EFA101404	4933	EFA1c0033_orf_55p	10663
E3M10000033G07	555	EFA101685	4952	EFA1c0041_orf_55p	10791

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000033G09	557	EFA102656	5004	EFA1c0039_orf_26p	10734
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E3M10000033H02	559	EFA101415	4940	EFA1c0022_orf_16p	10529
E3M10000033H04	560	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000033H05	561	EFA100741	4890	EFA1c0022_orf_21p	10535
E3M10000033H07	562	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000033H08	563	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000033H09	564	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000033H10	565	EFA101079	4908	#N/A	#N/A
E3M10000033H11	566	EFA100190	4867	EFA1c0010_orf_2p	10480
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E3M10000034A03	568	EFA100978	4904	EFA1c0022_orf_27p	10541
E3M10000034A04	569	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000034B02	570	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000034B04	571	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000034C04	572	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000034D01	573	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000034D02	574	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000034E01	575	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000034E04	576	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000034F02	577	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000034F03	578	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000034F04	579	EFA100190	4867	EFA1c0010_orf_2p	10480
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E3M10000034G03	581	EFA100740	4889	EFA1c0022_orf_22p	10536
E3M10000034H02	582	EFA101257	4925	EFA1c0045_orf_159p	10917
E3M10000034H03	583	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000035A02	584	EFA103268	5023	EFA1c0010_orf_1p	10479
E3M10000035A04	585	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000035A05	586	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000035A06	587	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000035A08	588	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000035A09	589	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000035A11	590	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000035B01	591	EFA101022	4906	EFA1c0043_orf_69p	10875
E3M10000035B03	592	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000035B06	593	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000035B07	594	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000035B08	595	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000035B10	596	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000035B11	597	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000035B12	598	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000035C01	599	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000035C03	600	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000035C04	601	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000035C05	602	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000035C06	603	EFA101160	4917	EFA1c0022_orf_3p	10549

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000035C08	605	EFA100741	4890	EFA1c0022_orf_21p	10535
E3M10000035C08	605	EFA100742	4891	EFA1c0022_orf_20p	10534
E3M10000035C09	606	EFA103062	5019	EFA1c0030_orf_19p	10615
E3M10000035C11	607	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000035C12	608	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000035D02	609	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000035D03	610	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000035D04	611	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000035D05	612	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000035D10	613	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000035D11	614	EFA100919	4901	EFA1c0013_orf_12p	10491
E3M10000035E03	615	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000035E04	616	EFA101141	4914	EFA1c0030_orf_18p	10614
E3M10000035E05	617	EFA102006	4973	EFA1c0025_orf_17p	10580
E3M10000035E07	618	EFA100919	4901	EFA1c0013_orf_12p	10491
E3M10000035E08	619	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000035E09	620	EFA100312	4874	EFA1c0032_orf_28p	10641
E3M10000035E10	621	EFA101022	4906	EFA1c0043_orf_69p	10875
E3M10000035E11	622	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000035E12	623	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000035F01	624	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000035F02	625	EFA101925	4971	EFA1c0044_orf_19p	10893
E3M10000035F03	626	EFA100312	4874	EFA1c0032_orf_28p	10641
E3M10000035F06	627	EFA101080	4909	#N/A	#N/A
E3M10000035F07	628	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000035F08	629	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000035F09	630	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000035F09	630	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000035F11	631	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000035F12	632	EFA101120	4911	EFA1c0036_orf_113p	10687
E3M10000035G02	633	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000035G02	633	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000035G04	634	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000035G05	635	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000035G08	636	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000035G09	637	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000035G09	637	EFA103508	5029	EFA1c0033_orf_95p	10672
E3M10000035G10	638	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000035G11	639	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000035H03	640	EFA101080	4909	#N/A	#N/A
E3M10000035H06	641	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000035H09	642	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000035H11	643	EFA101257	4925	EFA1c0045_orf_159p	10917
E3M10000035H11	643	EFA101258	4926	EFA1c0045_orf_160p	10918
E3M10000036A03	644	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000036A04	645	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000036A05	646	EFA102780	5010	EFA1c0045_orf_101p	10908

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E3M10000036A07	648	EFA103268	5023	EFA1c0010_orf_1p	10479
E3M10000036A08	649	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000036A09	650	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000036A10	651	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000036B01	652	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000036B03	653	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000036B06	654	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000036B07	655	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000036B08	656	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000036B09	657	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000036B11	658	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000036B12	659	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000036B12	659	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000036C01	660	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000036C03	661	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000036C06	662	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000036C07	663	EFA101141	4914	EFA1c0030_orf_18p	10614
E3M10000036C08	664	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000036C09	665	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000036C10	666	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000036C11	667	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000036D03	668	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000036D04	669	EFA102201	4982	#N/A	#N/A
E3M10000036D06	670	EFA100740	4889	EFA1c0022_orf_22p	10536
E3M10000036D08	671	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000036D09	672	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000036D10	673	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000036D11	674	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000036D12	675	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000036E01	676	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000036E04	677	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000036E05	678	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000036E07	679	EFA101022	4906	EFA1c0043_orf_69p	10875
E3M10000036E08	680	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000036F03	681	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000036F04	682	EFA101686	4953	EFA1c0045_orf_63p	10940
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E3M10000036F08	684	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000036F09	685	EFA101404	4933	EFA1c0033_orf_55p	10663
E3M10000036F10	686	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000036F12	687	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000036G01	688	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000036G01	688	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000036G02	689	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000036G03	690	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000036G04	691	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000036G06	692	EFA100295	4873	EFA1c0021_orf_15p	10517

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
E3M10000036G10	693	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000036H02	694	EFA103038	5017	EFA1c0030_orf_17p	10613
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E3M10000036H04	696	EFA103365	5026	EFA1c0022_orf_1p	10533
E3M10000036H05	697	EFA100194	4868	EFA1c0022_orf_26p	10540
E3M10000036H06	698	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000036H07	699	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000036H08	700	EFA103210	5022	EFA1c0036_orf_119p	10688
E3M10000036H09	701	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000036H10	702	EFA101141	4914	EFA1c0030_orf_18p	10614
E3M10000037A03	703	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000037A06	704	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000037A08	705	EFA103365	5026	EFA1c0022_orf_1p	10533
E3M10000037A09	706	EFA100756	4893	EFA1c0024_orf_39p	10575
E3M10000037A10	707	EFA103268	5023	EFA1c0010_orf_1p	10479
E3M10000037B02	708	EFA100641	4883	EFA1c0041_orf_57p	10793
E3M10000037B02	708	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000037B07	709	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000037B08	710	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000037B11	711	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000037C01	712	EFA101080	4909	#N/A	#N/A
E3M10000037C02	713	EFA102351	4989	EFA1c0032_orf_20p	10634
E3M10000037C04	714	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000037C05	715	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000037C07	716	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000037C07	716	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000037C11	717	EFA100615	4881	EFA1c0016_orf_29p	10501
E3M10000037C12	718	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000037D02	719	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000037D03	720	EFA100795	4896	EFA1c0043_orf_229p	10863
E3M10000037D03	720	EFA103081	5020	EFA1c0043_orf_228p	10862
E3M10000037D04	721	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000037D05	722	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000037D06	723	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000037D09	724	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000037D09	724	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000037D11	725	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000037E01	726	EFA102736	5007	EFA1c0022_orf_60p	10556
E3M10000037E02	727	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000037E03	728	EFA102503	4996	EFA1c0032_orf_32p	10643
E3M10000037E05	729	EFA101080	4909	#N/A	#N/A
E3M10000037E07	730	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000037E08	731	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000037E10	732	EFA101253	4924	EFA1c0043_orf_178p	10852
E3M10000037E12	733	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000037F01	734	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000037F02	735	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000037F06	736	EFA100210	4870	EFA1c0022_orf_9p	10560

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000037F12	738	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000037G01	739	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000037G02	740	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000037G03	741	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000037G05	742	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000037G06	743	EFA103295	5024	EFA1c0032_orf_1p	10633
E3M10000037G07	744	EFA101541	4948	EFA1c0012_orf_5p	10488
E3M10000037G08	745	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000037G10	746	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000037G11	747	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000037H02	748	EFA101413	4938	#N/A	#N/A
E3M10000037H05	749	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000037H07	750	EFA100955	4902	EFA1c0022_orf_28p	10542
E3M10000037H10	751	EFA101080	4909	#N/A	#N/A
E3M10000037H11	752	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000038A02	753	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000038A03	754	EFA103038	5017	EFA1c0030_orf_17p	10613
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E3M10000038A06	756	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000038A07	757	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000038A09	758	EFA102736	5007	EFA1c0022_orf_60p	10556
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E3M10000038A11	760	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000038B02	761	EFA103210	5022	EFA1c0036_orf_119p	10688
E3M10000038B03	762	EFA102389	4992	EFA1c0044_orf_83p	10904
E3M10000038B04	763	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000038B05	764	EFA100795	4896	EFA1c0043_orf_229p	10863
E3M10000038B05	764	EFA103081	5020	EFA1c0043_orf_228p	10862
E3M10000038B07	765	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000038B08	766	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000038B09	767	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000038B11	768	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000038C02	769	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000038C03	770	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000038C05	771	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000038C07	772	EFA101963	4972	EFA1c0043_orf_162p	10848
E3M10000038C10	773	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000038C12	774	EFA101080	4909	#N/A	#N/A
E3M10000038D01	775	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000038D02	776	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000038D04	777	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000038D08	778	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000038D10	779	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000038D11	780	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000038D12	781	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000038E02	782	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000038E03	783	EFA101159	4916	EFA1c0022_orf_2p	10543

TABLE IA

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000038E07	786	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000038E08	787	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000038E11	788	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000038F02	789	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000038F04	790	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000038F05	791	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000038F05	791	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000038F06	792	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000038F07	793	EFA103210	5022	EFA1c0036_orf_119p	10688
E3M10000038F09	794	EFA102185	4980	EFA1c0045_orf_95p	10950
E3M10000038F10	795	EFA101080	4909	#N/A	#N/A
E3M10000038F11	796	EFA100740	4889	EFA1c0022_orf_22p	10536
E3M10000038G02	797	EFA100919	4901	EFA1c0013_orf_12p	10491
E3M10000038G03	798	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000038G06	799	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000038G07	800	EFA102352	4990	EFA1c0032_orf_21p	10635
E3M10000038G07	800	EFA102353	4991	EFA1c0032_orf_22p	10636
E3M10000038G11	801	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000038H02	802	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000038H05	803	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000038H06	804	EFA100295	4873	EFA1c0021_orf_15p	10517
E3M10000038H07	805	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000038H08	806	EFA100295	4873	EFA1c0021_orf_15p	10517
E3M10000038H09	807	EFA102802	5012	EFA1c0043_orf_18p	10854
E3M10000038H10	808	EFA101541	4948	EFA1c0012_orf_5p	10488
E3M10000039A02	809	EFA101736	4955	EFA1c0041_orf_14p	10775
E3M10000039A02	809	EFA101737	4956	EFA1c0041_orf_15p	10778
E3M10000039A06	810	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000039A07	811	EFA102006	4973	EFA1c0025_orf_17p	10580
E3M10000039A08	812	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000039A10	813	EFA101257	4925	EFA1c0045_orf_159p	10917
E3M10000039A11	814	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000039B01	815	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000039B03	816	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000039B04	817	EFA101415	4940	EFA1c0022_orf_16p	10529
E3M10000039B04	817	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000039B06	818	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000039B07	819	EFA102110	4978	EFA1c0042_orf_99p	10841
E3M10000039B08	820	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000039B09	821	EFA101792	4961	EFA1c0042_orf_113p	10805
E3M10000039B11	822	EFA101080	4909	#N/A	#N/A
E3M10000039C02	823	EFA103062	5019	EFA1c0030_orf_19p	10615
E3M10000039C04	824	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000039C05	825	EFA100739	4888	EFA1c0022_orf_23p	10537
E3M10000039C06	826	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000039C07	827	EFA101791	4960	EFA1c0042_orf_112p	10804

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000039C08	828	EFA101159	4916	EFA1c0022_orf_2p	10543
E3M10000039C09	829	EFA102503	4996	EFA1c0032_orf_32p	10643
E3M10000039C10	830	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000039D02	831	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000039D03	832	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000039D04	833	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000039D06	834	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000039E01	835	EFA102201	4982	#N/A	#N/A
E3M10000039E02	836	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000039E03	837	EFA100919	4901	EFA1c0013_orf_12p	10491
E3M10000039E05	838	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000039E07	839	EFA103295	5024	EFA1c0032_orf_1p	10633
E3M10000039E08	840	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000039F01	841	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000039F02	842	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000039F03	843	EFA102788	5011	EFA1c0033_orf_41p	10661
E3M10000039F03	843	EFA103375	5027	EFA1c0033_orf_40p	10660
E3M10000039F06	844	EFA100739	4888	EFA1c0022_orf_23p	10537
E3M10000039F07	845	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000039F08	846	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000039G01	847	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000039G02	848	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000039G05	849	EFA100919	4901	EFA1c0013_orf_12p	10491
E3M10000039G07	850	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000039G09	851	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000039G10	852	EFA101682	4951	EFA1c0041_orf_53p	10789
E3M10000039H02	853	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000039H07	854	EFA101080	4909	#N/A	#N/A
E3M10000039H08	855	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000039H10	856	EFA101413	4938	#N/A	#N/A
E3M10000039H11	857	EFA101120	4911	EFA1c0036_orf_113p	10687
E3M10000039H11	857	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000040A03	858	EFA101123	4913	EFA1c0040_orf_22p	10748
E3M10000040A05	859	EFA101080	4909	#N/A	#N/A
E3M10000040A07	860	EFA100157	4865	EFA1c0034_orf_63p	10673
E3M10000040A09	861	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000040A10	862	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000040A11	863	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000040B01	864	EFA102788	5011	EFA1c0033_orf_41p	10661
E3M10000040B02	865	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000040B05	866	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000040B05	866	EFA103268	5023	EFA1c0010_orf_1p	10479
E3M10000040B06	867	EFA102518	4997	EFA1c0032_orf_46p	10647
E3M10000040B08	868	EFA100919	4901	EFA1c0013_orf_12p	10491
E3M10000040B09	869	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000040B10	870	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000040B11	871	EFA102764	5008	EFA1c0008_orf_3p	10478

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E3M10000040C05	874	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000040C06	875	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000040C07	876	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000040C08	877	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000040C09	878	EFA100165	4866	EFA1c0032_orf_23p	10637
E3M10000040C09	878	EFA102353	4991	EFA1c0032_orf_22p	10636
E3M10000040C10	879	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000040C11	880	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000040C12	881	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000040D03	882	EFA102201	4982	#N/A	#N/A
E3M10000040D04	883	EFA101080	4909	#N/A	#N/A
E3M10000040D08	884	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000040D12	885	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000040E02	886	EFA102051	4976	#N/A	#N/A
E3M10000040E10	887	EFA101415	4940	EFA1c0022_orf_16p	10529
E3M10000040E11	888	EFA103039	5018	EFA1c0043_orf_16p	10850
E3M10000040E12	889	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000040F01	890	EFA100295	4873	EFA1c0021_orf_15p	10517
E3M10000040F03	891	EFA102503	4996	EFA1c0032_orf_32p	10643
E3M10000040F08	892	EFA101080	4909	#N/A	#N/A
E3M10000040F09	893	EFA100919	4901	EFA1c0013_orf_12p	10491
E3M10000040F10	894	EFA102051	4976	#N/A	#N/A
E3M10000040G01	895	EFA101415	4940	EFA1c0022_orf_16p	10529
E3M10000040G02	896	EFA101424	4943	EFA1c0041_orf_39p	10784
E3M10000040G02	896	EFA101425	4944	EFA1c0041_orf_40p	10785
E3M10000040G04	897	EFA101141	4914	EFA1c0030_orf_18p	10614
E3M10000040G05	898	EFA101159	4916	EFA1c0022_orf_2p	10543
E3M10000040G07	899	EFA101079	4908	#N/A	#N/A
E3M10000040G07	899	EFA101080	4909	#N/A	#N/A
E3M10000040G08	900	EFA102186	4981	EFA1c0045_orf_94p	10949
E3M10000040G09	901	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000040G11	902	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000040H02	903	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000040H03	904	EFA100394	4876	EFA1c0034_orf_6p	10675
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E3M10000040H04	905	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000040H05	906	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000040H05	906	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000040H09	907	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000040H09	907	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000041A03	908	EFA100615	4881	EFA1c0016_orf_29p	10501
E3M10000041A05	909	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000041A08	910	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000041A09	911	EFA101354	4930	EFA1c0032_orf_69p	10648
E3M10000041A10	912	EFA100001	4861	EFA1c0030_orf_3p	10618
E3M10000041A11	913	EFA100642	4884	EFA1c0041_orf_56p	10792

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000041B03	915	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000041B05	916	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000041B06	917	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000041B08	918	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000041B09	919	EFA101924	4970	EFA1c0044_orf_18p	10891
E3M10000041B09	919	EFA101925	4971	EFA1c0044_orf_19p	10893
E3M10000041B10	920	EFA101080	4909	#N/A	#N/A
E3M10000041B11	921	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000041B11	921	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000041B12	922	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000041C01	923	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000041C07	924	EFA100739	4888	EFA1c0022_orf_23p	10537
E3M10000041C08	925	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000041C09	926	EFA103365	5026	EFA1c0022_orf_1p	10533
E3M10000041C10	927	EFA102503	4996	EFA1c0032_orf_32p	10643
E3M10000041C11	928	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000041C12	929	EFA100798	4897	EFA1c0042_orf_160p	10818
E3M10000041D02	930	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000041D03	931	EFA101060	4907	EFA1c0038_orf_73p	10722
E3M10000041D04	932	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000041D04	932	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000041D05	933	EFA101080	4909	#N/A	#N/A
E3M10000041D06	934	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000041D08	935	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000041D09	936	EFA101120	4911	EFA1c0036_orf_113p	10687
E3M10000041D10	937	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000041D11	938	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000041D12	939	EFA100394	4876	EFA1c0034_orf_6p	10675
E3M10000041E02	940	EFA101797	4963	EFA1c0045_orf_167p	10924
E3M10000041E03	941	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000041E05	942	EFA101415	4940	EFA1c0022_orf_16p	10529
E3M10000041E07	943	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000041E10	944	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000041E11	945	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000041F03	946	EFA102503	4996	EFA1c0032_orf_32p	10643
E3M10000041F05	947	EFA102006	4973	EFA1c0025_orf_17p	10580
E3M10000041F06	948	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000041F07	949	EFA101159	4916	EFA1c0022_orf_2p	10543
E3M10000041F08	950	EFA100295	4873	EFA1c0021_orf_15p	10517
E3M10000041F09	951	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000041F10	952	EFA101079	4908	#N/A	#N/A
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E3M10000041F11	953	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000041G02	954	EFA101141	4914	EFA1c0030_orf_18p	10614
E3M10000041G03	955	EFA102253	4984	EFA1c0038_orf_85p	10727
E3M10000041G04	956	EFA101685	4952	EFA1c0041_orf_55p	10791

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000041G08	959	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000041G09	960	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000041G10	961	EFA100394	4876	EFA1c0034_orf_6p	10675
E3M10000041G12	962	EFA100394	4876	EFA1c0034_orf_6p	10675
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E3M10000041H05	964	EFA100329	4875	EFA1c0041_orf_35p	10782
E3M10000041H06	965	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000041H07	966	EFA103062	5019	EFA1c0030_orf_19p	10615
E3M10000041H08	967	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000041H09	968	EFA102788	5011	EFA1c0033_orf_41p	10661
E3M10000041H10	969	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000041H11	970	EFA102253	4984	EFA1c0038_orf_85p	10727
E3M10000042A03	971	EFA101120	4911	EFA1c0036_orf_113p	10687
E3M10000042A03	971	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000042A08	972	EFA102351	4989	EFA1c0032_orf_20p	10634
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E3M10000042B01	974	EFA101404	4933	EFA1c0033_orf_55p	10663
E3M10000042B02	975	EFA100668	4885	EFA1c0035_orf_58p	10679
E3M10000042B04	976	EFA102186	4981	EFA1c0045_orf_94p	10949
E3M10000042B04	976	EFA102453	4993	EFA1c0045_orf_203p	10931
E3M10000042B08	977	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000042B09	978	EFA101797	4963	EFA1c0045_orf_167p	10924
E3M10000042B10	979	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000042B11	980	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000042C02	981	EFA101150	4915	EFA1c0038_orf_57p	10719
E3M10000042C03	982	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000042C04	983	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000042C10	984	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000042C10	984	EFA100295	4873	EFA1c0021_orf_15p	10517
E3M10000042D01	985	EFA100615	4881	EFA1c0016_orf_29p	10501
E3M10000042D02	986	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000042D03	987	EFA100394	4876	EFA1c0034_orf_6p	10675
E3M10000042D06	988	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000042D09	989	EFA101141	4914	EFA1c0030_orf_18p	10614
E3M10000042D11	990	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000042D12	991	EFA100795	4896	EFA1c0043_orf_229p	10863
E3M10000042E05	992	EFA102501	4994	EFA1c0031_orf_35p	10626
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E3M10000042G01	995	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000042G05	996	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000042G07	997	EFA101169	4923	EFA1c0024_orf_38p	10574
E3M10000042G08	998	EFA102780	5010	EFA1c0045_orf_101p	10908
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E3M10000042G11	999	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000042G12	1000	EFA102501	4994	EFA1c0031_orf_35p	10626

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E3M10000042H11	1003	EFA100668	4885	EFA1c0035_orf_58p	10679
E3M10000043A02	1004	EFA101799	4964	EFA1c0045_orf_169p	10926
E3M10000043A03	1005	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000043A05	1006	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000043A08	1007	EFA100689	4886	EFA1c0038_orf_54p	10717
E3M10000043A09	1008	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000043A09	1008	EFA101415	4940	EFA1c0022_orf_16p	10529
E3M10000043A10	1009	EFA101080	4909	#N/A	#N/A
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E3M10000043B01	1011	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000043B02	1012	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000043B03	1013	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000043B06	1014	EFA101404	4933	EFA1c0033_orf_55p	10663
E3M10000043B08	1015	EFA101123	4913	EFA1c0040_orf_22p	10748
E3M10000043B09	1016	EFA101892	4969	EFA1c0017_orf_21p	10506
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E3M10000043B11	1018	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000043B12	1019	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000043C01	1020	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000043C08	1021	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000043C09	1022	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000043D01	1023	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000043D02	1024	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000043D09	1025	EFA102351	4989	EFA1c0032_orf_20p	10634
E3M10000043D10	1026	EFA101872	4967	EFA1c0042_orf_152p	10815
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E3M10000043D12	1027	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000043E03	1028	EFA100397	4877	EFA1c0041_orf_148p	10773
E3M10000043E07	1029	EFA101339	4928	EFA1c0040_orf_13p	10743
E3M10000043E08	1030	EFA101872	4967	EFA1c0042_orf_152p	10815
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E3M10000043E10	1031	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000043E11	1032	EFA102813	5013	EFA1c0043_orf_9p	10878
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E3M10000043F08	1036	EFA101121	4912	EFA1c0036_orf_112p	10686
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E3M10000043G05	1041	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000043G07	1042	EFA100157	4865	EFA1c0034_orf_63p	10673
E3M10000043G08	1043	EFA101080	4909	#N/A	#N/A
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E3M10000043H05	1048	EFA101080	4909	#N/A	#N/A
E3M10000043H08	1049	EFA100615	4881	EFA1c0016_orf_29p	10501
E3M10000043H09	1050	EFA102006	4973	EFA1c0025_orf_17p	10580
E3M10000043H11	1051	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000044C02	1052	EFA100955	4902	EFA1c0022_orf_28p	10542
E3M10000044E01	1053	EFA102091	4977	EFA1c0010_orf_3p	10481
K1M10000002F02	1054	KPN101750	5037	KPN1c1723_orf_1p	11652
K1M10000003C01	1055	KPN103882	5040	KPN1c2848_orf_1p	11716
K1M10000007F01	1057	KPN104183	5041	KPN1c1646_orf_2p	11650
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K1M10000008C02	1058	KPN107626	5051	#N/A	#N/A
K1M10000008C10	1059	KPN101729	5036	KPN1c1566_orf_1p	11647
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K1M10000009D04	1061	KPN107776	5052	KPN1c4041_orf_1p	11771
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K1M10000020B02	1065	KPN101729	5036	KPN1c1566_orf_1p	11647
K1M10000022C10	1067	KPN100854	5033	KPN1c0845_orf_1p	11630
K1M10000030C07	1070	KPN104716	5045	KPN1c3094_orf_5p	11757
K1M10000030E07	1071	KPN104538	5044	KPN1c2918_orf_2p	11726
K1M10000032E11	1073	KPN101729	5036	KPN1c1566_orf_1p	11647
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K1M10000036G08	1076	KPN106044	5048	#N/A	#N/A
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P1M10000014H10	1095	PA4252	5168	#N/A	#N/A
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P1M10000024D06	1107	PA3160	5130	#N/A	#N/A
P1M10000024E06	1108	PA4888	5200	#N/A	#N/A
P1M10000024H03	1109	PA2313	5105	#N/A	#N/A
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P1M10000026H05	1117	PA3154	5129	#N/A	#N/A
P1M10000027A06	1118	PA4257	5172	#N/A	#N/A
P1M10000027B02	1119	PA3154	5129	#N/A	#N/A
P1M10000027G05	1120	PA2313	5105	#N/A	#N/A
P1M10000028A08	1121	PA0788	5075	#N/A	#N/A
P1M10000028B01	1122	PA4263	5176	#N/A	#N/A
P1M10000028E02	1123	PA2584	5112	#N/A	#N/A
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P1M10000032F04	1127	PA0265	5058	#N/A	#N/A
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P1M10000035A06	1133	PA4249	5165	#N/A	#N/A
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P1M10000038F04	1139	PA5207	5208	#N/A	#N/A
P1M10000038G02	1140	PA4542	5192	#N/A	#N/A
P1M10000039G05	1141	PA3764	5141	#N/A	#N/A
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P1M10000040C04	1144	PA1115	5081	#N/A	#N/A
P1M10000040D04	1145	PA0378	5062	#N/A	#N/A
P1M10000040D05	1146	PA5209	5209	#N/A	#N/A
P1M10000040E10	1147	PA2128	5100	#N/A	#N/A
P1M10000040H03	1148	PA1115	5081	#N/A	#N/A
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P1M10000042E08	1154	PA4252	5168	#N/A	#N/A
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P1M10000043A03	1155	PA3006	5121	#N/A	#N/A
P1M10000043D06	1156	PA3764	5141	#N/A	#N/A
P1M10000044F07	1157	PA4244	5160	#N/A	#N/A
P1M10000046B03	1158	PA1462	5087	#N/A	#N/A
P1M10000046C07	1159	PA2671	5116	#N/A	#N/A
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P1M10000046G11	1162	PA1115	5081	#N/A	#N/A
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P1M10000047F07	1165	PA4506	5190	#N/A	#N/A
P1M10000047G10	1166	PA4259	5174	#N/A	#N/A
P1M10000048A03	1167	PA4105	5154	#N/A	#N/A
P1M10000049E08	1168	PA4272	5181	#N/A	#N/A
P1M10000049G10	1169	PA4027	5149	#N/A	#N/A
P1M10000050G11	1170	PA4249	5165	#N/A	#N/A
P1M10000051D11	1171	PA1365	5085	#N/A	#N/A
P1M10000051F01	1172	PA1115	5081	#N/A	#N/A
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P1M10000055E05	1182	PA5507	5219	#N/A	#N/A
P1M10000056C07	1183	PA1360	5084	#N/A	#N/A
P1M10000056F05	1184	PA4258	5173	#N/A	#N/A
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P1M10000061B04	1197	PA2726	5119	#N/A	#N/A
P1M10000061E04	1198	PA4244	5160	#N/A	#N/A
P1M10000061F04	1199	PA3522	5136	#N/A	#N/A
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P1M10000062C03	1201	PA0321	5059	#N/A	#N/A
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P1M10000062C07	1203	PA4251	5167	#N/A	#N/A
P1M10000062C12	1204	PA5316	5212	#N/A	#N/A
P1M10000062D07	1205	PA4247	5163	#N/A	#N/A
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P1M10000068H05	1246	PA4268	5178	#N/A	#N/A
P1M10000069D09	1247	PA4246	5162	#N/A	#N/A
P1M10000069G06	1248	PA4246	5162	#N/A	#N/A
P1M10000069H02	1249	PA4433	5188	#N/A	#N/A
P1M10000070A05	1250	PA2470	5109	#N/A	#N/A
P1M10000070B10	1251	PA5393	5214	#N/A	#N/A
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P1M10000079A10	1283	PA4576	5193	#N/A	#N/A
P1M10000079B10	1284	PA4576	5193	#N/A	#N/A
P1M10000079C10	1285	PA4576	5193	#N/A	#N/A
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S1M10000001A09	1356	SAU101907	5574	SAU1c0040_orf_79p	12442
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S1M10000001D07	1362	SAU101360	5431	SAU1c0044_orf_109p	12555
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000002A10	1381	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000002A10	1381	SAU301148	5888	#N/A	#N/A
S1M10000002A12	1382	SAU200916	5797	SAU2c0373_orf_4p	12838
S1M10000002A12	1382	SAU300455	5872	#N/A	#N/A
S1M10000002A12	1382	SAU301620	5899	SAU3c1478_orf_2p	13140
S1M10000002B01	1383	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000002B03	1384	SAU101034	5371	SAU1c0044_orf_27p	12608
S1M10000002B04	1385	SAU101907	5574	SAU1c0040_orf_79p	12442
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S1M10000002B09	1389	SAU201810	5836	SAU2c0308_orf_2p	12769
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S1M10000002C02	1391	SAU201810	5836	SAU2c0308_orf_2p	12769
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S1M10000002C12	1395	SAU101039	5373	SAU1c0043_orf_181p	12522
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S1M10000002D05	1399	SAU202930	5856	SAU2c0396_orf_3p	12871
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S1M10000002E07	1406	SAU201810	5836	SAU2c0308_orf_2p	12769
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S1M10000002F02	1411	SAU301620	5899	SAU3c1478_orf_2p	13140
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S1M10000002G06	1418	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000002G07	1419	SAU103038	5757	#N/A	#N/A
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S1M10000004F09	1499	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000004F09	1499	SAU301148	5888	#N/A	#N/A
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S1M10000004G01	1501	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000004G01	1501	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000004G01	1501	SAU301148	5888	#N/A	#N/A
S1M10000004G02	1502	SAU102939	5747	#N/A	#N/A
S1M10000004G03	1503	SAU102449	5674	SAU1c0045_orf_22p	12677
S1M10000004G05	1504	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000004G06	1505	SAU102939	5747	#N/A	#N/A
S1M10000004G07	1506	SAU100964	5363	SAU1c0044_orf_86p	12641
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S1M10000004G09	1507	SAU101869	5566	SAU1c0036_orf_24p	12321
S1M10000004G12	1508	SAU100497	5280	SAU1c0018_orf_3p	12140
S1M10000005A01	1509	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000005A01	1509	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000005A01	1509	SAU301148	5888	#N/A	#N/A
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S1M10000005A05	1511	SAU102939	5747	#N/A	#N/A
S1M10000005A06	1512	SAU102939	5747	#N/A	#N/A
S1M10000005A07	1513	SAU100952	5358	SAU1c0043_orf_182p	12523
S1M10000005A08	1514	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000005A08	1514	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000005A08	1514	SAU301148	5888	#N/A	#N/A
S1M10000005A09	1515	SAU103038	5757	#N/A	#N/A
S1M10000005A10	1516	SAU101239	5402	SAU1c0044_orf_15p	12570
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S1M10000005A11	1517	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000005B02	1518	SAU102527	5693	SAU1c0032_orf_9p	12260
S1M10000005B04	1519	SAU101545	5474	SAU1c0037_orf_132p	12348
S1M10000005B07	1520	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000005B07	1520	SAU202174	5845	SAU2c0412_orf_3p	12895
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S1M10000005B08	1521	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000005B09	1522	SAU102422	5666	SAU1c0030_orf_22p	12207
S1M10000005B12	1523	SAU102284	5635	SAU1c0038_orf_5p	12389
S1M10000005B12	1523	SAU201469	5816	SAU2c0438_orf_6p	12967
S1M10000005C01	1524	SAU201810	5836	SAU2c0308_orf_2p	12769
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S1M10000005C06	1526	SAU100885	5348	SAU1c0038_orf_38p	12376
S1M10000005C09	1527	SAU302513	5906	SAU3c1298_orf_1p	13085
S1M10000005C11	1528	SAU101495	5467	SAU1c0037_orf_65p	12360
S1M10000005D01	1529	SAU103038	5757	#N/A	#N/A
S1M10000005D02	1530	SAU102007	5590	SAU1c0040_orf_108p	12428
S1M10000005D03	1531	SAU101907	5574	SAU1c0040_orf_79p	12442
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S1M10000005D05	1533	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000005D06	1534	SAU101545	5474	SAU1c0037_orf_132p	12348
S1M10000005D06	1534	SAU101546	5475	SAU1c0037_orf_133p	12349
S1M10000005D07	1535	SAU101869	5566	SAU1c0036_orf_24p	12321
S1M10000005D08	1536	SAU101624	5497	SAU1c0040_orf_25p	12429
S1M10000005D09	1537	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000005D11	1538	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000005D12	1539	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000005E01	1540	SAU100542	5288	SAU1c0043_orf_210p	12532
S1M10000005E02	1541	SAU102631	5721	SAU1c0045_orf_94p	12712
S1M10000005E05	1542	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000005E05	1542	SAU202174	5845	SAU2c0412_orf_3p	12895
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S1M10000005E07	1544	SAU102939	5747	#N/A	#N/A
S1M10000005E08	1545	SAU201810	5836	SAU2c0308_orf_2p	12769
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S1M10000005F02	1549	SAU100964	5363	SAU1c0044_orf_86p	12641
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S1M10000005F03	1550	SAU301433	5895	SAU3c1420_orf_2p	13118
S1M10000005F04	1551	SAU102044	5593	SAU1c0039_orf_65p	12414
S1M10000005F04	1551	SAU102046	5594	SAU1c0039_orf_66p	12415
S1M10000005F04	1551	SAU201961	5840	#N/A	#N/A
S1M10000006A03	1552	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000006A03	1552	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000006A03	1552	SAU301148	5888	#N/A	#N/A
S1M10000006A04	1553	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000006A05	1554	SAU101807	5547	SAU1c0032_orf_26p	12231
S1M10000006A05	1554	SAU101808	5548	SAU1c0032_orf_27p	12232
S1M10000006A07	1555	SAU100952	5358	SAU1c0043_orf_182p	12523
S1M10000006A08	1556	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000006A08	1556	SAU202174	5845	SAU2c0412_orf_3p	12895
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S1M10000006A12	1558	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000006B02	1559	SAU100741	5318	SAU1c0039_orf_48p	12409
S1M10000006B03	1560	SAU102631	5721	SAU1c0045_orf_94p	12712
S1M10000006B04	1561	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000006B04	1561	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000006B04	1561	SAU301148	5888	#N/A	#N/A
S1M10000006B07	1562	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000006B10	1563	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000006B11	1564	SAU101365	5432	SAU1c0044_orf_112p	12556
S1M10000006C02	1565	SAU102939	5747	#N/A	#N/A
S1M10000006C04	1566	SAU102287	5637	SAU1c0038_orf_7p	12398
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S1M10000006C06	1567	SAU102487	5688	SAU1c0039_orf_92p	12419
S1M10000006C07	1568	SAU100157	5237	SAU1c0040_orf_81p	12444
S1M10000006C08	1569	SAU102939	5747	#N/A	#N/A
S1M10000006C10	1570	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000006C10	1570	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000006C10	1570	SAU301148	5888	#N/A	#N/A
S1M10000006D03	1571	SAU100608	5297	SAU1c0034_orf_69p	12293
S1M10000006D05	1572	SAU201810	5836	SAU2c0308_orf_2p	12769
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S1M10000006D06	1573	SAU301148	5888	#N/A	#N/A
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S1M10000006E02	1576	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000006E02	1576	SAU301148	5888	#N/A	#N/A
S1M10000006E03	1577	SAU100275	5252	SAU1c0036_orf_15p	12314
S1M10000006E04	1578	SAU101777	5527	SAU1c0037_orf_39p	12352
S1M10000006E07	1579	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000006E07	1579	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000006E07	1579	SAU301148	5888	#N/A	#N/A
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S1M10000006F01	1581	SAU101869	5566	SAU1c0036_orf_24p	12321
S1M10000006F02	1582	SAU201469	5816	SAU2c0438_orf_6p	12967
S1M10000006F03	1583	SAU102294	5639	SAU1c0044_orf_288p	12610
S1M10000006F03	1583	SAU301080	5885	SAU3c1287_orf_1p	13083
S1M10000006F04	1584	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000006F06	1585	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000006G02	1586	SAU101833	5555	SAU1c0038_orf_34p	12373
S1M10000006G03	1587	SAU101400	5444	SAU1c0036_orf_35p	12326
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000006G07	1590	SAU202945	5857	SAU2c0394_orf_7p	12868
S1M10000006G09	1591	SAU102939	5747	#N/A	#N/A
S1M10000006G10	1592	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000006G11	1593	SAU101438	5450	SAU1c0038_orf_40p	12379
S1M10000007A02	1594	SAU102939	5747	#N/A	#N/A
S1M10000007A03	1595	SAU101653	5504	SAU1c0042_orf_124p	12493
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S1M10000007B11	1597	SAU101476	5459	SAU1c0032_orf_69p	12254
S1M10000007C02	1598	SAU102939	5747	#N/A	#N/A
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S1M10000007C05	1600	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000007C06	1601	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000007C07	1602	SAU101266	5408	SAU1c0042_orf_117p	12490
S1M10000007C08	1603	SAU101717	5513	SAU1c0016_orf_16p	12131
S1M10000007C09	1604	SAU102939	5747	#N/A	#N/A
S1M10000007D03	1605	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000007D03	1605	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000007D03	1605	SAU301148	5888	#N/A	#N/A
S1M10000007D06	1606	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000007D08	1607	SAU102939	5747	#N/A	#N/A
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S1M10000007E04	1610	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000007E04	1610	SAU301148	5888	#N/A	#N/A
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S1M10000007F02	1614	SAU101685	5512	SAU1c0023_orf_11p	12152
S1M10000007F04	1615	SAU101491	5464	SAU1c0025_orf_20p	12165
S1M10000007F08	1616	SAU100794	5330	SAU1c0028_orf_53p	12189
S1M10000007F09	1617	SAU202930	5856	SAU2c0396_orf_3p	12871
S1M10000007F10	1618	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000007F11	1619	SAU102939	5747	#N/A	#N/A
S1M10000007F12	1620	SAU102939	5747	#N/A	#N/A
S1M10000007G02	1621	SAU101270	5410	SAU1c0037_orf_89p	12365
S1M10000007G03	1622	SAU100952	5358	SAU1c0043_orf_182p	12523
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S1M10000007G07	1624	SAU102652	5725	SAU1c0045_orf_115p	12653
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S1M10000008A05	1628	SAU102939	5747	#N/A	#N/A
S1M10000008A08	1629	SAU102905	5742	SAU1c0033_orf_45p	12273
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000008B03	1632	SAU103144	5761	SAU1c0045_orf_15p	12663
S1M10000008B04	1633	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000008B04	1633	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000008B04	1633	SAU301148	5888	#N/A	#N/A
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S1M10000008B08	1635	SAU101652	5503	SAU1c0042_orf_123p	12492
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S1M10000008B10	1637	SAU100608	5297	SAU1c0034_orf_69p	12293
S1M10000008C05	1638	SAU102939	5747	#N/A	#N/A
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S1M10000008C09	1642	SAU101793	5534	SAU1c0032_orf_14p	12218
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S1M10000008D09	1644	SAU103038	5757	#N/A	#N/A
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S1M10000008E08	1646	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000008E09	1647	SAU101343	5425	SAU1c0044_orf_40p	12619
S1M10000008E10	1648	SAU101360	5431	SAU1c0044_orf_109p	12555
S1M10000008F01	1649	SAU102284	5635	SAU1c0038_orf_5p	12389
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S1M10000008G03	1658	SAU101637	5500	SAU1c0029_orf_8p	12201
S1M10000008G05	1659	SAU102870	5738	SAU1c0026_orf_17p	12170
S1M10000009A02	1660	SAU101159	5387	SAU1c0036_orf_46p	12331
S1M10000009A04	1661	SAU102979	5750	SAU1c0043_orf_227p	12536
S1M10000009A07	1662	SAU101371	5435	SAU1c0033_orf_7p	12275
S1M10000009A08	1663	SAU100658	5303	SAU1c0038_orf_59p	12388
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S1M10000009A09	1664	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000009A10	1665	SAU100658	5303	SAU1c0038_orf_59p	12388
S1M10000009A11	1666	SAU100114	5228	SAU1c0043_orf_225p	12535
S1M10000009B01	1667	SAU201506	5818	SAU2c0432_orf_18p	12946
S1M10000009B02	1668	SAU101159	5387	SAU1c0036_orf_46p	12331
S1M10000009B03	1669	SAU201506	5818	SAU2c0432_orf_18p	12946
S1M10000009B04	1670	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000009B05	1671	SAU101752	5522	SAU1c0040_orf_85p	12447

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000009B11	1675	SAU301898	5904	SAU3c1079_orf_1p	13057
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S1M10000009C07	1681	SAU102460	5678	SAU1c0026_orf_18p	12171
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S1M10000009F07	1705	SAU102607	5712	SAU1c0041_orf_51p	12472
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S1M10000009F09	1706	SAU202176	5846	SAU2c0412_orf_3p	12895
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S1M10000009F10	1707	SAU201541	5822	SAU2c0431_orf_14p	12942
S1M10000009G02	1708	SAU101572	5484	SAU1c0044_orf_211p	12586
S1M10000009G02	1708	SAU101573	5485	SAU1c0044_orf_212p	12587
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S1M10000009G09	1713	SAU102693	5731	SAU1c0044_orf_58p	12627
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S1M10000009G11	1715	SAU100131	5232	SAU1c0043_orf_156p	12517
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S1M10000009H11	1722	SAU101801	5541	#N/A	#N/A
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S1M10000011A03	1724	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000011A04	1725	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000011A06	1726	SAU101574	5486	SAU1c0044_orf_213p	12588
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S1M10000011B04	1730	SAU101574	5486	SAU1c0044_orf_213p	12588
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S1M10000011C05	1733	SAU202756	5852	SAU2c0470_orf_1p	13027
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S1M10000011D01	1735	SAU101293	5414	SAU1c0044_orf_61p	12631
S1M10000011D02	1736	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000011D04	1737	SAU102280	5632	SAU1c0038_orf_3p	12378
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S1M10000011E03	1740	SAU101632	5499	SAU1c0039_orf_3p	12407
S1M10000011E04	1741	SAU101572	5484	SAU1c0044_orf_211p	12586
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S1M10000011F03	1743	SAU102350	5649	SAU1c0040_orf_36p	12433
S1M10000011F04	1744	SAU101155	5385	SAU1c0036_orf_11p	12310
S1M10000011F06	1745	SAU101481	5460	SAU1c0015_orf_9p	12130
S1M10000011F06	1745	SAU101482	5461	SAU1c0015_orf_10p	12123
S1M10000011G01	1746	SAU301465	5896	SAU3c1429_orf_4p	13121
S1M10000011G03	1747	SAU302626	5907	SAU3c1367_orf_3p	13105
S1M10000011G04	1748	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000011G05	1749	SAU102350	5649	SAU1c0040_orf_36p	12433
S1M10000011G06	1750	SAU102298	5641	SAU1c0045_orf_42p	12705
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000012A06	1755	SAU100157	5237	SAU1c0040_orf_81p	12444
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S1M10000012A09	1757	SAU102356	5652	SAU1c0040_orf_41p	12436
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S1M10000012B05	1761	SAU101573	5485	SAU1c0044_orf_212p	12587
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S1M10000012B07	1763	SAU101814	5551	SAU1c0032_orf_32p	12237
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S1M10000012B11	1764	SAU102551	5698	SAU1c0045_orf_206p	12672
S1M10000012C01	1765	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000012C03	1766	SAU100776	5327	SAU1c0041_orf_72p	12482
S1M10000012C04	1767	SAU100776	5327	SAU1c0041_orf_72p	12482
S1M10000012C05	1768	SAU201558	5823	SAU2c0434_orf_5p	12954
S1M10000012C06	1769	SAU101570	5482	SAU1c0044_orf_209p	12584
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S1M10000012C11	1770	SAU100547	5290	SAU1c0032_orf_3p	12240
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S1M10000012D12	1777	SAU102621	5719	SAU1c0041_orf_63p	12480
S1M10000012D12	1777	SAU202006	5842	SAU2c0456_orf_20p	13018
S1M10000012E01	1778	SAU100733	5314	SAU1c0044_orf_254p	12602
S1M10000012E01	1778	SAU100734	5315	SAU1c0044_orf_255p	12603
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S1M10000012E12	1783	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000012E12	1783	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000012E12	1783	SAU301148	5888	#N/A	#N/A
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S1M10000012F07	1785	SAU102284	5635	SAU1c0038_orf_5p	12389
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000012F11	1789	SAU101781	5528	SAU1c0037_orf_43p	12353
S1M10000012F12	1790	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000012F12	1790	SAU202174	5845	SAU2c0412_orf_3p	12895
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S1M10000012G03	1793	SAU201301	5809	SAU2c0416_orf_17p	12899
S1M10000012G06	1794	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000012G07	1795	SAU101572	5484	SAU1c0044_orf_211p	12586
S1M10000012G07	1795	SAU101573	5485	SAU1c0044_orf_212p	12587
S1M10000012G08	1796	SAU102593	5704	SAU1c0041_orf_39p	12463
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S1M10000012H08	1799	SAU202186	5847	SAU2c0222_orf_1p	12731
S1M10000012H09	1800	SAU100227	5244	SAU1c0043_orf_188p	12525
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S1M10000013B05	1815	SAU100300	5253	SAU1c0040_orf_90p	12451
S1M10000013B06	1816	SAU100118	5229	SAU1c0015_orf_13p	12125
S1M10000013B07	1817	SAU202174	5845	SAU2c0412_orf_3p	12895
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S1M10000013B11	1819	SAU103042	5758	#N/A	#N/A
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S1M10000013C05	1821	SAU101038	5372	SAU1c0043_orf_180p	12521
S1M10000013C07	1822	SAU100300	5253	SAU1c0040_orf_90p	12451
S1M10000013C08	1823	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000013C09	1824	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000013C10	1825	SAU100736	5316	SAU1c0038_orf_64p	12391
S1M10000013C11	1826	SAU102059	5597	SAU1c0034_orf_51p	12286

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S1M10000013D09	1829	SAU302956	5915	SAU3c1513_orf_9p	13161
S1M10000013D11	1830	SAU102433	5668	SAU1c0045_orf_37p	12701
S1M10000013E01	1831	SAU102674	5730	SAU1c0024_orf_12p	12156
S1M10000013E02	1832	SAU101184	5391	SAU1c0035_orf_80p	12305
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S1M10000013E08	1835	SAU100831	5335	SAU1c0038_orf_93p	12403
S1M10000013E09	1836	SAU101571	5483	SAU1c0044_orf_210p	12585
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S1M10000013F02	1838	SAU101570	5482	SAU1c0044_orf_209p	12584
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S1M10000013F12	1844	SAU102437	5670	SAU1c0045_orf_33p	12695
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S1M10000014A05	1862	SAU101991	5582	SAU1c0040_orf_94p	12454
S1M10000014A07	1863	SAU101526	5470	SAU1c0027_orf_32p	12179
S1M10000014A08	1864	SAU103038	5757	#N/A	#N/A
S1M10000014A11	1865	SAU100866	5344	SAU1c0044_orf_100p	12553
S1M10000014A12	1866	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000014B01	1867	SAU100547	5290	SAU1c0032_orf_3p	12240
S1M10000014B02	1868	SAU100432	5271	SAU1c0040_orf_88p	12450
S1M10000014B02	1868	SAU100433	5272	SAU1c0040_orf_87p	12449
S1M10000014B03	1869	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000014B04	1870	SAU100778	5328	SAU1c0043_orf_140p	12514

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
S1M10000014B05	1871	SAU102476	5682	SAU1c0026_orf_33p	12175
S1M10000014B06	1872	SAU101199	5395	SAU1c0035_orf_62p	12302
S1M10000014B07	1873	SAU101756	5524	SAU1c0040_orf_82p	12445
S1M10000014B08	1874	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000014B10	1875	SAU200006	5770	SAU2c0157_orf_1p	12723
S1M10000014B11	1876	SAU102534	5696	#N/A	#N/A
S1M10000014B12	1877	SAU102534	5696	#N/A	#N/A
S1M10000014C01	1878	SAU101575	5487	SAU1c0044_orf_214p	12589
S1M10000014C05	1879	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000014C06	1880	SAU100305	5256	SAU1c0038_orf_77p	12397
S1M10000014C07	1881	SAU101801	5541	#N/A	#N/A
S1M10000014C09	1882	SAU100547	5290	SAU1c0032_orf_3p	12240
S1M10000014C09	1882	SAU102881	5740	SAU1c0032_orf_4p	12242
S1M10000014C10	1883	SAU302901	5912	SAU3c1497_orf_8p	13146
S1M10000014C11	1884	SAU100514	5281	SAU1c0044_orf_57p	12626
S1M10000014C12	1885	SAU101814	5551	SAU1c0032_orf_32p	12237
S1M10000014C12	1885	SAU101815	5552	SAU1c0032_orf_33p	12238
S1M10000014D03	1886	SAU100885	5348	SAU1c0038_orf_38p	12376
S1M10000014D06	1887	SAU100305	5256	SAU1c0038_orf_77p	12397
S1M10000014D08	1888	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000014D09	1889	SAU100808	5332	SAU1c0037_orf_12p	12345
S1M10000014D10	1890	SAU102292	5638	SAU1c0038_orf_10p	12368
S1M10000014E01	1891	SAU101793	5534	SAU1c0032_orf_14p	12218
S1M10000014E01	1891	SAU101794	5535	#N/A	#N/A
S1M10000014E04	1892	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000014E05	1893	SAU101565	5480	SAU1c0022_orf_8p	12151
S1M10000014E07	1894	SAU100658	5303	SAU1c0038_orf_59p	12388
S1M10000014E07	1894	SAU100659	5304	SAU1c0038_orf_60p	12390
S1M10000014E08	1895	SAU202176	5846	SAU2c0412_orf_3p	12895
S1M10000014E09	1896	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000014E09	1896	SAU300269	5869	#N/A	#N/A
S1M10000014E10	1897	SAU102453	5677	SAU1c0045_orf_19p	12669
S1M10000014E12	1898	SAU102284	5635	SAU1c0038_orf_5p	12389
S1M10000014E12	1898	SAU201469	5816	SAU2c0438_orf_6p	12967
S1M10000014F02	1899	SAU100128	5231	#N/A	#N/A
S1M10000014F02	1899	SAU101549	5476	SAU1c0043_orf_64p	12549
S1M10000014F02	1899	SAU101576	5488	SAU1c0044_orf_105p	12554
S1M10000014F03	1900	SAU102200	5611	SAU1c0045_orf_168p	12665
S1M10000014F03	1900	SAU102201	5612	SAU1c0045_orf_169p	12666
S1M10000014F04	1901	SAU102449	5674	SAU1c0045_orf_22p	12677
S1M10000014F05	1902	SAU200914	5796	SAU2c0373_orf_2p	12837
S1M10000014F08	1903	SAU102433	5668	SAU1c0045_orf_37p	12701
S1M10000014F09	1904	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000014F09	1904	SAU300269	5869	#N/A	#N/A
S1M10000014F10	1905	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000014G02	1906	SAU102054	5596	SAU1c0039_orf_74p	12417
S1M10000014G04	1907	SAU101242	5404	SAU1c0044_orf_18p	12578
S1M10000014G06	1908	SAU100275	5252	SAU1c0036_orf_15p	12314

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
S1M10000014G07	1909	SAU201620	5827	#N/A	#N/A
S1M10000014G08	1910	SAU100157	5237	SAU1c0040_orf_81p	12444
S1M10000014G12	1911	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000014H02	1912	SAU100242	5246	SAU1c0036_orf_5p	12336
S1M10000014H03	1913	SAU102264	5628	SAU1c0032_orf_60p	12250
S1M10000014H04	1914	SAU100275	5252	SAU1c0036_orf_15p	12314
S1M10000014H05	1915	SAU102116	5602	SAU1c0027_orf_5p	12180
S1M10000014H06	1916	SAU100275	5252	SAU1c0036_orf_15p	12314
S1M10000014H07	1917	SAU103038	5757	#N/A	#N/A
S1M10000014H08	1918	SAU100157	5237	SAU1c0040_orf_81p	12444
S1M10000014H11	1919	SAU102534	5696	#N/A	#N/A
S1M10000015A02	1920	SAU100865	5343	SAU1c0044_orf_99p	12648
S1M10000015A03	1921	SAU102388	5655	SAU1c0033_orf_35p	12267
S1M10000015A05	1922	SAU101815	5552	SAU1c0032_orf_33p	12238
S1M10000015A06	1923	SAU101857	5560	SAU1c0044_orf_156p	12569
S1M10000015A09	1924	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000015A10	1925	SAU103038	5757	#N/A	#N/A
S1M10000015A11	1926	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000015A12	1927	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000015B02	1928	SAU102340	5647	SAU1c0045_orf_149p	12660
S1M10000015B05	1929	SAU103038	5757	#N/A	#N/A
S1M10000015B08	1930	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000015B08	1930	SAU101792	5533	SAU1c0032_orf_13p	12217
S1M10000015B09	1931	SAU102585	5703	SAU1c0044_orf_289p	12611
S1M10000015B09	1931	SAU201773	5834	SAU2c0446_orf_4p	12996
S1M10000015B09	1931	SAU302685	5908	SAU3c1403_orf_1p	13113
S1M10000015B10	1932	SAU102308	5642	SAU1c0045_orf_50p	12706
S1M10000015C01	1933	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000015C02	1934	SAU102340	5647	SAU1c0045_orf_149p	12660
S1M10000015C03	1935	SAU102390	5657	SAU1c0033_orf_38p	12269
S1M10000015C03	1935	SAU201333	5810	SAU2c0418_orf_8p	12905
S1M10000015C05	1936	SAU100690	5309	#N/A	#N/A
S1M10000015C06	1937	SAU101815	5552	SAU1c0032_orf_33p	12238
S1M10000015C08	1938	SAU100133	5233	SAU1c0044_orf_170p	12574
S1M10000015C08	1938	SAU100323	5261	SAU1c0044_orf_171p	12575
S1M10000015C10	1939	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000015C12	1940	SAU100305	5256	SAU1c0038_orf_77p	12397
S1M10000015D02	1941	SAU100794	5330	SAU1c0028_orf_53p	12189
S1M10000015D03	1942	SAU102032	5591	SAU1c0029_orf_47p	12198
S1M10000015D04	1943	SAU100131	5232	SAU1c0043_orf_156p	12517
S1M10000015D05	1944	SAU100793	5329	SAU1c0028_orf_52p	12188
S1M10000015D06	1945	SAU100736	5316	SAU1c0038_orf_64p	12391
S1M10000015D12	1946	SAU101814	5551	SAU1c0032_orf_32p	12237
S1M10000015E02	1947	SAU102390	5657	SAU1c0033_orf_38p	12269
S1M10000015E02	1947	SAU201333	5810	SAU2c0418_orf_8p	12905
S1M10000015E03	1948	SAU200468	5781	SAU2c0429_orf_19p	12937
S1M10000015E06	1949	SAU101320	5420	SAU1c0015_orf_16p	12128
S1M10000015E07	1950	SAU101545	5474	SAU1c0037_orf_132p	12348

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000015E10	1952	SAU100114	5228	SAU1c0043_orf_225p	12535
S1M10000015E11	1953	SAU102286	5636	SAU1c0038_orf_6p	12393
S1M10000015E11	1953	SAU102287	5637	SAU1c0038_orf_7p	12398
S1M10000015E12	1954	SAU102352	5650	SAU1c0040_orf_38p	12434
S1M10000015F01	1955	SAU100123	5230	SAU1c0043_orf_189p	12526
S1M10000015F01	1955	SAU102001	5586	SAU1c0040_orf_102p	12424
S1M10000015F01	1955	SAU103159	5762	SAU1c0045_orf_204p	12670
S1M10000015F01	1955	SAU201827	5837	SAU2c0449_orf_21p	13002
S1M10000015F02	1956	SAU101561	5479	SAU1c0022_orf_4p	12149
S1M10000015F03	1957	SAU201403	5815	SAU2c0423_orf_3p	12913
S1M10000015F04	1958	SAU201403	5815	SAU2c0423_orf_3p	12913
S1M10000015F06	1959	SAU201385	5814	#N/A	#N/A
S1M10000015F07	1960	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000015F08	1961	SAU102102	5600	SAU1c0045_orf_340p	12696
S1M10000015F09	1962	SAU101800	5540	SAU1c0032_orf_20p	12225
S1M10000015F09	1962	SAU101801	5541	#N/A	#N/A
S1M10000015F10	1963	SAU100114	5228	SAU1c0043_orf_225p	12535
S1M10000015G01	1964	SAU102481	5685	SAU1c0039_orf_99p	12422
S1M10000015G02	1965	SAU200058	5773	SAU2c0134_orf_1p	12719
S1M10000015G02	1965	SAU200059	5774	SAU2c0134_orf_3p	12720
S1M10000015G03	1966	SAU101070	5376	SAU1c0034_orf_60p	12291
S1M10000015G04	1967	SAU101242	5404	SAU1c0044_orf_18p	12578
S1M10000015G05	1968	SAU101573	5485	SAU1c0044_orf_212p	12587
S1M10000015G06	1969	SAU101156	5386	SAU1c0036_orf_12p	12311
S1M10000015G07	1970	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000015G08	1971	SAU101814	5551	SAU1c0032_orf_32p	12237
S1M10000015G09	1972	SAU102143	5607	SAU1c0041_orf_14p	12458
S1M10000015G09	1972	SAU102144	5608	SAU1c0041_orf_15p	12459
S1M10000015G10	1973	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000015G11	1974	SAU100275	5252	SAU1c0036_orf_15p	12314
S1M10000015H04	1975	SAU101801	5541	#N/A	#N/A
S1M10000015H04	1975	SAU101802	5542	SAU1c0032_orf_22p	12227
S1M10000015H06	1976	SAU201385	5814	#N/A	#N/A
S1M10000016A03	1977	SAU101803	5543	SAU1c0032_orf_23p	12228
S1M10000016A03	1977	SAU101804	5544	#N/A	#N/A
S1M10000016A04	1978	SAU100432	5271	SAU1c0040_orf_88p	12450
S1M10000016A04	1978	SAU100433	5272	SAU1c0040_orf_87p	12449
S1M10000016A06	1979	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000016A07	1980	SAU100932	5356	SAU1c0044_orf_308p	12615
S1M10000016A09	1981	SAU101067	5375	SAU1c0034_orf_58p	12290
S1M10000016A09	1981	SAU300732	5877	SAU3c1116_orf_1p	13061
S1M10000016A10	1982	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000016A12	1983	SAU100522	5284	SAU1c0044_orf_249p	12599
S1M10000016B02	1984	SAU102449	5674	SAU1c0045_orf_22p	12677
S1M10000016B05	1985	SAU101320	5420	SAU1c0015_orf_16p	12128
S1M10000016B06	1986	SAU100432	5271	SAU1c0040_orf_88p	12450
S1M10000016B06	1986	SAU100433	5272	SAU1c0040_orf_87p	12449

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
S1M10000016B07	1987	SAU103077	5759	SAU1c0039_orf_44p	12408
S1M10000016B08	1988	SAU101491	5464	SAU1c0025_orf_20p	12165
S1M10000016B09	1989	SAU301465	5896	SAU3c1429_orf_4p	13121
S1M10000016B10	1990	SAU101006	5367	SAU1c0028_orf_59p	12190
S1M10000016B11	1991	SAU101242	5404	SAU1c0044_orf_18p	12578
S1M10000016B12	1992	SAU101794	5535	#N/A	#N/A
S1M10000016B12	1992	SAU101795	5536	SAU1c0032_orf_15p	12219
S1M10000016C01	1993	SAU100845	5340	SAU1c0036_orf_41p	12329
S1M10000016C02	1994	SAU102049	5595	SAU1c0039_orf_68p	12416
S1M10000016C04	1995	SAU100921	5355	SAU1c0038_orf_76p	12396
S1M10000016C05	1996	SAU101777	5527	SAU1c0037_orf_39p	12352
S1M10000016C06	1997	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000016C06	1997	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000016C06	1997	SAU301148	5888	#N/A	#N/A
S1M10000016C08	1998	SAU101491	5464	SAU1c0025_orf_20p	12165
S1M10000016C09	1999	SAU102233	5616	SAU1c0043_orf_20p	12531
S1M10000016C10	2000	SAU201513	5820	SAU2c0432_orf_10p	12944
S1M10000016C10	2000	SAU203196	5861	SAU2c0432_orf_11p	12945
S1M10000016C11	2001	SAU101573	5485	SAU1c0044_orf_212p	12587
S1M10000016C12	2002	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000016D01	2003	SAU102355	5651	SAU1c0040_orf_40p	12435
S1M10000016D02	2004	SAU200242	5777	SAU2c0250_orf_2p	12734
S1M10000016D04	2005	SAU100921	5355	SAU1c0038_orf_76p	12396
S1M10000016D05	2006	SAU100770	5324	#N/A	#N/A
S1M10000016D06	2007	SAU100952	5358	SAU1c0043_orf_182p	12523
S1M10000016D08	2008	SAU101070	5376	SAU1c0034_orf_60p	12291
S1M10000016D09	2009	SAU101868	5565	SAU1c0036_orf_23p	12320
S1M10000016D10	2010	SAU201513	5820	SAU2c0432_orf_10p	12944
S1M10000016D10	2010	SAU203196	5861	SAU2c0432_orf_11p	12945
S1M10000016D11	2011	SAU101573	5485	SAU1c0044_orf_212p	12587
S1M10000016E04	2012	SAU101371	5435	SAU1c0033_orf_7p	12275
S1M10000016E05	2013	SAU101320	5420	SAU1c0015_orf_16p	12128
S1M10000016E06	2014	SAU102639	5724	#N/A	#N/A
S1M10000016E07	2015	SAU102636	5722	SAU1c0045_orf_101p	12650
S1M10000016E07	2015	SAU102637	5723	SAU1c0045_orf_102p	12651
S1M10000016E08	2016	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000016E09	2017	SAU102527	5693	SAU1c0032_orf_9p	12260
S1M10000016E10	2018	SAU102983	5751	SAU1c0045_orf_224p	12676
S1M10000016E11	2019	SAU102281	5633	SAU1c0038_orf_4p	12384
S1M10000016E12	2020	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000016F02	2021	SAU102113	5601	SAU1c0027_orf_2p	12178
S1M10000016F02	2021	SAU301223	5889	SAU3c1345_orf_3p	13090
S1M10000016F03	2022	SAU101864	5562	SAU1c0044_orf_163p	12572
S1M10000016F05	2023	SAU201168	5804	SAU2c0407_orf_8p	12889
S1M10000016F06	2024	SAU102407	5662	#N/A	#N/A
S1M10000016F08	2025	SAU101491	5464	SAU1c0025_orf_20p	12165
S1M10000016F09	2026	SAU102527	5693	SAU1c0032_orf_9p	12260
S1M10000016F11	2027	SAU102113	5601	SAU1c0027_orf_2p	12178

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
S1M10000016F11	2027	SAU301223	5889	SAU3c1345_orf_3p	13090
S1M10000016G01	2028	SAU102434	5669	SAU1c0045_orf_36p	12700
S1M10000016G03	2029	SAU101300	5415	SAU1c0044_orf_113p	12557
S1M10000016G03	2029	SAU101365	5432	SAU1c0044_orf_112p	12556
S1M10000016G04	2030	SAU102450	5675	SAU1c0045_orf_21p	12675
S1M10000016G05	2031	SAU102292	5638	SAU1c0038_orf_10p	12368
S1M10000016H03	2032	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000016H04	2033	SAU101545	5474	SAU1c0037_orf_132p	12348
S1M10000016H08	2034	SAU101067	5375	SAU1c0034_orf_58p	12290
S1M10000016H08	2034	SAU300732	5877	SAU3c1116_orf_1p	13061
S1M10000016H10	2035	SAU101756	5524	SAU1c0040_orf_82p	12445
S1M10000017A02	2036	SAU101866	5564	SAU1c0036_orf_21p	12319
S1M10000017A03	2037	SAU101545	5474	SAU1c0037_orf_132p	12348
S1M10000017A03	2037	SAU101546	5475	SAU1c0037_orf_133p	12349
S1M10000017A04	2038	SAU102292	5638	SAU1c0038_orf_10p	12368
S1M10000017A08	2039	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000017A11	2040	SAU102437	5670	SAU1c0045_orf_33p	12695
S1M10000017A12	2041	SAU301357	5893	SAU3c1394_orf_2p	13111
S1M10000017B02	2042	SAU102242	5618	SAU1c0043_orf_26p	12540
S1M10000017B05	2043	SAU302513	5906	SAU3c1298_orf_1p	13085
S1M10000017B07	2044	SAU101806	5546	SAU1c0032_orf_25p	12230
S1M10000017B08	2045	SAU101546	5475	SAU1c0037_orf_133p	12349
S1M10000017B09	2046	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000017B10	2047	SAU101754	5523	SAU1c0040_orf_84p	12446
S1M10000017B11	2048	SAU101754	5523	SAU1c0040_orf_84p	12446
S1M10000017B12	2049	SAU201375	5811	SAU2c0426_orf_4p	12926
S1M10000017C01	2050	SAU101224	5397	SAU1c0044_orf_98p	12647
S1M10000017C03	2051	SAU101910	5576	SAU1c0040_orf_76p	12440
S1M10000017C05	2052	SAU200657	5789	#N/A	#N/A
S1M10000017C08	2053	SAU101890	5570	SAU1c0034_orf_29p	12280
S1M10000017C09	2054	SAU101398	5442	SAU1c0036_orf_33p	12324
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S1M10000017C10	2055	SAU102615	5717	SAU1c0041_orf_57p	12477
S1M10000017C11	2056	SAU101799	5539	SAU1c0032_orf_19p	12223
S1M10000017C11	2056	SAU101800	5540	SAU1c0032_orf_20p	12225
S1M10000017C12	2057	SAU101782	5529	SAU1c0037_orf_44p	12354
S1M10000017C12	2057	SAU200994	5802	SAU2c0428_orf_4p	12935
S1M10000017D03	2058	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000017D09	2059	SAU101799	5539	SAU1c0032_orf_19p	12223
S1M10000017D09	2059	SAU101800	5540	SAU1c0032_orf_20p	12225
S1M10000017D10	2060	SAU100633	5301	SAU1c0043_orf_147p	12515
S1M10000017E04	2061	SAU101801	5541	#N/A	#N/A
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S1M10000017E08	2063	SAU101198	5394	SAU1c0035_orf_61p	12301
S1M10000017E11	2064	SAU102883	5741	SAU1c0045_orf_38p	12702
S1M10000017F01	2065	SAU100157	5237	SAU1c0040_orf_81p	12444
S1M10000017F04	2066	SAU100140	5235	SAU1c0032_orf_7p	12258
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000017F11	2069	SAU101463	5458	SAU1c0045_orf_232p	12679
S1M10000017G02	2070	SAU102433	5668	SAU1c0045_orf_37p	12701
S1M10000017G05	2071	SAU102259	5624	SAU1c0032_orf_55p	12245
S1M10000017G06	2072	SAU200565	5785	SAU2c0324_orf_7p	12781
S1M10000018A03	2073	SAU100139	5234	SAU1c0032_orf_6p	12255
S1M10000018A03	2073	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000018A04	2074	SAU102142	5606	SAU1c0041_orf_13p	12457
S1M10000018A05	2075	SAU100886	5349	SAU1c0018_orf_16p	12139
S1M10000018A05	2075	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000018A06	2076	SAU100970	5365	SAU1c0043_orf_197p	12529
S1M10000018A08	2077	SAU100139	5234	SAU1c0032_orf_6p	12255
S1M10000018A08	2077	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000018A09	2078	SAU102142	5606	SAU1c0041_orf_13p	12457
S1M10000018A10	2079	SAU100866	5344	SAU1c0044_orf_100p	12553
S1M10000018A11	2080	SAU100139	5234	SAU1c0032_orf_6p	12255
S1M10000018A11	2080	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000018B02	2081	SAU100886	5349	SAU1c0018_orf_16p	12139
S1M10000018B02	2081	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000018B03	2082	SAU101839	5556	SAU1c0042_orf_12p	12495
S1M10000018B05	2083	SAU100300	5253	SAU1c0040_orf_90p	12451
S1M10000018B09	2084	SAU100836	5336	SAU1c0031_orf_13p	12212
S1M10000018B09	2084	SAU202731	5850	#N/A	#N/A
S1M10000018B10	2085	SAU100401	5268	SAU1c0044_orf_174p	12576
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S1M10000018C02	2088	SAU102447	5672	SAU1c0045_orf_24p	12685
S1M10000018C03	2089	SAU100778	5328	SAU1c0043_orf_140p	12514
S1M10000018C04	2090	SAU100141	5236	SAU1c0032_orf_8p	12259
S1M10000018C05	2091	SAU103038	5757	#N/A	#N/A
S1M10000018C06	2092	SAU100684	5306	SAU1c0044_orf_68p	12632
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S1M10000018C09	2094	SAU101065	5374	SAU1c0034_orf_56p	12289
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S1M10000018C10	2095	SAU100112	5227	SAU1c0044_orf_70p	12634
S1M10000018C11	2096	SAU102663	5727	SAU1c0024_orf_2p	12158
S1M10000018C12	2097	SAU101948	5579	SAU1c0045_orf_69p	12709
S1M10000018D01	2098	SAU101452	5455	SAU1c0045_orf_247p	12684
S1M10000018D02	2099	SAU102284	5635	SAU1c0038_orf_5p	12389
S1M10000018D02	2099	SAU201469	5816	SAU2c0438_orf_6p	12967
S1M10000018D03	2100	SAU101793	5534	SAU1c0032_orf_14p	12218
S1M10000018D04	2101	SAU101798	5538	SAU1c0032_orf_18p	12222
S1M10000018D09	2102	SAU101067	5375	SAU1c0034_orf_58p	12290
S1M10000018D10	2103	SAU301898	5904	SAU3c1079_orf_1p	13057
S1M10000018D11	2104	SAU101752	5522	SAU1c0040_orf_85p	12447

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S1M10000018E02	2107	SAU100265	5249	SAU1c0014_orf_11p	12122
S1M10000018E03	2108	SAU102420	5665	SAU1c0030_orf_20p	12206
S1M10000018E04	2109	SAU102035	5592	SAU1c0029_orf_50p	12199
S1M10000018E05	2110	SAU100596	5295	SAU1c0043_orf_63p	12548
S1M10000018E08	2111	SAU100793	5329	SAU1c0028_orf_52p	12188
S1M10000018E09	2112	SAU301898	5904	SAU3c1079_orf_1p	13057
S1M10000018E11	2113	SAU101799	5539	SAU1c0032_orf_19p	12223
S1M10000018E11	2113	SAU101800	5540	SAU1c0032_orf_20p	12225
S1M10000018E12	2114	SAU200914	5796	SAU2c0373_orf_2p	12837
S1M10000018F03	2115	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000018F04	2116	SAU102396	5660	SAU1c0033_orf_43p	12272
S1M10000018F04	2116	SAU301118	5886	SAU3c1305_orf_3p	13086
S1M10000018F07	2117	SAU102629	5720	SAU1c0041_orf_71p	12481
S1M10000018F09	2118	SAU101810	5549	SAU1c0032_orf_28p	12233
S1M10000018F09	2118	SAU300110	5865	SAU3c0533_orf_2p	13031
S1M10000018F10	2119	SAU100432	5271	SAU1c0040_orf_88p	12450
S1M10000018F10	2119	SAU100433	5272	SAU1c0040_orf_87p	12449
S1M10000018F12	2120	SAU201469	5816	SAU2c0438_orf_6p	12967
S1M10000018G03	2121	SAU101808	5548	SAU1c0032_orf_27p	12232
S1M10000018G05	2122	SAU101999	5585	SAU1c0040_orf_101p	12423
S1M10000018G07	2123	SAU101727	5516	SAU1c0016_orf_6p	12133
S1M10000018G08	2124	SAU102200	5611	SAU1c0045_orf_168p	12665
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S1M10000018G10	2126	SAU100141	5236	SAU1c0032_orf_8p	12259
S1M10000018G10	2126	SAU102527	5693	SAU1c0032_orf_9p	12260
S1M10000018G12	2127	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000018H01	2128	SAU101663	5506	SAU1c0033_orf_14p	12261
S1M10000018H02	2129	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000018H02	2129	SAU101653	5504	SAU1c0042_orf_124p	12493
S1M10000018H07	2130	SAU102437	5670	SAU1c0045_orf_33p	12695
S1M10000018H09	2131	SAU101622	5496	SAU1c0040_orf_27p	12430
S1M10000018H10	2132	SAU100157	5237	SAU1c0040_orf_81p	12444
S1M10000019A02	2133	SAU103077	5759	SAU1c0039_orf_44p	12408
S1M10000019A03	2134	SAU102352	5650	SAU1c0040_orf_38p	12434
S1M10000019A05	2135	SAU201469	5816	SAU2c0438_orf_6p	12967
S1M10000019A06	2136	SAU101311	5419	SAU1c0044_orf_126p	12563
S1M10000019A07	2137	SAU101727	5516	SAU1c0016_orf_6p	12133
S1M10000019A07	2137	SAU101728	5517	SAU1c0016_orf_5p	12132
S1M10000019A09	2138	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000019A11	2139	SAU102292	5638	SAU1c0038_orf_10p	12368
S1M10000019A12	2140	SAU102693	5731	SAU1c0044_orf_58p	12627
S1M10000019A12	2140	SAU102694	5732	SAU1c0044_orf_59p	12628
S1M10000019B03	2141	SAU101156	5386	SAU1c0036_orf_12p	12311
S1M10000019B04	2142	SAU100899	5351	SAU1c0034_orf_11p	12277

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000019B08	2144	SAU102423	5667	SAU1c0030_orf_23p	12208
S1M10000019B09	2145	SAU100182	5241	SAU1c0037_orf_82p	12362
S1M10000019B09	2145	SAU100251	5248	SAU1c0037_orf_83p	12363
S1M10000019B10	2146	SAU101570	5482	SAU1c0044_orf_209p	12584
S1M10000019B11	2147	SAU100879	5345	SAU1c0041_orf_82p	12483
S1M10000019B12	2148	SAU101793	5534	SAU1c0032_orf_14p	12218
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S1M10000019C04	2150	SAU103175	5764	SAU1c0045_orf_269p	12687
S1M10000019C04	2150	SAU301472	5897	SAU3c1431_orf_4p	13124
S1M10000019C05	2151	SAU101756	5524	SAU1c0040_orf_82p	12445
S1M10000019C06	2152	SAU101790	5531	SAU1c0032_orf_11p	12215
S1M10000019C06	2152	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000019C07	2153	SAU101400	5444	SAU1c0036_orf_35p	12326
S1M10000019C08	2154	SAU202126	5844	SAU2c0045_orf_1p	12714
S1M10000019C11	2155	SAU100301	5254	SAU1c0040_orf_91p	12452
S1M10000019C12	2156	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000019D01	2157	SAU102270	5631	SAU1c0032_orf_65p	12253
S1M10000019D02	2158	SAU101145	5384	SAU1c0035_orf_43p	12299
S1M10000019D04	2159	SAU102292	5638	SAU1c0038_orf_10p	12368
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S1M10000019E01	2165	SAU100962	5361	SAU1c0044_orf_84p	12639
S1M10000019E02	2166	SAU101624	5497	SAU1c0040_orf_25p	12429
S1M10000019E07	2167	SAU102352	5650	SAU1c0040_orf_38p	12434
S1M10000019F01	2168	SAU102241	5617	SAU1c0043_orf_25p	12539
S1M10000019F05	2169	SAU101612	5493	SAU1c0044_orf_7p	12637
S1M10000019F05	2169	SAU202945	5857	SAU2c0394_orf_7p	12868
S1M10000019F06	2170	SAU101864	5562	SAU1c0044_orf_163p	12572
S1M10000019F08	2171	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000019F09	2172	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000019F11	2173	SAU101242	5404	SAU1c0044_orf_18p	12578
S1M10000019G04	2174	SAU101793	5534	SAU1c0032_orf_14p	12218
S1M10000019G07	2175	SAU100522	5284	SAU1c0044_orf_249p	12599
S1M10000019G09	2176	SAU100300	5253	SAU1c0040_orf_90p	12451
S1M10000019G10	2177	SAU101235	5400	SAU1c0044_orf_11p	12561
S1M10000019G10	2177	SAU101236	5401	SAU1c0044_orf_12p	12564
S1M10000019G11	2178	SAU101802	5542	SAU1c0032_orf_22p	12227
S1M10000019H05	2179	SAU101802	5542	SAU1c0032_orf_22p	12227
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S1M10000019H08	2180	SAU102449	5674	SAU1c0045_orf_22p	12677
S1M10000020A05	2181	SAU101868	5565	SAU1c0036_orf_23p	12320

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S1M10000020A07	2183	SAU101567	5481	SAU1c0022_orf_10p	12144
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S1M10000020A11	2184	SAU102437	5670	SAU1c0045_orf_33p	12695
S1M10000020A12	2185	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000020B02	2186	SAU100475	5276	SAU1c0036_orf_61p	12337
S1M10000020B03	2187	SAU100059	5224	SAU1c0045_orf_10p	12652
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S1M10000020B12	2192	SAU102143	5607	SAU1c0041_orf_14p	12458
S1M10000020C09	2193	SAU101545	5474	SAU1c0037_orf_132p	12348
S1M10000020C10	2194	SAU101799	5539	SAU1c0032_orf_19p	12223
S1M10000020C10	2194	SAU101800	5540	SAU1c0032_orf_20p	12225
S1M10000020C11	2195	SAU101452	5455	SAU1c0045_orf_247p	12684
S1M10000020D03	2196	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000020D04	2197	SAU102481	5685	SAU1c0039_orf_99p	12422
S1M10000020D06	2198	SAU102578	5701	SAU1c0039_orf_61p	12411
S1M10000020D07	2199	SAU100198	5243	SAU1c0009_orf_1p	12120
S1M10000020D08	2200	SAU100547	5290	SAU1c0032_orf_3p	12240
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S1M10000020E04	2205	SAU101805	5545	SAU1c0032_orf_24p	12229
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S1M10000020E08	2207	SAU101756	5524	SAU1c0040_orf_82p	12445
S1M10000020E11	2208	SAU101876	5567	SAU1c0025_orf_9p	12169
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S1M10000020F05	2211	SAU100547	5290	SAU1c0032_orf_3p	12240
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S1M10000020F07	2213	SAU200731	5793	SAU2c0352_orf_2p	12808
S1M10000020F09	2214	SAU100114	5228	SAU1c0043_orf_225p	12535
S1M10000020F11	2215	SAU101663	5506	SAU1c0033_orf_14p	12261
S1M10000020F11	2215	SAU101664	5507	SAU1c0033_orf_15p	12262
S1M10000020F12	2216	SAU100745	5319	SAU1c0044_orf_233p	12596
S1M10000020G01	2217	SAU102905	5742	SAU1c0033_orf_45p	12273
S1M10000020G05	2218	SAU100114	5228	SAU1c0043_orf_225p	12535
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S1M10000020G10	2222	SAU101807	5547	SAU1c0032_orf_26p	12231
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S1M10000020G11	2223	SAU101592	5490	SAU1c0039_orf_37p	12406
S1M10000020G12	2224	SAU100865	5343	SAU1c0044_orf_99p	12648

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000020H04	2227	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000020H06	2228	SAU101541	5472	SAU1c0037_orf_128p	12344
S1M10000020H08	2229	SAU201558	5823	SAU2c0434_orf_5p	12954
S1M10000020H10	2230	SAU101754	5523	SAU1c0040_orf_84p	12446
S1M10000020H11	2231	SAU100053	5222	SAU1c0020_orf_1p	12143
S1M10000021A04	2232	SAU200752	5795	SAU2c0354_orf_5p	12809
S1M10000021A04	2232	SAU300975	5880	SAU3c1240_orf_3p	13075
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S1M10000021A06	2234	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000021A07	2235	SAU100496	5279	SAU1c0041_orf_83p	12484
S1M10000021A07	2235	SAU301004	5882	SAU3c1255_orf_1p	13079
S1M10000021A08	2236	SAU101183	5390	SAU1c0035_orf_79p	12304
S1M10000021A09	2237	SAU102933	5744	SAU1c0039_orf_62p	12412
S1M10000021A09	2237	SAU201184	5805	SAU2c0351_orf_19p	12807
S1M10000021A10	2238	SAU101545	5474	SAU1c0037_orf_132p	12348
S1M10000021B05	2239	SAU100139	5234	SAU1c0032_orf_6p	12255
S1M10000021B05	2239	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000021B06	2240	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000021B07	2241	SAU101632	5499	SAU1c0039_orf_3p	12407
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S1M10000021C04	2243	SAU200928	5798	SAU2c0365_orf_5p	12815
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S1M10000021C08	2246	SAU102575	5700	SAU1c0044_orf_283p	12609
S1M10000021C10	2247	SAU101320	5420	SAU1c0015_orf_16p	12128
S1M10000021C11	2248	SAU200006	5770	SAU2c0157_orf_1p	12723
S1M10000021C12	2249	SAU101726	5515	SAU1c0016_orf_7p	12134
S1M10000021D01	2250	SAU102503	5691	SAU1c0045_orf_274p	12690
S1M10000021D03	2251	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000021D03	2251	SAU101286	5413	SAU1c0034_orf_67p	12292
S1M10000021D04	2252	SAU100858	5341	SAU1c0038_orf_86p	12401
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S1M10000021D06	2253	SAU100865	5343	SAU1c0044_orf_99p	12648
S1M10000021D09	2254	SAU101868	5565	SAU1c0036_orf_23p	12320
S1M10000021D10	2255	SAU100714	5312	SAU1c0044_orf_74p	12635
S1M10000021E01	2256	SAU101655	5505	SAU1c0042_orf_125p	12494
S1M10000021E02	2257	SAU102200	5611	SAU1c0045_orf_168p	12665
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S1M10000021E03	2258	SAU101857	5560	SAU1c0044_orf_156p	12569
S1M10000021E05	2259	SAU101777	5527	SAU1c0037_orf_39p	12352
S1M10000021E06	2260	SAU102663	5727	SAU1c0024_orf_2p	12158
S1M10000021E09	2261	SAU200006	5770	SAU2c0157_orf_1p	12723
S1M10000021E12	2262	SAU102292	5638	SAU1c0038_orf_10p	12368
S1M10000021F02	2263	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000021F04	2264	SAU100139	5234	SAU1c0032_orf_6p	12255
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000021F06	2266	SAU101235	5400	SAU1c0044_orf_11p	12561
S1M10000021F07	2267	SAU101383	5438	SAU1c0022_orf_20p	12147
S1M10000021F09	2268	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000021F09	2268	SAU301465	5896	SAU3c1429_orf_4p	13121
S1M10000021F11	2269	SAU101371	5435	SAU1c0033_orf_7p	12275
S1M10000021G01	2270	SAU200468	5781	SAU2c0429_orf_19p	12937
S1M10000021G03	2271	SAU301357	5893	SAU3c1394_orf_2p	13111
S1M10000021G08	2272	SAU100714	5312	SAU1c0044_orf_74p	12635
S1M10000021H04	2273	SAU100139	5234	SAU1c0032_orf_6p	12255
S1M10000021H04	2273	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000021H05	2274	SAU300131	5866	SAU3c0560_orf_2p	13034
S1M10000021H07	2275	SAU101806	5546	SAU1c0032_orf_25p	12230
S1M10000021H08	2276	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000021H11	2277	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000022A02	2278	SAU100865	5343	SAU1c0044_orf_99p	12648
S1M10000022A02	2278	SAU301230	5890	SAU3c1347_orf_6p	13092
S1M10000022A03	2279	SAU201197	5806	SAU2c0429_orf_2p	12938
S1M10000022A05	2280	SAU101807	5547	SAU1c0032_orf_26p	12231
S1M10000022A08	2281	SAU101365	5432	SAU1c0044_orf_112p	12556
S1M10000022A09	2282	SAU102939	5747	#N/A	#N/A
S1M10000022A12	2283	SAU101868	5565	SAU1c0036_orf_23p	12320
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S1M10000022B02	2284	SAU301230	5890	SAU3c1347_orf_6p	13092
S1M10000022B03	2285	SAU200468	5781	SAU2c0429_orf_19p	12937
S1M10000022B05	2286	SAU100920	5354	SAU1c0038_orf_75p	12395
S1M10000022B06	2287	SAU100714	5312	SAU1c0044_orf_74p	12635
S1M10000022B08	2288	SAU102292	5638	SAU1c0038_orf_10p	12368
S1M10000022B09	2289	SAU102939	5747	#N/A	#N/A
S1M10000022B10	2290	SAU101546	5475	SAU1c0037_orf_133p	12349
S1M10000022B11	2291	SAU101726	5515	SAU1c0016_orf_7p	12134
S1M10000022B12	2292	SAU101868	5565	SAU1c0036_orf_23p	12320
S1M10000022C02	2293	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000022C03	2294	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000022C04	2295	SAU100714	5312	SAU1c0044_orf_74p	12635
S1M10000022C06	2296	SAU100246	5247	SAU1c0042_orf_130p	12496
S1M10000022C06	2296	SAU300998	5881	SAU3c1253_orf_3p	13077
S1M10000022C07	2297	SAU101546	5475	SAU1c0037_orf_133p	12349
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S1M10000022C08	2298	SAU103115	5760	SAU1c0042_orf_88p	12508
S1M10000022C11	2299	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000022D03	2300	SAU101805	5545	SAU1c0032_orf_24p	12229
S1M10000022D05	2301	SAU101777	5527	SAU1c0037_orf_39p	12352
S1M10000022D06	2302	SAU100921	5355	SAU1c0038_orf_76p	12396
S1M10000022D07	2303	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000022D08	2304	SAU101189	5392	SAU1c0033_orf_25p	12264
S1M10000022D09	2305	SAU101726	5515	SAU1c0016_orf_7p	12134
S1M10000022D11	2306	SAU101447	5454	SAU1c0045_orf_244p	12683

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S1M10000022E03	2308	SAU200468	5781	SAU2c0429_orf_19p	12937
S1M10000022E05	2309	SAU301465	5896	SAU3c1429_orf_4p	13121
S1M10000022E09	2310	SAU101235	5400	SAU1c0044_orf_11p	12561
S1M10000022E09	2310	SAU101236	5401	SAU1c0044_orf_12p	12564
S1M10000022F04	2311	SAU101592	5490	SAU1c0039_orf_37p	12406
S1M10000022F06	2312	SAU101868	5565	SAU1c0036_orf_23p	12320
S1M10000022F07	2313	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000022F08	2314	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000022F11	2315	SAU101592	5490	SAU1c0039_orf_37p	12406
S1M10000022G03	2316	SAU301465	5896	SAU3c1429_orf_4p	13121
S1M10000022G04	2317	SAU101777	5527	SAU1c0037_orf_39p	12352
S1M10000022G07	2318	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000022G08	2319	SAU100557	5291	SAU1c0044_orf_132p	12565
S1M10000022G12	2320	SAU101546	5475	SAU1c0037_orf_133p	12349
S1M10000022H03	2321	SAU101006	5367	SAU1c0028_orf_59p	12190
S1M10000022H05	2322	SAU101814	5551	SAU1c0032_orf_32p	12237
S1M10000022H06	2323	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000022H07	2324	SAU100866	5344	SAU1c0044_orf_100p	12553
S1M10000022H08	2325	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000022H11	2326	SAU101610	5492	SAU1c0044_orf_5p	12629
S1M10000023A05	2327	SAU301465	5896	SAU3c1429_orf_4p	13121
S1M10000023A09	2328	SAU101340	5423	SAU1c0038_orf_82p	12400
S1M10000023A11	2329	SAU100547	5290	SAU1c0032_orf_3p	12240
S1M10000023A12	2330	SAU101651	5502	SAU1c0042_orf_122p	12491
S1M10000023A12	2330	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000023B01	2331	SAU100886	5349	SAU1c0018_orf_16p	12139
S1M10000023B03	2332	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000023B03	2332	SAU101653	5504	SAU1c0042_orf_124p	12493
S1M10000023B07	2333	SAU101857	5560	SAU1c0044_orf_156p	12569
S1M10000023B08	2334	SAU100140	5235	SAU1c0032_orf_7p	12258
S1M10000023B08	2334	SAU100141	5236	SAU1c0032_orf_8p	12259
S1M10000023B09	2335	SAU101340	5423	SAU1c0038_orf_82p	12400
S1M10000023B10	2336	SAU102578	5701	SAU1c0039_orf_61p	12411
S1M10000023B11	2337	SAU102613	5715	SAU1c0041_orf_55p	12475
S1M10000023B12	2338	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000023B12	2338	SAU301148	5888	#N/A	#N/A
S1M10000023C02	2339	SAU100140	5235	SAU1c0032_orf_7p	12258
S1M10000023C02	2339	SAU100141	5236	SAU1c0032_orf_8p	12259
S1M10000023C10	2340	SAU102554	5699	SAU1c0045_orf_209p	12673
S1M10000023C11	2341	SAU102352	5650	SAU1c0040_orf_38p	12434
S1M10000023C12	2342	SAU100077	5226	SAU1c0043_orf_178p	12520
S1M10000023D01	2343	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000023D03	2344	SAU101996	5584	SAU1c0040_orf_99p	12456
S1M10000023D04	2345	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000023D07	2346	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000023D08	2347	SAU100887	5350	SAU1c0018_orf_15p	12138
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S1M10000023E04	2352	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000023E07	2353	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000023E10	2354	SAU203293	5862	SAU2c0441_orf_21p	12979
S1M10000023E11	2355	SAU102292	5638	SAU1c0038_orf_10p	12368
S1M10000023F04	2356	SAU101736	5518	SAU1c0043_orf_166p	12519
S1M10000023F04	2356	SAU101737	5519	SAU1c0043_orf_165p	12518
S1M10000023F07	2357	SAU100546	5289	SAU1c0032_orf_2p	12235
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S1M10000023F10	2359	SAU102352	5650	SAU1c0040_orf_38p	12434
S1M10000023F11	2360	SAU100617	5300	SAU1c0035_orf_102p	12295
S1M10000023F12	2361	SAU102352	5650	SAU1c0040_orf_38p	12434
S1M10000023G02	2362	SAU301465	5896	SAU3c1429_orf_4p	13121
S1M10000023G03	2363	SAU101996	5584	SAU1c0040_orf_99p	12456
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S1M10000023G08	2366	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000023G09	2367	SAU101968	5581	SAU1c0028_orf_43p	12187
S1M10000023G11	2368	SAU102613	5715	SAU1c0041_orf_55p	12475
S1M10000023H02	2369	SAU101996	5584	SAU1c0040_orf_99p	12456
S1M10000023H06	2370	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000023H07	2371	SAU100300	5253	SAU1c0040_orf_90p	12451
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S1M10000023H10	2373	SAU101365	5432	SAU1c0044_orf_112p	12556
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S1M10000024A04	2375	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000024A07	2376	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000024A08	2377	SAU101231	5399	SAU1c0035_orf_6p	12303
S1M10000024A11	2378	SAU103226	5768	SAU1c0045_orf_95p	12713
S1M10000024B05	2379	SAU102418	5664	SAU1c0030_orf_18p	12205
S1M10000024B06	2380	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000024B08	2381	SAU100601	5296	SAU1c0044_orf_313p	12616
S1M10000024B09	2382	SAU200468	5781	SAU2c0429_orf_19p	12937
S1M10000024B10	2383	SAU101265	5407	#N/A	#N/A
S1M10000024C02	2384	SAU101197	5393	SAU1c0035_orf_60p	12300
S1M10000024C04	2385	SAU101862	5561	SAU1c0044_orf_161p	12571
S1M10000024C07	2386	SAU101039	5373	SAU1c0043_orf_181p	12522
S1M10000024D02	2387	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000024D03	2388	SAU100714	5312	SAU1c0044_orf_74p	12635
S1M10000024D10	2389	SAU100140	5235	SAU1c0032_orf_7p	12258
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S1M10000024D11	2390	SAU101198	5394	SAU1c0035_orf_61p	12301
S1M10000024E03	2391	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000024E05	2392	SAU101800	5540	SAU1c0032_orf_20p	12225
S1M10000024E05	2392	SAU101801	5541	#N/A	#N/A
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S1M10000024E08	2395	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000024F02	2396	SAU101447	5454	SAU1c0045_orf_244p	12683
S1M10000024F03	2397	SAU102992	5752	SAU1c0044_orf_60p	12630
S1M10000024F05	2398	SAU201197	5806	SAU2c0429_orf_2p	12938
S1M10000024F08	2399	SAU101726	5515	SAU1c0016_orf_7p	12134
S1M10000024F10	2400	SAU200468	5781	SAU2c0429_orf_19p	12937
S1M10000024G05	2401	SAU101800	5540	SAU1c0032_orf_20p	12225
S1M10000024G05	2401	SAU101801	5541	#N/A	#N/A
S1M10000024G06	2402	SAU102418	5664	SAU1c0030_orf_18p	12205
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S1M10000024G08	2404	SAU101632	5499	SAU1c0039_orf_3p	12407
S1M10000024G10	2405	SAU202176	5846	SAU2c0412_orf_3p	12895
S1M10000024G12	2406	SAU100141	5236	SAU1c0032_orf_8p	12259
S1M10000024H02	2407	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000024H04	2408	SAU100770	5324	#N/A	#N/A
S1M10000024H07	2409	SAU200725	5792	SAU2c0428_orf_20p	12933
S1M10000024H08	2410	SAU102002	5587	SAU1c0040_orf_103p	12425
S1M10000024H08	2410	SAU102003	5588	SAU1c0040_orf_104p	12426
S1M10000025A03	2411	SAU101247	5405	SAU1c0043_orf_136p	12512
S1M10000025A08	2412	SAU102766	5735	#N/A	#N/A
S1M10000025A08	2412	SAU201236	5808	SAU2c0409_orf_10p	12891
S1M10000025A08	2412	SAU300338	5871	#N/A	#N/A
S1M10000025A09	2413	SAU102292	5638	SAU1c0038_orf_10p	12368
S1M10000025A10	2414	SAU101455	5456	SAU1c0045_orf_250p	12686
S1M10000025A10	2414	SAU200916	5797	SAU2c0373_orf_4p	12838
S1M10000025A10	2414	SAU301620	5899	SAU3c1478_orf_2p	13140
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S1M10000025B12	2421	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000025C01	2422	SAU102292	5638	SAU1c0038_orf_10p	12368
S1M10000025C03	2423	SAU100139	5234	SAU1c0032_orf_6p	12255
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S1M10000025C09	2425	SAU100793	5329	SAU1c0028_orf_52p	12188
S1M10000025C09	2425	SAU301433	5895	SAU3c1420_orf_2p	13118
S1M10000025C10	2426	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000025C11	2427	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000025D01	2428	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000025D03	2429	SAU101771	5525	SAU1c0037_orf_33p	12350
S1M10000025D03	2429	SAU101772	5526	SAU1c0037_orf_34p	12351
S1M10000025D04	2430	SAU100970	5365	SAU1c0043_orf_197p	12529
S1M10000025D06	2431	SAU101543	5473	SAU1c0037_orf_130p	12346

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S1M10000025D08	2432	SAU103191	5765	SAU1c0041_orf_44p	12465
S1M10000025D09	2433	SAU100522	5284	SAU1c0044_orf_249p	12599
S1M10000025D10	2434	SAU102200	5611	SAU1c0045_orf_168p	12665
S1M10000025D10	2434	SAU102201	5612	SAU1c0045_orf_169p	12666
S1M10000025E01	2435	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000025E04	2436	SAU100389	5266	SAU1c0034_orf_14p	12279
S1M10000025E09	2437	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000025E11	2438	SAU102437	5670	SAU1c0045_orf_33p	12695
S1M10000025F03	2439	SAU102297	5640	SAU1c0045_orf_41p	12704
S1M10000025F05	2440	SAU102200	5611	SAU1c0045_orf_168p	12665
S1M10000025F05	2440	SAU102201	5612	SAU1c0045_orf_169p	12666
S1M10000025F08	2441	SAU200685	5790	SAU2c0344_orf_9p	12801
S1M10000025F09	2442	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000025F10	2443	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000025F12	2444	SAU102200	5611	SAU1c0045_orf_168p	12665
S1M10000025F12	2444	SAU102201	5612	SAU1c0045_orf_169p	12666
S1M10000025G04	2445	SAU300617	5874	SAU3c1046_orf_2p	13056
S1M10000025G06	2446	SAU300617	5874	SAU3c1046_orf_2p	13056
S1M10000025G10	2447	SAU101869	5566	SAU1c0036_orf_24p	12321
S1M10000025H05	2448	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000025H06	2449	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000025H07	2450	SAU200752	5795	SAU2c0354_orf_5p	12809
S1M10000025H07	2450	SAU300975	5880	SAU3c1240_orf_3p	13075
S1M10000025H10	2451	SAU100590	5293	SAU1c0013_orf_5p	12121
S1M10000025H10	2451	SAU301268	5891	SAU3c1364_orf_2p	13102
S1M10000026A02	2452	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000026A04	2453	SAU102340	5647	SAU1c0045_orf_149p	12660
S1M10000026A05	2454	SAU200934	5799	SAU2c0375_orf_9p	12842
S1M10000026A06	2455	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000026A07	2456	SAU100970	5365	SAU1c0043_orf_197p	12529
S1M10000026A08	2457	SAU100266	5250	SAU1c0032_orf_75p	12256
S1M10000026A09	2458	SAU102452	5676	SAU1c0045_orf_20p	12674
S1M10000026A09	2458	SAU102453	5677	SAU1c0045_orf_19p	12669
S1M10000026A10	2459	SAU100970	5365	SAU1c0043_orf_197p	12529
S1M10000026A11	2460	SAU102259	5624	SAU1c0032_orf_55p	12245
S1M10000026A11	2460	SAU102260	5625	SAU1c0032_orf_56p	12246
S1M10000026A11	2460	SAU102261	5626	SAU1c0032_orf_57p	12247
S1M10000026A11	2460	SAU300868	5879	#N/A	#N/A
S1M10000026B02	2461	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000026B03	2462	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000026B05	2463	SAU101546	5475	SAU1c0037_orf_133p	12349
S1M10000026B06	2464	SAU101570	5482	SAU1c0044_orf_209p	12584
S1M10000026B07	2465	SAU101341	5424	SAU1c0044_orf_38p	12618
S1M10000026B07	2465	SAU301275	5892	SAU3c1365_orf_2p	13103
S1M10000026B10	2466	SAU101592	5490	SAU1c0039_orf_37p	12406
S1M10000026B11	2467	SAU101999	5585	SAU1c0040_orf_101p	12423

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000026C01	2469	SAU100266	5250	SAU1c0032_orf_75p	12256
S1M10000026C06	2470	SAU101772	5526	SAU1c0037_orf_34p	12351
S1M10000026C07	2471	SAU101842	5557	SAU1c0042_orf_9p	12510
S1M10000026C08	2472	SAU100139	5234	SAU1c0032_orf_6p	12255
S1M10000026C11	2473	SAU200657	5789	#N/A	#N/A
S1M10000026C12	2474	SAU101726	5515	SAU1c0016_orf_7p	12134
S1M10000026D04	2475	SAU100658	5303	SAU1c0038_orf_59p	12388
S1M10000026D05	2476	SAU101491	5464	SAU1c0025_orf_20p	12165
S1M10000026D06	2477	SAU100139	5234	SAU1c0032_orf_6p	12255
S1M10000026D07	2478	SAU101815	5552	SAU1c0032_orf_33p	12238
S1M10000026D08	2479	SAU100690	5309	#N/A	#N/A
S1M10000026D10	2480	SAU203296	5863	SAU2c0442_orf_18p	12983
S1M10000026D12	2481	SAU100546	5289	SAU1c0032_orf_2p	12235
S1M10000026E01	2482	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000026E07	2483	SAU102939	5747	#N/A	#N/A
S1M10000026E09	2484	SAU102001	5586	SAU1c0040_orf_102p	12424
S1M10000026E09	2484	SAU102002	5587	SAU1c0040_orf_103p	12425
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S1M10000026E11	2486	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000026E12	2487	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000026F01	2488	SAU101784	5530	SAU1c0037_orf_46p	12355
S1M10000026F03	2489	SAU102200	5611	SAU1c0045_orf_168p	12665
S1M10000026F03	2489	SAU102201	5612	SAU1c0045_orf_169p	12666
S1M10000026F04	2490	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000026F05	2491	SAU100139	5234	SAU1c0032_orf_6p	12255
S1M10000026F06	2492	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000026F07	2493	SAU101869	5566	SAU1c0036_orf_24p	12321
S1M10000026F08	2494	SAU101756	5524	SAU1c0040_orf_82p	12445
S1M10000026F09	2495	SAU102939	5747	#N/A	#N/A
S1M10000026F10	2496	SAU101869	5566	SAU1c0036_orf_24p	12321
S1M10000026F11	2497	SAU102939	5747	#N/A	#N/A
S1M10000026F12	2498	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000026G01	2499	SAU101869	5566	SAU1c0036_orf_24p	12321
S1M10000026G03	2500	SAU100547	5290	SAU1c0032_orf_3p	12240
S1M10000026G04	2501	SAU100690	5309	#N/A	#N/A
S1M10000026G05	2502	SAU101756	5524	SAU1c0040_orf_82p	12445
S1M10000026G06	2503	SAU101784	5530	SAU1c0037_orf_46p	12355
S1M10000026G07	2504	SAU100886	5349	SAU1c0018_orf_16p	12139
S1M10000026G09	2505	SAU100542	5288	SAU1c0043_orf_210p	12532
S1M10000026G10	2506	SAU100613	5299	SAU1c0015_orf_14p	12126
S1M10000026G10	2506	SAU102812	5736	SAU1c0015_orf_15p	12127
S1M10000026G12	2507	SAU101551	5477	SAU1c0043_orf_67p	12550
S1M10000026H01	2508	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000026H02	2509	SAU102355	5651	SAU1c0040_orf_40p	12435
S1M10000026H03	2510	SAU101801	5541	#N/A	#N/A
S1M10000026H04	2511	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000026H04	2511	SAU202174	5845	SAU2c0412_orf_3p	12895

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000026H07	2513	SAU101807	5547	SAU1c0032_orf_26p	12231
S1M10000026H09	2514	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000026H09	2514	SAU301148	5888	#N/A	#N/A
S1M10000026H10	2515	SAU102479	5683	SAU1c0039_orf_101p	12405
S1M10000027A04	2516	SAU101756	5524	SAU1c0040_orf_82p	12445
S1M10000027A05	2517	SAU101805	5545	SAU1c0032_orf_24p	12229
S1M10000027A08	2518	SAU101772	5526	SAU1c0037_orf_34p	12351
S1M10000027A11	2519	SAU101551	5477	SAU1c0043_orf_67p	12550
S1M10000027B04	2520	SAU102939	5747	#N/A	#N/A
S1M10000027B06	2521	SAU100275	5252	SAU1c0036_orf_15p	12314
S1M10000027B07	2522	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000027B08	2523	SAU101807	5547	SAU1c0032_orf_26p	12231
S1M10000027B09	2524	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000027B11	2525	SAU101265	5407	#N/A	#N/A
S1M10000027C02	2526	SAU101327	5421	SAU1c0044_orf_296p	12612
S1M10000027C04	2527	SAU201236	5808	SAU2c0409_orf_10p	12891
S1M10000027C05	2528	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000027C06	2529	SAU100114	5228	SAU1c0043_orf_225p	12535
S1M10000027C08	2530	SAU101807	5547	SAU1c0032_orf_26p	12231
S1M10000027C09	2531	SAU101545	5474	SAU1c0037_orf_132p	12348
S1M10000027D02	2532	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000027D02	2532	SAU101653	5504	SAU1c0042_orf_124p	12493
S1M10000027D03	2533	SAU100300	5253	SAU1c0040_orf_90p	12451
S1M10000027D05	2534	SAU101554	5478	SAU1c0043_orf_70p	12551
S1M10000027D06	2535	SAU202708	5849	SAU2c0385_orf_1p	12855
S1M10000027D08	2536	SAU100714	5312	SAU1c0044_orf_74p	12635
S1M10000027D09	2537	SAU203524	5864	SAU2c0435_orf_1p	12957
S1M10000027D10	2538	SAU102283	5634	SAU1c0006_orf_1p	12119
S1M10000027D11	2539	SAU101996	5584	SAU1c0040_orf_99p	12456
S1M10000027E05	2540	SAU200916	5797	SAU2c0373_orf_4p	12838
S1M10000027E05	2540	SAU301620	5899	SAU3c1478_orf_2p	13140
S1M10000027E06	2541	SAU100690	5309	#N/A	#N/A
S1M10000027E07	2542	SAU100547	5290	SAU1c0032_orf_3p	12240
S1M10000027E08	2543	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000027E09	2544	SAU101807	5547	SAU1c0032_orf_26p	12231
S1M10000027E11	2545	SAU101551	5477	SAU1c0043_orf_67p	12550
S1M10000027F01	2546	SAU103038	5757	#N/A	#N/A
S1M10000027F02	2547	SAU101491	5464	SAU1c0025_orf_20p	12165
S1M10000027F05	2548	SAU100882	5347	SAU1c0038_orf_35p	12374
S1M10000027F06	2549	SAU100690	5309	#N/A	#N/A
S1M10000027F08	2550	SAU200006	5770	SAU2c0157_orf_1p	12723
S1M10000027F09	2551	SAU100858	5341	SAU1c0038_orf_86p	12401
S1M10000027G03	2552	SAU101756	5524	SAU1c0040_orf_82p	12445
S1M10000027G04	2553	SAU101777	5527	SAU1c0037_orf_39p	12352
S1M10000027G05	2554	SAU102526	5692	SAU1c0045_orf_299p	12691

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000027G07	2556	SAU102265	5629	SAU1c0032_orf_61p	12251
S1M10000027G09	2557	SAU101807	5547	SAU1c0032_orf_26p	12231
S1M10000027G11	2558	SAU102533	5695	#N/A	#N/A
S1M10000027G11	2558	SAU102534	5696	#N/A	#N/A
S1M10000027H02	2559	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000027H04	2560	SAU101777	5527	SAU1c0037_orf_39p	12352
S1M10000027H05	2561	SAU102526	5692	SAU1c0045_orf_299p	12691
S1M10000027H06	2562	SAU100690	5309	#N/A	#N/A
S1M10000027H07	2563	SAU100542	5288	SAU1c0043_orf_210p	12532
S1M10000027H08	2564	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000027H09	2565	SAU101382	5437	SAU1c0022_orf_19p	12146
S1M10000027H10	2566	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000027H11	2567	SAU102533	5695	#N/A	#N/A
S1M10000027H11	2567	SAU102534	5696	#N/A	#N/A
S1M10000028A02	2568	SAU101085	5378	SAU1c0034_orf_42p	12284
S1M10000028A02	2568	SAU101086	5379	SAU1c0034_orf_43p	12285
S1M10000028A04	2569	SAU101028	5370	SAU1c0043_orf_7p	12552
S1M10000028A06	2570	SAU100478	5277	SAU1c0044_orf_265p	12605
S1M10000028A06	2570	SAU100996	5366	SAU1c0044_orf_266p	12606
S1M10000028A08	2571	SAU102054	5596	SAU1c0039_orf_74p	12417
S1M10000028B01	2572	SAU101085	5378	SAU1c0034_orf_42p	12284
S1M10000028B01	2572	SAU101086	5379	SAU1c0034_orf_43p	12285
S1M10000028B02	2573	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000028B02	2573	SAU301465	5896	SAU3c1429_orf_4p	13121
S1M10000028B03	2574	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000028B04	2575	SAU102764	5734	SAU1c0044_orf_56p	12625
S1M10000028B05	2576	SAU101869	5566	SAU1c0036_orf_24p	12321
S1M10000028B06	2577	SAU201558	5823	SAU2c0434_orf_5p	12954
S1M10000028B08	2578	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000028B09	2579	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000028C02	2580	SAU203296	5863	SAU2c0442_orf_18p	12983
S1M10000028C04	2581	SAU101381	5436	SAU1c0022_orf_18p	12145
S1M10000028C05	2582	SAU100313	5259	SAU1c0045_orf_153p	12661
S1M10000028C05	2582	SAU100359	5264	SAU1c0032_orf_35p	12239
S1M10000028C05	2582	SAU200297	5778	SAU2c0274_orf_2p	12739
S1M10000028C06	2583	SAU103226	5768	SAU1c0045_orf_95p	12713
S1M10000028C08	2584	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000028D03	2585	SAU301898	5904	SAU3c1079_orf_1p	13057
S1M10000028D04	2586	SAU101381	5436	SAU1c0022_orf_18p	12145
S1M10000028D06	2587	SAU200006	5770	SAU2c0157_orf_1p	12723
S1M10000028D07	2588	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000028D08	2589	SAU100858	5341	SAU1c0038_orf_86p	12401
S1M10000028D09	2590	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000028E01	2591	SAU100062	5225	SAU1c0035_orf_98p	12309
S1M10000028E01	2591	SAU100231	5245	#N/A	#N/A
S1M10000028E03	2592	SAU100770	5324	#N/A	#N/A
S1M10000028E08	2593	SAU101865	5563	SAU1c0036_orf_20p	12318

TABLE 1A

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000028F01	2594	SAU101086	5379	SAU1c0034_orf_43p	12285
S1M10000028F03	2595	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000028F04	2596	SAU100301	5254	SAU1c0040_orf_91p	12452
S1M10000028F04	2596	SAU100302	5255	SAU1c0040_orf_92p	12453
S1M10000028F05	2597	SAU100301	5254	SAU1c0040_orf_91p	12452
S1M10000028F05	2597	SAU100302	5255	SAU1c0040_orf_92p	12453
S1M10000028F06	2598	SAU100432	5271	SAU1c0040_orf_88p	12450
S1M10000028F06	2598	SAU202756	5852	SAU2c0470_orf_1p	13027
S1M10000028F07	2599	SAU101006	5367	SAU1c0028_orf_59p	12190
S1M10000028G01	2600	SAU102554	5699	SAU1c0045_orf_209p	12673
S1M10000028G02	2601	SAU201236	5808	SAU2c0409_orf_10p	12891
S1M10000028G02	2601	SAU300338	5871	#N/A	#N/A
S1M10000028G03	2602	SAU101231	5399	SAU1c0035_orf_6p	12303
S1M10000028G04	2603	SAU200916	5797	SAU2c0373_orf_4p	12838
S1M10000028G04	2603	SAU301620	5899	SAU3c1478_orf_2p	13140
S1M10000028G05	2604	SAU100690	5309	#N/A	#N/A
S1M10000028G06	2605	SAU101865	5563	SAU1c0036_orf_20p	12318
S1M10000028G08	2606	SAU101341	5424	SAU1c0044_orf_38p	12618
S1M10000028G08	2606	SAU301275	5892	SAU3c1365_orf_2p	13103
S1M10000028H03	2607	SAU101815	5552	SAU1c0032_orf_33p	12238
S1M10000028H04	2608	SAU103038	5757	#N/A	#N/A
S1M10000028H05	2609	SAU101869	5566	SAU1c0036_orf_24p	12321
S1M10000029A02	2610	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000029A04	2611	SAU100489	5278	SAU1c0044_orf_133p	12566
S1M10000029A04	2611	SAU100557	5291	SAU1c0044_orf_132p	12565
S1M10000029A09	2612	SAU101495	5467	SAU1c0037_orf_65p	12360
S1M10000029A10	2613	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000029A11	2614	SAU101868	5565	SAU1c0036_orf_23p	12320
S1M10000029A12	2615	SAU100865	5343	SAU1c0044_orf_99p	12648
S1M10000029B02	2616	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000029B03	2617	SAU201225	5807	SAU2c0412_orf_5p	12896
S1M10000029B04	2618	SAU201621	5828	SAU2c0437_orf_4p	12966
S1M10000029B05	2619	SAU100355	5263	SAU1c0023_orf_6p	12155
S1M10000029B06	2620	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000029B08	2621	SAU101360	5431	SAU1c0044_orf_109p	12555
S1M10000029B10	2622	SAU101891	5571	SAU1c0034_orf_30p	12281
S1M10000029C02	2623	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000029C03	2624	SAU100690	5309	#N/A	#N/A
S1M10000029C05	2625	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000029C07	2626	SAU102222	5613	SAU1c0043_orf_12p	12511
S1M10000029C09	2627	SAU101495	5467	SAU1c0037_orf_65p	12360
S1M10000029C10	2628	SAU101995	5583	SAU1c0040_orf_98p	12455
S1M10000029C12	2629	SAU100859	5342	SAU1c0038_orf_87p	12402
S1M10000029D02	2630	SAU101400	5444	SAU1c0036_orf_35p	12326
S1M10000029D05	2631	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000029D09	2632	SAU101495	5467	SAU1c0037_orf_65p	12360
S1M10000029D10	2633	SAU101891	5571	SAU1c0034_orf_30p	12281

TABLE IA

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000029E02	2635	SAU101400	5444	SAU1c0036_orf_35p	12326
S1M10000029E05	2636	SAU100522	5284	SAU1c0044_orf_249p	12599
S1M10000029E10	2637	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000029E11	2638	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000029F01	2639	SAU101803	5543	SAU1c0032_orf_23p	12228
S1M10000029F01	2639	SAU101804	5544	#N/A	#N/A
S1M10000029F02	2640	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000029F02	2640	SAU101286	5413	SAU1c0034_orf_67p	12292
S1M10000029F04	2641	SAU102639	5724	#N/A	#N/A
S1M10000029F09	2642	SAU100793	5329	SAU1c0028_orf_52p	12188
S1M10000029F09	2642	SAU301433	5895	SAU3c1420_orf_2p	13118
S1M10000029F10	2643	SAU102621	5719	SAU1c0041_orf_63p	12480
S1M10000029F11	2644	SAU102883	5741	SAU1c0045_orf_38p	12702
S1M10000029F12	2645	SAU102603	5709	SAU1c0041_orf_48p	12469
S1M10000029F12	2645	SAU102609	5713	SAU1c0041_orf_52p	12473
S1M10000029G01	2646	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000029G02	2647	SAU101622	5496	SAU1c0040_orf_27p	12430
S1M10000029G03	2648	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000029G05	2649	SAU101156	5386	SAU1c0036_orf_12p	12311
S1M10000029G07	2650	SAU101622	5496	SAU1c0040_orf_27p	12430
S1M10000029G08	2651	SAU101365	5432	SAU1c0044_orf_112p	12556
S1M10000029G12	2652	SAU101270	5410	SAU1c0037_orf_89p	12365
S1M10000029H01	2653	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000029H05	2654	SAU102613	5715	SAU1c0041_orf_55p	12475
S1M10000029H06	2655	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000029H08	2656	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000029H09	2657	SAU101365	5432	SAU1c0044_orf_112p	12556
S1M10000029H10	2658	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000030A02	2659	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000030A05	2660	SAU101491	5464	SAU1c0025_orf_20p	12165
S1M10000030A09	2661	SAU101242	5404	SAU1c0044_orf_18p	12578
S1M10000030A10	2662	SAU101092	5381	SAU1c0028_orf_9p	12192
S1M10000030A10	2662	SAU202882	5855	SAU2c0381_orf_3p	12848
S1M10000030A11	2663	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000030B02	2664	SAU101573	5485	SAU1c0044_orf_212p	12587
S1M10000030B05	2665	SAU100275	5252	SAU1c0036_orf_15p	12314
S1M10000030B07	2666	SAU101180	5389	SAU1c0045_orf_126p	12656
S1M10000030B09	2667	SAU301898	5904	SAU3c1079_orf_1p	13057
S1M10000030C02	2668	SAU102531	5694	SAU1c0045_orf_186p	12667
S1M10000030C03	2669	SAU102629	5720	SAU1c0041_orf_71p	12481
S1M10000030C04	2670	SAU101999	5585	SAU1c0040_orf_101p	12423
S1M10000030C05	2671	SAU101999	5585	SAU1c0040_orf_101p	12423
S1M10000030C08	2672	SAU101175	5388	SAU1c0031_orf_1p	12213
S1M10000030C09	2673	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000030C10	2674	SAU301592	5898	SAU3c1467_orf_2p	13137
S1M10000030C12	2675	SAU100961	5360	SAU1c0044_orf_83p	12638
S1M10000030C12	2675	SAU100962	5361	SAU1c0044_orf_84p	12639

TABLE IA

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
S1M10000030D01	2676	SAU101495	5467	SAU1c0037_orf_65p	12360
S1M10000030D02	2677	SAU101573	5485	SAU1c0044_orf_212p	12587
S1M10000030D03	2678	SAU100731	5313	SAU1c0044_orf_252p	12601
S1M10000030D05	2679	SAU102222	5613	SAU1c0043_orf_12p	12511
S1M10000030D06	2680	SAU102392	5658	SAU1c0033_orf_40p	12270
S1M10000030D06	2680	SAU201541	5822	SAU2c0431_orf_14p	12942
S1M10000030D07	2681	SAU102392	5658	SAU1c0033_orf_40p	12270
S1M10000030D07	2681	SAU201541	5822	SAU2c0431_orf_14p	12942
S1M10000030D09	2682	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000030D10	2683	SAU100313	5259	SAU1c0045_orf_153p	12661
S1M10000030D10	2683	SAU100359	5264	SAU1c0032_orf_35p	12239
S1M10000030D11	2684	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000030E02	2685	SAU100731	5313	SAU1c0044_orf_252p	12601
S1M10000030E06	2686	SAU102909	5743	SAU1c0036_orf_16p	12315
S1M10000030E07	2687	SAU102939	5747	#N/A	#N/A
S1M10000030E11	2688	SAU101790	5531	SAU1c0032_orf_11p	12215
S1M10000030E12	2689	SAU100300	5253	SAU1c0040_orf_90p	12451
S1M10000030F01	2690	SAU100731	5313	SAU1c0044_orf_252p	12601
S1M10000030F07	2691	SAU102939	5747	#N/A	#N/A
S1M10000030F08	2692	SAU101800	5540	SAU1c0032_orf_20p	12225
S1M10000030F08	2692	SAU101801	5541	#N/A	#N/A
S1M10000030F09	2693	SAU101266	5408	SAU1c0042_orf_117p	12490
S1M10000030F10	2694	SAU102453	5677	SAU1c0045_orf_19p	12669
S1M10000030G03	2695	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000030G05	2696	SAU102246	5619	SAU1c0043_orf_30p	12542
S1M10000030G05	2696	SAU102247	5620	SAU1c0043_orf_31p	12543
S1M10000030G07	2697	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000030G08	2698	SAU100546	5289	SAU1c0032_orf_2p	12235
S1M10000030G09	2699	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000030G10	2700	SAU102453	5677	SAU1c0045_orf_19p	12669
S1M10000030G11	2701	SAU101529	5471	SAU1c0043_orf_39p	12544
S1M10000030G12	2702	SAU201197	5806	SAU2c0429_orf_2p	12938
S1M10000030H01	2703	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000030H02	2704	SAU200392	5780	SAU2c0298_orf_3p	12755
S1M10000030H03	2705	SAU102162	5609	SAU1c0041_orf_27p	12462
S1M10000030H05	2706	SAU102380	5654	SAU1c0033_orf_29p	12265
S1M10000030H07	2707	SAU100123	5230	SAU1c0043_orf_189p	12526
S1M10000030H07	2707	SAU102001	5586	SAU1c0040_orf_102p	12424
S1M10000030H07	2707	SAU103159	5762	SAU1c0045_orf_204p	12670
S1M10000030H07	2707	SAU201827	5837	SAU2c0449_orf_21p	13002
S1M10000030H09	2708	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000031A03	2709	SAU100546	5289	SAU1c0032_orf_2p	12235
S1M10000031A08	2710	SAU101641	5501	SAU1c0029_orf_12p	12193
S1M10000031A10	2711	SAU102242	5618	SAU1c0043_orf_26p	12540
S1M10000031B01	2712	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000031B02	2713	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000031B04	2714	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000031B11	2715	SAU101262	5406	SAU1c0042_orf_113p	12488

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
S1M10000031B12	2716	SAU101360	5431	SAU1c0044_orf_109p	12555
S1M10000031C04	2717	SAU100062	5225	SAU1c0035_orf_98p	12309
S1M10000031C04	2717	SAU100231	5245	#N/A	#N/A
S1M10000031C07	2718	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000031C09	2719	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000031C11	2720	SAU102935	5745	#N/A	#N/A
S1M10000031D06	2721	SAU201197	5806	SAU2c0429_orf_2p	12938
S1M10000031D07	2722	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000031D08	2723	SAU101891	5571	SAU1c0034_orf_30p	12281
S1M10000031D09	2724	SAU102453	5677	SAU1c0045_orf_19p	12669
S1M10000031E02	2725	SAU101350	5429	SAU1c0042_orf_109p	12487
S1M10000031E03	2726	SAU101267	5409	SAU1c0037_orf_86p	12364
S1M10000031E03	2726	SAU300719	5876	SAU3c1108_orf_3p	13059
S1M10000031E04	2727	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000031E07	2728	SAU102449	5674	SAU1c0045_orf_22p	12677
S1M10000031E08	2729	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000031E10	2730	SAU102433	5668	SAU1c0045_orf_37p	12701
S1M10000031E12	2731	SAU101400	5444	SAU1c0036_orf_35p	12326
S1M10000031F02	2732	SAU101800	5540	SAU1c0032_orf_20p	12225
S1M10000031F02	2732	SAU101801	5541	#N/A	#N/A
S1M10000031F03	2733	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000031F04	2734	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000031F04	2734	SAU101572	5484	SAU1c0044_orf_211p	12586
S1M10000031F05	2735	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000031F08	2736	SAU101869	5566	SAU1c0036_orf_24p	12321
S1M10000031F10	2737	SAU102593	5704	SAU1c0041_orf_39p	12463
S1M10000031F11	2738	SAU102469	5679	SAU1c0026_orf_25p	12172
S1M10000031F12	2739	SAU102593	5704	SAU1c0041_orf_39p	12463
S1M10000031G02	2740	SAU101797	5537	SAU1c0032_orf_17p	12221
S1M10000031G03	2741	SAU101679	5509	SAU1c0044_orf_222p	12593
S1M10000031G04	2742	SAU103198	5766	#N/A	#N/A
S1M10000031G06	2743	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000031G09	2744	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000031G10	2745	SAU100077	5226	SAU1c0043_orf_178p	12520
S1M10000031G11	2746	SAU100118	5229	SAU1c0015_orf_13p	12125
S1M10000031H01	2747	SAU103144	5761	SAU1c0045_orf_15p	12663
S1M10000031H02	2748	SAU100886	5349	SAU1c0018_orf_16p	12139
S1M10000031H06	2749	SAU100690	5309	#N/A	#N/A
S1M10000031H09	2750	SAU201743	5831	#N/A	#N/A
S1M10000031H11	2751	SAU100077	5226	SAU1c0043_orf_178p	12520
S1M10000032A03	2752	SAU202039	5843	SAU2c0452_orf_20p	13009
S1M10000032A05	2753	SAU100275	5252	SAU1c0036_orf_15p	12314
S1M10000032A06	2754	SAU100610	5298	SAU1c0034_orf_71p	12294
S1M10000032A07	2755	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000032A08	2756	SAU102142	5606	SAU1c0041_orf_13p	12457
S1M10000032A08	2756	SAU102143	5607	SAU1c0041_orf_14p	12458
S1M10000032A10	2757	SAU101777	5527	SAU1c0037_orf_39p	12352
S1M10000032B01	2758	SAU301898	5904	SAU3c1079_orf_1p	13057

TABLE IA

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
S1M10000032B05	2759	SAU102607	5712	SAU1c0041_orf_51p	12472
S1M10000032B05	2759	SAU102944	5749	SAU1c0041_orf_47p	12468
S1M10000032B07	2760	SAU100157	5237	SAU1c0040_orf_81p	12444
S1M10000032B08	2761	SAU100175	5240	SAU1c0044_orf_204p	12582
S1M10000032B11	2762	SAU100944	5357	SAU1c0042_orf_5p	12505
S1M10000032B12	2763	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000032C01	2764	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000032C03	2765	SAU102241	5617	SAU1c0043_orf_25p	12539
S1M10000032C04	2766	SAU102241	5617	SAU1c0043_orf_25p	12539
S1M10000032C05	2767	SAU101632	5499	SAU1c0039_orf_3p	12407
S1M10000032C09	2768	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000032C10	2769	SAU201615	5826	SAU2c0440_orf_10p	12972
S1M10000032C11	2770	SAU102863	5737	#N/A	#N/A
S1M10000032C12	2771	SAU102863	5737	#N/A	#N/A
S1M10000032D03	2772	SAU100613	5299	SAU1c0015_orf_14p	12126
S1M10000032D06	2773	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000032D07	2774	SAU200468	5781	SAU2c0429_orf_19p	12937
S1M10000032D09	2775	SAU100128	5231	#N/A	#N/A
S1M10000032D09	2775	SAU101549	5476	SAU1c0043_orf_64p	12549
S1M10000032D09	2775	SAU101576	5488	SAU1c0044_orf_105p	12554
S1M10000032D11	2776	SAU100128	5231	#N/A	#N/A
S1M10000032D11	2776	SAU101549	5476	SAU1c0043_orf_64p	12549
S1M10000032D11	2776	SAU101576	5488	SAU1c0044_orf_105p	12554
S1M10000032E02	2777	SAU101784	5530	SAU1c0037_orf_46p	12355
S1M10000032E03	2778	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000032E04	2779	SAU201197	5806	SAU2c0429_orf_2p	12938
S1M10000032E06	2780	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000032E08	2781	SAU102281	5633	SAU1c0038_orf_4p	12384
S1M10000032E09	2782	SAU100521	5283	SAU1c0044_orf_250p	12600
S1M10000032E10	2783	SAU101868	5565	SAU1c0036_orf_23p	12320
S1M10000032E11	2784	SAU101592	5490	SAU1c0039_orf_37p	12406
S1M10000032E12	2785	SAU101999	5585	SAU1c0040_orf_101p	12423
S1M10000032F01	2786	SAU102001	5586	SAU1c0040_orf_102p	12424
S1M10000032F01	2786	SAU102002	5587	SAU1c0040_orf_103p	12425
S1M10000032F04	2787	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000032F05	2788	SAU101339	5422	SAU1c0038_orf_81p	12399
S1M10000032F10	2789	SAU102585	5703	SAU1c0044_orf_289p	12611
S1M10000032F10	2789	SAU201773	5834	SAU2c0446_orf_4p	12996
S1M10000032F11	2790	SAU101189	5392	SAU1c0033_orf_25p	12264
S1M10000032F12	2791	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000032G02	2792	SAU100710	5311	SAU1c0043_orf_54p	12546
S1M10000032G02	2792	SAU200628	5788	SAU2c0334_orf_4p	12790
S1M10000032G03	2793	SAU100813	5334	SAU1c0036_orf_29p	12322
S1M10000032G04	2794	SAU101904	5573	SAU1c0044_orf_36p	12617
S1M10000032G06	2795	SAU101509	5469	SAU1c0039_orf_81p	12418
S1M10000032G08	2796	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000032G10	2797	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000032G12	2798	SAU101084	5377	SAU1c0034_orf_41p	12283

TABLE IA

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
S1M10000032H01	2799	SAU101445	5452	SAU1c0038_orf_47p	12382
S1M10000032H01	2799	SAU101446	5453	SAU1c0038_orf_48p	12383
S1M10000032H04	2800	SAU101868	5565	SAU1c0036_orf_23p	12320
S1M10000032H07	2801	SAU101797	5537	SAU1c0032_orf_17p	12221
S1M10000032H07	2801	SAU101798	5538	SAU1c0032_orf_18p	12222
S1M10000032H09	2802	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000032H11	2803	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000032H11	2803	SAU301148	5888	#N/A	#N/A
S1M10000033A02	2804	SAU201775	5835	SAU2c0446_orf_4p	12996
S1M10000033A02	2804	SAU301080	5885	SAU3c1287_orf_1p	13083
S1M10000033A07	2805	SAU200949	5800	SAU2c0380_orf_11p	12846
S1M10000033A08	2806	SAU101231	5399	SAU1c0035_orf_6p	12303
S1M10000033A10	2807	SAU202039	5843	SAU2c0452_orf_20p	13009
S1M10000033B02	2808	SAU101808	5548	SAU1c0032_orf_27p	12232
S1M10000033B07	2809	SAU102044	5593	SAU1c0039_orf_65p	12414
S1M10000033B08	2810	SAU101868	5565	SAU1c0036_orf_23p	12320
S1M10000033B11	2811	SAU100793	5329	SAU1c0028_orf_52p	12188
S1M10000033B11	2811	SAU301433	5895	SAU3c1420_orf_2p	13118
S1M10000033B12	2812	SAU101104	5382	SAU1c0029_orf_20p	12195
S1M10000033B12	2812	SAU103010	5753	SAU1c0029_orf_19p	12194
S1M10000033C04	2813	SAU102933	5744	SAU1c0039_orf_62p	12412
S1M10000033D02	2814	SAU102333	5644	SAU1c0045_orf_143p	12657
S1M10000033D03	2815	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000033D04	2816	SAU100745	5319	SAU1c0044_orf_233p	12596
S1M10000033D05	2817	SAU100301	5254	SAU1c0040_orf_91p	12452
S1M10000033D06	2818	SAU102113	5601	SAU1c0027_orf_2p	12178
S1M10000033D10	2819	SAU100813	5334	SAU1c0036_orf_29p	12322
S1M10000033D12	2820	SAU101360	5431	SAU1c0044_orf_109p	12555
S1M10000033E04	2821	SAU102318	5643	SAU1c0045_orf_60p	12707
S1M10000033E10	2822	SAU100162	5239	SAU1c0044_orf_206p	12583
S1M10000033E12	2823	SAU100770	5324	#N/A	#N/A
S1M10000033F02	2824	SAU101724	5514	SAU1c0016_orf_9p	12136
S1M10000033F03	2825	SAU101784	5530	SAU1c0037_orf_46p	12355
S1M10000033F06	2826	SAU102449	5674	SAU1c0045_orf_22p	12677
S1M10000033F07	2827	SAU102044	5593	SAU1c0039_orf_65p	12414
S1M10000033F09	2828	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000033F11	2829	SAU100689	5308	SAU1c0036_orf_2p	12323
S1M10000033G05	2830	SAU101904	5573	SAU1c0044_orf_36p	12617
S1M10000033G07	2831	SAU101824	5554	SAU1c0038_orf_26p	12371
S1M10000033G09	2832	SAU102380	5654	SAU1c0033_orf_29p	12265
S1M10000033G10	2833	SAU100793	5329	SAU1c0028_orf_52p	12188
S1M10000033G10	2833	SAU301433	5895	SAU3c1420_orf_2p	13118
S1M10000033G11	2834	SAU101968	5581	SAU1c0028_orf_43p	12187
S1M10000033G12	2835	SAU100300	5253	SAU1c0040_orf_90p	12451
S1M10000033H01	2836	SAU301465	5896	SAU3c1429_orf_4p	13121
S1M10000033H02	2837	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000033H03	2838	SAU101833	5555	SAU1c0038_orf_34p	12373
S1M10000033H07	2839	SAU101996	5584	SAU1c0040_orf_99p	12456

TABLE IA

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000033H09	2841	SAU100710	5311	SAU1c0043_orf_54p	12546
S1M10000033H10	2842	SAU100690	5309	#N/A	#N/A
S1M10000033H11	2843	SAU102453	5677	SAU1c0045_orf_19p	12669
S1M10000034A02	2844	SAU101197	5393	SAU1c0035_orf_60p	12300
S1M10000034A03	2845	SAU102939	5747	#N/A	#N/A
S1M10000034A04	2846	SAU102578	5701	SAU1c0039_orf_61p	12411
S1M10000034A05	2847	SAU101242	5404	SAU1c0044_orf_18p	12578
S1M10000034A08	2848	SAU101020	5368	SAU1c0045_orf_86p	12710
S1M10000034A09	2849	SAU100773	5326	SAU1c0038_orf_39p	12377
S1M10000034A11	2850	SAU102389	5656	SAU1c0033_orf_36p	12268
S1M10000034A12	2851	SAU101632	5499	SAU1c0039_orf_3p	12407
S1M10000034B03	2852	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000034B05	2853	SAU101630	5498	SAU1c0039_orf_4p	12410
S1M10000034B06	2854	SAU102607	5712	SAU1c0041_orf_51p	12472
S1M10000034B06	2854	SAU102944	5749	SAU1c0041_orf_47p	12468
S1M10000034B07	2855	SAU100077	5226	SAU1c0043_orf_178p	12520
S1M10000034B08	2856	SAU101341	5424	SAU1c0044_orf_38p	12618
S1M10000034B09	2857	SAU101909	5575	SAU1c0040_orf_77p	12441
S1M10000034B10	2858	SAU101882	5569	SAU1c0025_orf_15p	12163
S1M10000034B12	2859	SAU200593	5786	SAU2c0327_orf_1p	12784
S1M10000034C02	2860	SAU100557	5291	SAU1c0044_orf_132p	12565
S1M10000034C06	2861	SAU200157	5776	#N/A	#N/A
S1M10000034C07	2862	SAU101343	5425	SAU1c0044_orf_40p	12619
S1M10000034C09	2863	SAU102281	5633	SAU1c0038_orf_4p	12384
S1M10000034C12	2864	SAU100859	5342	SAU1c0038_orf_87p	12402
S1M10000034D01	2865	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000034D05	2866	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000034D06	2867	SAU200157	5776	#N/A	#N/A
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S1M10000034D08	2869	SAU102284	5635	SAU1c0038_orf_5p	12389
S1M10000034D08	2869	SAU201469	5816	SAU2c0438_orf_6p	12967
S1M10000034D10	2870	SAU102474	5681	SAU1c0026_orf_31p	12174
S1M10000034D11	2871	SAU101881	5568	SAU1c0025_orf_14p	12162
S1M10000034D12	2872	SAU101632	5499	SAU1c0039_orf_3p	12407
S1M10000034E01	2873	SAU102433	5668	SAU1c0045_orf_37p	12701
S1M10000034E02	2874	SAU100557	5291	SAU1c0044_orf_132p	12565
S1M10000034E04	2875	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000034E05	2876	SAU100738	5317	SAU1c0044_orf_52p	12624
S1M10000034E06	2877	SAU100347	5262	SAU1c0036_orf_56p	12334
S1M10000034E06	2877	SAU100443	5274	SAU1c0036_orf_55p	12333
S1M10000034E07	2878	SAU100617	5300	SAU1c0035_orf_102p	12295
S1M10000034E10	2879	SAU102401	5661	SAU1c0030_orf_4p	12209
S1M10000034E11	2880	SAU101881	5568	SAU1c0025_orf_14p	12162
S1M10000034E12	2881	SAU200960	5801	SAU2c0377_orf_5p	12843
S1M10000034F01	2882	SAU202731	5850	#N/A	#N/A
S1M10000034F02	2883	SAU201621	5828	SAU2c0437_orf_4p	12966
S1M10000034F03	2884	SAU201971	5841	SAU2c0455_orf_17p	13015

TABLE IA

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000034F05	2886	SAU101630	5498	SAU1c0039_orf_4p	12410
S1M10000034F07	2887	SAU101175	5388	SAU1c0031_orf_1p	12213
S1M10000034F08	2888	SAU202736	5851	SAU2c0426_orf_7p	12927
S1M10000034F09	2889	SAU101869	5566	SAU1c0036_orf_24p	12321
S1M10000034F10	2890	SAU102350	5649	SAU1c0040_orf_36p	12433
S1M10000034F12	2891	SAU100522	5284	SAU1c0044_orf_249p	12599
S1M10000034G02	2892	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000034G03	2893	SAU101198	5394	SAU1c0035_orf_61p	12301
S1M10000034G06	2894	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000034G07	2895	SAU102380	5654	SAU1c0033_orf_29p	12265
S1M10000034G08	2896	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000034G09	2897	SAU102294	5639	SAU1c0044_orf_288p	12610
S1M10000034G09	2897	SAU201775	5835	SAU2c0446_orf_4p	12996
S1M10000034G11	2898	SAU200558	5782	SAU2c0322_orf_5p	12777
S1M10000034G12	2899	SAU100557	5291	SAU1c0044_orf_132p	12565
S1M10000034H01	2900	SAU101293	5414	SAU1c0044_orf_61p	12631
S1M10000034H02	2901	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000034H03	2902	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000034H06	2903	SAU101570	5482	SAU1c0044_orf_209p	12584
S1M10000034H07	2904	SAU100077	5226	SAU1c0043_orf_178p	12520
S1M10000034H08	2905	SAU200740	5794	SAU2c0340_orf_3p	12798
S1M10000034H09	2906	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000034H10	2907	SAU102422	5666	SAU1c0030_orf_22p	12207
S1M10000035A03	2908	SAU101360	5431	SAU1c0044_orf_109p	12555
S1M10000035A08	2909	SAU201403	5815	SAU2c0423_orf_3p	12913
S1M10000035A09	2910	SAU101350	5429	SAU1c0042_orf_109p	12487
S1M10000035A09	2910	SAU101351	5430	SAU1c0042_orf_108p	12486
S1M10000035A10	2911	SAU203296	5863	SAU2c0442_orf_18p	12983
S1M10000035A11	2912	SAU101756	5524	SAU1c0040_orf_82p	12445
S1M10000035A12	2913	SAU101455	5456	SAU1c0045_orf_250p	12686
S1M10000035A12	2913	SAU200916	5797	SAU2c0373_orf_4p	12838
S1M10000035A12	2913	SAU301620	5899	SAU3c1478_orf_2p	13140
S1M10000035B01	2914	SAU102584	5702	SAU1c0043_orf_239p	12537
S1M10000035B03	2915	SAU102246	5619	SAU1c0043_orf_30p	12542
S1M10000035B04	2916	SAU102246	5619	SAU1c0043_orf_30p	12542
S1M10000035B08	2917	SAU103232	5769	SAU1c0045_orf_341p	12697
S1M10000035B11	2918	SAU101756	5524	SAU1c0040_orf_82p	12445
S1M10000035C01	2919	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000035C02	2920	SAU101039	5373	SAU1c0043_orf_181p	12522
S1M10000035C04	2921	SAU100114	5228	SAU1c0043_orf_225p	12535
S1M10000035C06	2922	SAU101497	5468	SAU1c0037_orf_66p	12361
S1M10000035C11	2923	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000035D01	2924	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000035D04	2925	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000035D06	2926	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000035D09	2927	SAU100970	5365	SAU1c0043_orf_197p	12529

TABLE IA

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000035E03	2930	SAU102447	5672	SAU1c0045_orf_24p	12685
S1M10000035E04	2931	SAU103025	5755	SAU1c0029_orf_9p	12202
S1M10000035E08	2932	SAU100690	5309	#N/A	#N/A
S1M10000035E09	2933	SAU101197	5393	SAU1c0035_orf_60p	12300
S1M10000035E12	2934	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000035F03	2935	SAU101092	5381	SAU1c0028_orf_9p	12192
S1M10000035F03	2935	SAU202882	5855	SAU2c0381_orf_3p	12848
S1M10000035F04	2936	SAU101784	5530	SAU1c0037_orf_46p	12355
S1M10000035F09	2937	SAU203296	5863	SAU2c0442_orf_18p	12983
S1M10000035F12	2938	SAU101427	5447	SAU1c0042_orf_144p	12500
S1M10000035F12	2938	SAU103204	5767	SAU1c0042_orf_143p	12499
S1M10000035G02	2939	SAU101365	5432	SAU1c0044_orf_112p	12556
S1M10000035G09	2940	SAU203296	5863	SAU2c0442_orf_18p	12983
S1M10000035G11	2941	SAU101344	5426	SAU1c0044_orf_41p	12620
S1M10000035G12	2942	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000035H01	2943	SAU100140	5235	SAU1c0032_orf_7p	12258
S1M10000035H07	2944	SAU100313	5259	SAU1c0045_orf_153p	12661
S1M10000035H07	2944	SAU100359	5264	SAU1c0032_orf_35p	12239
S1M10000035H07	2944	SAU200297	5778	SAU2c0274_orf_2p	12739
S1M10000035H08	2945	SAU101772	5526	SAU1c0037_orf_34p	12351
S1M10000035H09	2946	SAU100496	5279	SAU1c0041_orf_83p	12484
S1M10000035H09	2946	SAU301004	5882	SAU3c1255_orf_1p	13079
S1M10000035H10	2947	SAU101756	5524	SAU1c0040_orf_82p	12445
S1M10000035H11	2948	SAU101344	5426	SAU1c0044_orf_41p	12620
S1M10000036A02	2949	SAU102447	5672	SAU1c0045_orf_24p	12685
S1M10000036A03	2950	SAU101242	5404	SAU1c0044_orf_18p	12578
S1M10000036A04	2951	SAU200994	5802	SAU2c0428_orf_4p	12935
S1M10000036A05	2952	SAU101810	5549	SAU1c0032_orf_28p	12233
S1M10000036A05	2952	SAU101811	5550	SAU1c0032_orf_29p	12234
S1M10000036A05	2952	SAU300110	5865	SAU3c0533_orf_2p	13031
S1M10000036A08	2953	SAU101220	5396	SAU1c0044_orf_94p	12645
S1M10000036A11	2954	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000036A12	2955	SAU100813	5334	SAU1c0036_orf_29p	12322
S1M10000036B04	2956	SAU101570	5482	SAU1c0044_orf_209p	12584
S1M10000036B04	2956	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000036B06	2957	SAU101653	5504	SAU1c0042_orf_124p	12493
S1M10000036B07	2958	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000036B08	2959	SAU101653	5504	SAU1c0042_orf_124p	12493
S1M10000036B11	2960	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000036B12	2961	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000036C01	2962	SAU100242	5246	SAU1c0036_orf_5p	12336
S1M10000036C03	2963	SAU101592	5490	SAU1c0039_orf_37p	12406
S1M10000036C04	2964	SAU102433	5668	SAU1c0045_orf_37p	12701
S1M10000036C05	2965	SAU100497	5280	SAU1c0018_orf_3p	12140
S1M10000036C06	2966	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000036C07	2967	SAU101800	5540	SAU1c0032_orf_20p	12225

TABLE IA

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000036C09	2968	SAU201773	5834	SAU2c0446_orf_4p	12996
S1M10000036C09	2968	SAU302685	5908	SAU3c1403_orf_1p	13113
S1M10000036C10	2969	SAU100433	5272	SAU1c0040_orf_87p	12449
S1M10000036C10	2969	SAU101751	5521	SAU1c0040_orf_86p	12448
S1M10000036D02	2970	SAU201197	5806	SAU2c0429_orf_2p	12938
S1M10000036D03	2971	SAU103038	5757	#N/A	#N/A
S1M10000036D06	2972	SAU103024	5754	SAU1c0029_orf_6p	12200
S1M10000036D08	2973	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000036D10	2974	SAU102933	5744	SAU1c0039_orf_62p	12412
S1M10000036D11	2975	SAU101197	5393	SAU1c0035_orf_60p	12300
S1M10000036D11	2975	SAU101198	5394	SAU1c0035_orf_61p	12301
S1M10000036D12	2976	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000036E06	2977	SAU100432	5271	SAU1c0040_orf_88p	12450
S1M10000036E06	2977	SAU202756	5852	SAU2c0470_orf_1p	13027
S1M10000036E08	2978	SAU101028	5370	SAU1c0043_orf_7p	12552
S1M10000036E11	2979	SAU101343	5425	SAU1c0044_orf_40p	12619
S1M10000036F06	2980	SAU101242	5404	SAU1c0044_orf_18p	12578
S1M10000036F07	2981	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000036F08	2982	SAU200914	5796	SAU2c0373_orf_2p	12837
S1M10000036F09	2983	SAU100532	5287	SAU1c0044_orf_198p	12580
S1M10000036F10	2984	SAU101586	5489	SAU1c0044_orf_242p	12598
S1M10000036F11	2985	SAU201506	5818	SAU2c0432_orf_18p	12946
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S1M10000036G07	2987	SAU102355	5651	SAU1c0040_orf_40p	12435
S1M10000036G08	2988	SAU102336	5646	SAU1c0045_orf_146p	12659
S1M10000036G11	2989	SAU101340	5423	SAU1c0038_orf_82p	12400
S1M10000036H01	2990	SAU101793	5534	SAU1c0032_orf_14p	12218
S1M10000036H02	2991	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000036H03	2992	SAU102909	5743	SAU1c0036_orf_16p	12315
S1M10000036H04	2993	SAU102909	5743	SAU1c0036_orf_16p	12315
S1M10000036H05	2994	SAU101798	5538	SAU1c0032_orf_18p	12222
S1M10000036H06	2995	SAU102292	5638	SAU1c0038_orf_10p	12368
S1M10000036H08	2996	SAU102909	5743	SAU1c0036_orf_16p	12315
S1M10000036H11	2997	SAU101653	5504	SAU1c0042_orf_124p	12493
S1M10000037A02	2998	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000037A02	2998	SAU101653	5504	SAU1c0042_orf_124p	12493
S1M10000037A03	2999	SAU100128	5231	#N/A	#N/A
S1M10000037A03	2999	SAU101549	5476	SAU1c0043_orf_64p	12549
S1M10000037A03	2999	SAU101576	5488	SAU1c0044_orf_105p	12554
S1M10000037A06	3000	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000037A08	3001	SAU102669	5728	SAU1c0024_orf_7p	12160
S1M10000037A09	3002	SAU101455	5456	SAU1c0045_orf_250p	12686
S1M10000037A09	3002	SAU200916	5797	SAU2c0373_orf_4p	12838
S1M10000037A11	3003	SAU101436	5449	SAU1c0028_orf_23p	12183
S1M10000037A12	3004	SAU200914	5796	SAU2c0373_orf_2p	12837
S1M10000037B03	3005	SAU101999	5585	SAU1c0040_orf_101p	12423

TABLE IA

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000037B06	3008	SAU101806	5546	SAU1c0032_orf_25p	12230
S1M10000037B06	3008	SAU101807	5547	SAU1c0032_orf_26p	12231
S1M10000037B07	3009	SAU101915	5577	SAU1c0040_orf_72p	12439
S1M10000037B08	3010	SAU101592	5490	SAU1c0039_orf_37p	12406
S1M10000037B10	3011	SAU101346	5427	SAU1c0044_orf_43p	12621
S1M10000037B11	3012	SAU101399	5443	SAU1c0036_orf_34p	12325
S1M10000037B12	3013	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000037C05	3014	SAU101482	5461	SAU1c0015_orf_10p	12123
S1M10000037C06	3015	SAU101653	5504	SAU1c0042_orf_124p	12493
S1M10000037C07	3016	SAU101641	5501	SAU1c0029_orf_12p	12193
S1M10000037C08	3017	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000037C09	3018	SAU101818	5553	SAU1c0038_orf_20p	12369
S1M10000037C10	3019	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000037D04	3020	SAU102283	5634	SAU1c0006_orf_1p	12119
S1M10000037D05	3021	SAU100114	5228	SAU1c0043_orf_225p	12535
S1M10000037D06	3022	SAU101996	5584	SAU1c0040_orf_99p	12456
S1M10000037D09	3023	SAU102246	5619	SAU1c0043_orf_30p	12542
S1M10000037D12	3024	SAU101999	5585	SAU1c0040_orf_101p	12423
S1M10000037E02	3025	SAU102447	5672	SAU1c0045_orf_24p	12685
S1M10000037E02	3025	SAU102448	5673	SAU1c0045_orf_23p	12681
S1M10000037E03	3026	SAU100813	5334	SAU1c0036_orf_29p	12322
S1M10000037E06	3027	SAU100921	5355	SAU1c0038_orf_76p	12396
S1M10000037E08	3028	SAU100139	5234	SAU1c0032_orf_6p	12255
S1M10000037E08	3028	SAU100140	5235	SAU1c0032_orf_7p	12258
S1M10000037E09	3029	SAU102049	5595	SAU1c0039_orf_68p	12416
S1M10000037E10	3030	SAU101444	5451	SAU1c0038_orf_46p	12381
S1M10000037E11	3031	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000037E12	3032	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000037F02	3033	SAU100776	5327	SAU1c0041_orf_72p	12482
S1M10000037F03	3034	SAU101339	5422	SAU1c0038_orf_81p	12399
S1M10000037F04	3035	SAU200468	5781	SAU2c0429_orf_19p	12937
S1M10000037F05	3036	SAU101807	5547	SAU1c0032_orf_26p	12231
S1M10000037F06	3037	SAU102585	5703	SAU1c0044_orf_289p	12611
S1M10000037F06	3037	SAU201773	5834	SAU2c0446_orf_4p	12996
S1M10000037F07	3038	SAU100793	5329	SAU1c0028_orf_52p	12188
S1M10000037F07	3038	SAU301433	5895	SAU3c1420_orf_2p	13118
S1M10000037F08	3039	SAU203001	5859	SAU2c0412_orf_15p	12894
S1M10000037F08	3039	SAU203007	5860	SAU2c0412_orf_10p	12893
S1M10000037F09	3040	SAU101592	5490	SAU1c0039_orf_37p	12406
S1M10000037F10	3041	SAU200468	5781	SAU2c0429_orf_19p	12937
S1M10000037G01	3042	SAU102502	5690	SAU1c0045_orf_273p	12689
S1M10000037G01	3042	SAU102503	5691	SAU1c0045_orf_274p	12690
S1M10000037G02	3043	SAU100658	5303	SAU1c0038_orf_59p	12388
S1M10000037G03	3044	SAU101344	5426	SAU1c0044_orf_41p	12620
S1M10000037G06	3045	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000037G07	3046	SAU103038	5757	#N/A	#N/A

TABLE IA

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
S1M10000037G08	3047	SAU100970	5365	SAU1c0043_orf_197p	12529
S1M10000037G10	3048	SAU100062	5225	SAU1c0035_orf_98p	12309
S1M10000037H02	3049	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000037H03	3050	SAU100114	5228	SAU1c0043_orf_225p	12535
S1M10000037H05	3051	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000037H07	3052	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000037H08	3053	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000037H09	3054	SAU100140	5235	SAU1c0032_orf_7p	12258
S1M10000037H11	3055	SAU100608	5297	SAU1c0034_orf_69p	12293
S1M10000038A04	3056	SAU101275	5412	SAU1c0044_orf_257p	12604
S1M10000038A07	3057	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000038A08	3058	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000038A09	3059	SAU100307	5257	SAU1c0036_orf_134p	12313
S1M10000038A11	3060	SAU100547	5290	SAU1c0032_orf_3p	12240
S1M10000038A12	3061	SAU101799	5539	SAU1c0032_orf_19p	12223
S1M10000038B01	3062	SAU101483	5462	SAU1c0015_orf_11p	12124
S1M10000038B03	3063	SAU101360	5431	SAU1c0044_orf_109p	12555
S1M10000038B07	3064	SAU102433	5668	SAU1c0045_orf_37p	12701
S1M10000038B08	3065	SAU100308	5258	SAU1c0036_orf_133p	12312
S1M10000038B09	3066	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000038B09	3066	SAU101653	5504	SAU1c0042_orf_124p	12493
S1M10000038B12	3067	SAU102764	5734	SAU1c0044_orf_56p	12625
S1M10000038C01	3068	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000038C02	3069	SAU200657	5789	#N/A	#N/A
S1M10000038C06	3070	SAU101320	5420	SAU1c0015_orf_16p	12128
S1M10000038C08	3071	SAU102132	5605	SAU1c0027_orf_19p	12177
S1M10000038C10	3072	SAU101346	5427	SAU1c0044_orf_43p	12621
S1M10000038C10	3072	SAU101347	5428	SAU1c0044_orf_44p	12622
S1M10000038C11	3073	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000038C12	3074	SAU101792	5533	SAU1c0032_orf_13p	12217
S1M10000038D02	3075	SAU101842	5557	SAU1c0042_orf_9p	12510
S1M10000038D05	3076	SAU101653	5504	SAU1c0042_orf_124p	12493
S1M10000038D07	3077	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000038D08	3078	SAU101341	5424	SAU1c0044_orf_38p	12618
S1M10000038D08	3078	SAU301275	5892	SAU3c1365_orf_2p	13103
S1M10000038D09	3079	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000038D10	3080	SAU101653	5504	SAU1c0042_orf_124p	12493
S1M10000038D11	3081	SAU101300	5415	SAU1c0044_orf_113p	12557
S1M10000038D11	3081	SAU101365	5432	SAU1c0044_orf_112p	12556
S1M10000038D12	3082	SAU100752	5322	SAU1c0043_orf_183p	12524
S1M10000038D12	3082	SAU100952	5358	SAU1c0043_orf_182p	12523
S1M10000038E01	3083	SAU101814	5551	SAU1c0032_orf_32p	12237
S1M10000038E02	3084	SAU101842	5557	SAU1c0042_orf_9p	12510
S1M10000038E03	3085	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000038E04	3086	SAU101573	5485	SAU1c0044_orf_212p	12587
S1M10000038E05	3087	SAU101653	5504	SAU1c0042_orf_124p	12493
S1M10000038E06	3088	SAU102231	5614	SAU1c0043_orf_18p	12527
S1M10000038E06	3088	SAU102232	5615	SAU1c0043_orf_19p	12530

TABLE IA

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000038E10	3090	SAU201558	5823	SAU2c0434_orf_5p	12954
S1M10000038E12	3091	SAU100838	5337	SAU1c0031_orf_12p	12211
S1M10000038E12	3091	SAU100839	5338	SAU1c0031_orf_11p	12210
S1M10000038F03	3092	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000038F04	3093	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000038F04	3093	SAU100965	5364	SAU1c0044_orf_87p	12642
S1M10000038F05	3094	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000038F05	3094	SAU100965	5364	SAU1c0044_orf_87p	12642
S1M10000038F06	3095	SAU101189	5392	SAU1c0033_orf_25p	12264
S1M10000038F08	3096	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000038F09	3097	SAU201666	5830	SAU2c0442_orf_11p	12981
S1M10000038F10	3098	SAU101197	5393	SAU1c0035_orf_60p	12300
S1M10000038F11	3099	SAU100747	5320	SAU1c0044_orf_235p	12597
S1M10000038F12	3100	SAU202039	5843	SAU2c0452_orf_20p	13009
S1M10000038G01	3101	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000038G03	3102	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000038G04	3103	SAU100475	5276	SAU1c0036_orf_61p	12337
S1M10000038G06	3104	SAU101189	5392	SAU1c0033_orf_25p	12264
S1M10000038G08	3105	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000038G10	3106	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000038G11	3107	SAU100123	5230	SAU1c0043_orf_189p	12526
S1M10000038G11	3107	SAU102001	5586	SAU1c0040_orf_102p	12424
S1M10000038G12	3108	SAU101184	5391	SAU1c0035_orf_80p	12305
S1M10000038H03	3109	SAU101798	5538	SAU1c0032_orf_18p	12222
S1M10000038H07	3110	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000038H09	3111	SAU102340	5647	SAU1c0045_orf_149p	12660
S1M10000038H11	3112	SAU101452	5455	SAU1c0045_orf_247p	12684
S1M10000039A02	3113	SAU100496	5279	SAU1c0041_orf_83p	12484
S1M10000039A02	3113	SAU301004	5882	SAU3c1255_orf_1p	13079
S1M10000039A05	3114	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000039A05	3114	SAU100965	5364	SAU1c0044_orf_87p	12642
S1M10000039A07	3115	SAU100131	5232	SAU1c0043_orf_156p	12517
S1M10000039A08	3116	SAU100522	5284	SAU1c0044_orf_249p	12599
S1M10000039A11	3117	SAU100613	5299	SAU1c0015_orf_14p	12126
S1M10000039A12	3118	SAU301465	5896	SAU3c1429_orf_4p	13121
S1M10000039B02	3119	SAU101455	5456	SAU1c0045_orf_250p	12686
S1M10000039B02	3119	SAU200916	5797	SAU2c0373_orf_4p	12838
S1M10000039B06	3120	SAU102350	5649	SAU1c0040_orf_36p	12433
S1M10000039B07	3121	SAU101869	5566	SAU1c0036_orf_24p	12321
S1M10000039B10	3122	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000039B12	3123	SAU301118	5886	SAU3c1305_orf_3p	13086
S1M10000039C04	3124	SAU102252	5621	SAU1c0032_orf_48p	12241
S1M10000039C06	3125	SAU100633	5301	SAU1c0043_orf_147p	12515
S1M10000039C07	3126	SAU200657	5789	#N/A	#N/A
S1M10000039C08	3127	SAU200468	5781	SAU2c0429_orf_19p	12937
S1M10000039C09	3128	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000039C10	3129	SAU101543	5473	SAU1c0037_orf_130p	12346

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
S1M10000039C11	3130	SAU200657	5789	#N/A	#N/A
S1M10000039D02	3131	SAU201403	5815	SAU2c0423_orf_3p	12913
S1M10000039D09	3132	SAU102294	5639	SAU1c0044_orf_288p	12610
S1M10000039D09	3132	SAU301080	5885	SAU3c1287_orf_1p	13083
S1M10000039D10	3133	SAU100323	5261	SAU1c0044_orf_171p	12575
S1M10000039E01	3134	SAU102264	5628	SAU1c0032_orf_60p	12250
S1M10000039E08	3135	SAU100412	5269	SAU1c0029_orf_38p	12197
S1M10000039E09	3136	SAU100056	5223	SAU1c0044_orf_176p	12577
S1M10000039E10	3137	SAU102394	5659	SAU1c0033_orf_41p	12271
S1M10000039E10	3137	SAU301118	5886	SAU3c1305_orf_3p	13086
S1M10000039E11	3138	SAU102473	5680	SAU1c0026_orf_30p	12173
S1M10000039F02	3139	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000039F03	3140	SAU102527	5693	SAU1c0032_orf_9p	12260
S1M10000039F05	3141	SAU100118	5229	SAU1c0015_orf_13p	12125
S1M10000039F07	3142	SAU102531	5694	SAU1c0045_orf_186p	12667
S1M10000039F08	3143	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000039F09	3144	SAU200157	5776	#N/A	#N/A
S1M10000039F10	3145	SAU100059	5224	SAU1c0045_orf_10p	12652
S1M10000039F12	3146	SAU101565	5480	SAU1c0022_orf_8p	12151
S1M10000039G03	3147	SAU101653	5504	SAU1c0042_orf_124p	12493
S1M10000039G04	3148	SAU102292	5638	SAU1c0038_orf_10p	12368
S1M10000039G07	3149	SAU100952	5358	SAU1c0043_orf_182p	12523
S1M10000039G07	3149	SAU101039	5373	SAU1c0043_orf_181p	12522
S1M10000039G10	3150	SAU101815	5552	SAU1c0032_orf_33p	12238
S1M10000039H02	3151	SAU102585	5703	SAU1c0044_orf_289p	12611
S1M10000039H02	3151	SAU201773	5834	SAU2c0446_orf_4p	12996
S1M10000039H03	3152	SAU100313	5259	SAU1c0045_orf_153p	12661
S1M10000039H03	3152	SAU100359	5264	SAU1c0032_orf_35p	12239
S1M10000039H03	3152	SAU200297	5778	SAU2c0274_orf_2p	12739
S1M10000039H04	3153	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000039H06	3154	SAU102283	5634	SAU1c0006_orf_1p	12119
S1M10000039H07	3155	SAU100793	5329	SAU1c0028_orf_52p	12188
S1M10000039H07	3155	SAU301433	5895	SAU3c1420_orf_2p	13118
S1M10000039H08	3156	SAU102440	5671	SAU1c0045_orf_30p	12692
S1M10000040A04	3157	SAU100040	5221	SAU1c0043_orf_217p	12533
S1M10000040A05	3158	SAU102671	5729	SAU1c0024_orf_9p	12161
S1M10000040A07	3159	SAU101028	5370	SAU1c0043_orf_7p	12552
S1M10000040A08	3160	SAU200157	5776	#N/A	#N/A
S1M10000040A10	3161	SAU103038	5757	#N/A	#N/A
S1M10000040A11	3162	SAU101801	5541	#N/A	#N/A
S1M10000040B01	3163	SAU101461	5457	SAU1c0045_orf_234p	12680
S1M10000040B03	3164	SAU102102	5600	SAU1c0045_orf_340p	12696
S1M10000040B07	3165	SAU101432	5448	SAU1c0028_orf_27p	12184
S1M10000040B11	3166	SAU101198	5394	SAU1c0035_orf_61p	12301
S1M10000040C03	3167	SAU201971	5841	SAU2c0455_orf_17p	13015
S1M10000040C03	3167	SAU301363	5894	#N/A	#N/A
S1M10000040C04	3168	SAU102551	5698	SAU1c0045_orf_206p	12672
S1M10000040C05	3169	SAU102534	5696	#N/A	#N/A

TABLE IA

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
S1M10000040C06	3170	SAU101247	5405	SAU1c0043_orf_136p	12512
S1M10000040C07	3171	SAU100970	5365	SAU1c0043_orf_197p	12529
S1M10000040C08	3172	SAU101197	5393	SAU1c0035_orf_60p	12300
S1M10000040C10	3173	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000040C10	3173	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000040C10	3173	SAU301148	5888	#N/A	#N/A
S1M10000040C11	3174	SAU101869	5566	SAU1c0036_orf_24p	12321
S1M10000040D01	3175	SAU101806	5546	SAU1c0032_orf_25p	12230
S1M10000040D01	3175	SAU101807	5547	SAU1c0032_orf_26p	12231
S1M10000040D03	3176	SAU102200	5611	SAU1c0045_orf_168p	12665
S1M10000040D03	3176	SAU102201	5612	SAU1c0045_orf_169p	12666
S1M10000040D08	3177	SAU100633	5301	SAU1c0043_orf_147p	12515
S1M10000040D09	3178	SAU101632	5499	SAU1c0039_orf_3p	12407
S1M10000040D11	3179	SAU101546	5475	SAU1c0037_orf_133p	12349
S1M10000040E01	3180	SAU100916	5353	SAU1c0038_orf_71p	12394
S1M10000040E02	3181	SAU101845	5558	SAU1c0042_orf_7p	12506
S1M10000040E04	3182	SAU101546	5475	SAU1c0037_orf_133p	12349
S1M10000040E05	3183	SAU101632	5499	SAU1c0039_orf_3p	12407
S1M10000040E06	3184	SAU101545	5474	SAU1c0037_orf_132p	12348
S1M10000040E07	3185	SAU101006	5367	SAU1c0028_orf_59p	12190
S1M10000040E09	3186	SAU102605	5710	SAU1c0041_orf_49p	12470
S1M10000040E10	3187	SAU100714	5312	SAU1c0044_orf_74p	12635
S1M10000040E11	3188	SAU101226	5398	SAU1c0035_orf_2p	12298
S1M10000040E12	3189	SAU102503	5691	SAU1c0045_orf_274p	12690
S1M10000040E12	3189	SAU201380	5812	SAU2c0426_orf_11p	12922
S1M10000040F01	3190	SAU101226	5398	SAU1c0035_orf_2p	12298
S1M10000040F02	3191	SAU101614	5494	SAU1c0044_orf_9p	12649
S1M10000040F03	3192	SAU101592	5490	SAU1c0039_orf_37p	12406
S1M10000040F04	3193	SAU100123	5230	SAU1c0043_orf_189p	12526
S1M10000040F04	3193	SAU102001	5586	SAU1c0040_orf_102p	12424
S1M10000040F04	3193	SAU103159	5762	SAU1c0045_orf_204p	12670
S1M10000040F04	3193	SAU201827	5837	SAU2c0449_orf_21p	13002
S1M10000040F05	3194	SAU102232	5615	SAU1c0043_orf_19p	12530
S1M10000040F06	3195	SAU100547	5290	SAU1c0032_orf_3p	12240
S1M10000040F08	3196	SAU300713	5875	SAU3c1104_orf_1p	13058
S1M10000040F09	3197	SAU101610	5492	SAU1c0044_orf_5p	12629
S1M10000040F12	3198	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000040G01	3199	SAU200006	5770	SAU2c0157_orf_1p	12723
S1M10000040G02	3200	SAU200561	5783	SAU2c0324_orf_3p	12779
S1M10000040G02	3200	SAU301773	5901	SAU3c1509_orf_2p	13157
S1M10000040G04	3201	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000040G07	3202	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000040G08	3203	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000040G12	3204	SAU101421	5446	SAU1c0042_orf_138p	12498
S1M10000040H02	3205	SAU100773	5326	SAU1c0038_orf_39p	12377
S1M10000040H03	3206	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000040H04	3207	SAU200914	5796	SAU2c0373_orf_2p	12837
S1M10000040H05	3208	SAU101400	5444	SAU1c0036_orf_35p	12326

TABLE IA

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000041B02	3212	SAU101592	5490	SAU1c0039_orf_37p	12406
S1M10000041B03	3213	SAU101592	5490	SAU1c0039_orf_37p	12406
S1M10000041B05	3214	SAU101798	5538	SAU1c0032_orf_18p	12222
S1M10000041B06	3215	SAU301620	5899	SAU3c1478_orf_2p	13140
S1M10000041B07	3216	SAU101145	5384	SAU1c0035_orf_43p	12299
S1M10000041B12	3217	SAU102725	5733	SAU1c0036_orf_68p	12338
S1M10000041C08	3218	SAU102607	5712	SAU1c0041_orf_51p	12472
S1M10000041C08	3218	SAU102944	5749	SAU1c0041_orf_47p	12468
S1M10000041C10	3219	SAU101784	5530	SAU1c0037_orf_46p	12355
S1M10000041C11	3220	SAU101570	5482	SAU1c0044_orf_209p	12584
S1M10000041D06	3221	SAU101777	5527	SAU1c0037_orf_39p	12352
S1M10000041D07	3222	SAU102639	5724	#N/A	#N/A
S1M10000041D08	3223	SAU200030	5772	SAU2c0282_orf_3p	12745
S1M10000041D10	3224	SAU101573	5485	SAU1c0044_orf_212p	12587
S1M10000041D12	3225	SAU102658	5726	SAU1c0045_orf_121p	12654
S1M10000041E03	3226	SAU101573	5485	SAU1c0044_orf_212p	12587
S1M10000041E06	3227	SAU101996	5584	SAU1c0040_orf_99p	12456
S1M10000041E09	3228	SAU201236	5808	SAU2c0409_orf_10p	12891
S1M10000041E12	3229	SAU100952	5358	SAU1c0043_orf_182p	12523
S1M10000041F03	3230	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000041F03	3230	SAU101572	5484	SAU1c0044_orf_211p	12586
S1M10000041F11	3231	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000041F12	3232	SAU102480	5684	SAU1c0039_orf_100p	12404
S1M10000041F12	3232	SAU102481	5685	SAU1c0039_orf_99p	12422
S1M10000041G01	3233	SAU100532	5287	SAU1c0044_orf_198p	12580
S1M10000041G06	3234	SAU102345	5648	SAU1c0045_orf_125p	12655
S1M10000041G08	3235	SAU101546	5475	SAU1c0037_orf_133p	12349
S1M10000041G10	3236	SAU100866	5344	SAU1c0044_orf_100p	12553
S1M10000041G11	3237	SAU101802	5542	SAU1c0032_orf_22p	12227
S1M10000041H01	3238	SAU101198	5394	SAU1c0035_orf_61p	12301
S1M10000041H04	3239	SAU100497	5280	SAU1c0018_orf_3p	12140
S1M10000041H05	3240	SAU100242	5246	SAU1c0036_orf_5p	12336
S1M10000041H07	3241	SAU102486	5687	SAU1c0039_orf_93p	12420
S1M10000041H07	3241	SAU102487	5688	SAU1c0039_orf_92p	12419
S1M10000041H08	3242	SAU301133	5887	SAU3c1311_orf_3p	13087
S1M10000041H09	3243	SAU103169	5763	SAU1c0045_orf_230p	12678
S1M10000042A04	3244	SAU201236	5808	SAU2c0409_orf_10p	12891
S1M10000042A05	3245	SAU102433	5668	SAU1c0045_orf_37p	12701
S1M10000042A06	3246	SAU102578	5701	SAU1c0039_orf_61p	12411
S1M10000042A07	3247	SAU100633	5301	SAU1c0043_orf_147p	12515
S1M10000042A09	3248	SAU101495	5467	SAU1c0037_orf_65p	12360
S1M10000042A11	3249	SAU101815	5552	SAU1c0032_orf_33p	12238
S1M10000042A12	3250	SAU101632	5499	SAU1c0039_orf_3p	12407
S1M10000042B02	3251	SAU202736	5851	SAU2c0426_orf_7p	12927
S1M10000042B03	3252	SAU101907	5574	SAU1c0040_orf_79p	12442

TABLE IA

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
S1M10000042B06	3253	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000042B07	3254	SAU101343	5425	SAU1c0044_orf_40p	12619
S1M10000042B08	3255	SAU100443	5274	SAU1c0036_orf_55p	12333
S1M10000042B09	3256	SAU101802	5542	SAU1c0032_orf_22p	12227
S1M10000042B10	3257	SAU100141	5236	SAU1c0032_orf_8p	12259
S1M10000042B10	3257	SAU102527	5693	SAU1c0032_orf_9p	12260
S1M10000042B11	3258	SAU101815	5552	SAU1c0032_orf_33p	12238
S1M10000042B12	3259	SAU101653	5504	SAU1c0042_orf_124p	12493
S1M10000042C02	3260	SAU100617	5300	SAU1c0035_orf_102p	12295
S1M10000042C06	3261	SAU102032	5591	SAU1c0029_orf_47p	12198
S1M10000042C10	3262	SAU101495	5467	SAU1c0037_orf_65p	12360
S1M10000042C11	3263	SAU103037	5756	SAU1c0044_orf_303p	12613
S1M10000042D04	3264	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000042D07	3265	SAU101632	5499	SAU1c0039_orf_3p	12407
S1M10000042D10	3266	SAU203296	5863	SAU2c0442_orf_18p	12983
S1M10000042D11	3267	SAU102663	5727	SAU1c0024_orf_2p	12158
S1M10000042E03	3268	SAU101495	5467	SAU1c0037_orf_65p	12360
S1M10000042E06	3269	SAU102433	5668	SAU1c0045_orf_37p	12701
S1M10000042E08	3270	SAU103198	5766	#N/A	#N/A
S1M10000042F01	3271	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000042F02	3272	SAU101891	5571	SAU1c0034_orf_30p	12281
S1M10000042F05	3273	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000042F06	3274	SAU100773	5326	SAU1c0038_orf_39p	12377
S1M10000042F08	3275	SAU100162	5239	SAU1c0044_orf_206p	12583
S1M10000042F09	3276	SAU100246	5247	SAU1c0042_orf_130p	12496
S1M10000042F09	3276	SAU300998	5881	SAU3c1253_orf_3p	13077
S1M10000042F10	3277	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000042F11	3278	SAU101653	5504	SAU1c0042_orf_124p	12493
S1M10000042G01	3279	SAU100140	5235	SAU1c0032_orf_7p	12258
S1M10000042G03	3280	SAU101220	5396	SAU1c0044_orf_94p	12645
S1M10000042G08	3281	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000042G09	3282	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000042G12	3283	SAU100521	5283	SAU1c0044_orf_250p	12600
S1M10000042H05	3284	SAU101491	5464	SAU1c0025_orf_20p	12165
S1M10000042H07	3285	SAU100433	5272	SAU1c0040_orf_87p	12449
S1M10000042H11	3286	SAU101632	5499	SAU1c0039_orf_3p	12407
S1M10000043A02	3287	SAU203001	5859	SAU2c0412_orf_15p	12894
S1M10000043A03	3288	SAU101400	5444	SAU1c0036_orf_35p	12326
S1M10000043A04	3289	SAU200088	5775	SAU2c0159_orf_1p	12724
S1M10000043A06	3290	SAU100077	5226	SAU1c0043_orf_178p	12520
S1M10000043A07	3291	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000043A08	3292	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000043A10	3293	SAU100865	5343	SAU1c0044_orf_99p	12648
S1M10000043A11	3294	SAU100865	5343	SAU1c0044_orf_99p	12648
S1M10000043A12	3295	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000043B01	3296	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000043B02	3297	SAU100059	5224	SAU1c0045_orf_10p	12652
S1M10000043B07	3298	SAU101922	5578	SAU1c0040_orf_66p	12438

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000043B08	3299	SAU100313	5259	SAU1c0045_orf_153p	12661
S1M10000043B08	3299	SAU100359	5264	SAU1c0032_orf_35p	12239
S1M10000043B08	3299	SAU200297	5778	SAU2c0274_orf_2p	12739
S1M10000043B09	3300	SAU100521	5283	SAU1c0044_orf_250p	12600
S1M10000043B10	3301	SAU100436	5273	SAU1c0023_orf_20p	12154
S1M10000043B12	3302	SAU102142	5606	SAU1c0041_orf_13p	12457
S1M10000043C02	3303	SAU101777	5527	SAU1c0037_orf_39p	12352
S1M10000043C07	3304	SAU101784	5530	SAU1c0037_orf_46p	12355
S1M10000043C11	3305	SAU201403	5815	SAU2c0423_orf_3p	12913
S1M10000043C12	3306	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000043D01	3307	SAU100866	5344	SAU1c0044_orf_100p	12553
S1M10000043D02	3308	SAU301465	5896	SAU3c1429_orf_4p	13121
S1M10000043D04	3309	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000043D10	3310	SAU102631	5721	SAU1c0045_orf_94p	12712
S1M10000043D12	3311	SAU100496	5279	SAU1c0041_orf_83p	12484
S1M10000043D12	3311	SAU301004	5882	SAU3c1255_orf_1p	13079
S1M10000043E02	3312	SAU100793	5329	SAU1c0028_orf_52p	12188
S1M10000043E02	3312	SAU301433	5895	SAU3c1420_orf_2p	13118
S1M10000043E03	3313	SAU102032	5591	SAU1c0029_orf_47p	12198
S1M10000043E05	3314	SAU102067	5598	SAU1c0034_orf_54p	12287
S1M10000043E07	3315	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000043E08	3316	SAU101344	5426	SAU1c0044_orf_41p	12620
S1M10000043E10	3317	SAU100186	5242	SAU1c0036_orf_19p	12317
S1M10000043E11	3318	SAU102498	5689	SAU1c0045_orf_270p	12688
S1M10000043E11	3318	SAU201381	5813	SAU2c0426_orf_16p	12923
S1M10000043E12	3319	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000043F01	3320	SAU101797	5537	SAU1c0032_orf_17p	12221
S1M10000043F01	3320	SAU101798	5538	SAU1c0032_orf_18p	12222
S1M10000043F05	3321	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000043F07	3322	SAU102447	5672	SAU1c0045_orf_24p	12685
S1M10000043F07	3322	SAU102448	5673	SAU1c0045_orf_23p	12681
S1M10000043F08	3323	SAU101344	5426	SAU1c0044_orf_41p	12620
S1M10000043F09	3324	SAU101801	5541	#N/A	#N/A
S1M10000043G01	3325	SAU100059	5224	SAU1c0045_orf_10p	12652
S1M10000043G04	3326	SAU102423	5667	SAU1c0030_orf_23p	12208
S1M10000043G05	3327	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000043G09	3328	SAU102585	5703	SAU1c0044_orf_289p	12611
S1M10000043G09	3328	SAU201773	5834	SAU2c0446_orf_4p	12996
S1M10000043G10	3329	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000043H01	3330	SAU101797	5537	SAU1c0032_orf_17p	12221
S1M10000043H01	3330	SAU101798	5538	SAU1c0032_orf_18p	12222
S1M10000043H03	3331	SAU101803	5543	SAU1c0032_orf_23p	12228
S1M10000043H03	3331	SAU101804	5544	#N/A	#N/A
S1M10000043H04	3332	SAU100128	5231	#N/A	#N/A
S1M10000043H04	3332	SAU101549	5476	SAU1c0043_orf_64p	12549
S1M10000043H04	3332	SAU101576	5488	SAU1c0044_orf_105p	12554
S1M10000043H05	3333	SAU200058	5773	SAU2c0134_orf_1p	12719

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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000043H06	3334	SAU102417	5663	SAU1c0030_orf_17p	12204
S1M10000043H06	3334	SAU102863	5737	#N/A	#N/A
S1M10000043H09	3335	SAU302950	5914	SAU3c1512_orf_12p	13160
S1M10000043H10	3336	SAU101024	5369	SAU1c0045_orf_90p	12711
S1M10000043H11	3337	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000044A02	3338	SAU101092	5381	SAU1c0028_orf_9p	12192
S1M10000044A06	3339	SAU101777	5527	SAU1c0037_orf_39p	12352
S1M10000044A08	3340	SAU101175	5388	SAU1c0031_orf_1p	12213
S1M10000044A09	3341	SAU102292	5638	SAU1c0038_orf_10p	12368
S1M10000044A11	3342	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000044A12	3343	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000044B01	3344	SAU102268	5630	SAU1c0032_orf_63p	12252
S1M10000044B02	3345	SAU101968	5581	SAU1c0028_orf_43p	12187
S1M10000044B05	3346	SAU100690	5309	#N/A	#N/A
S1M10000044B06	3347	SAU100547	5290	SAU1c0032_orf_3p	12240
S1M10000044B06	3347	SAU102881	5740	SAU1c0032_orf_4p	12242
S1M10000044B08	3348	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000044B11	3349	SAU101573	5485	SAU1c0044_orf_212p	12587
S1M10000044B12	3350	SAU201197	5806	SAU2c0429_orf_2p	12938
S1M10000044C04	3351	SAU101793	5534	SAU1c0032_orf_14p	12218
S1M10000044C06	3352	SAU101614	5494	SAU1c0044_orf_9p	12649
S1M10000044C07	3353	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000044C07	3353	SAU100965	5364	SAU1c0044_orf_87p	12642
S1M10000044C08	3354	SAU102909	5743	SAU1c0036_orf_16p	12315
S1M10000044C11	3355	SAU101793	5534	SAU1c0032_orf_14p	12218
S1M10000044C12	3356	SAU102280	5632	SAU1c0038_orf_3p	12378
S1M10000044D01	3357	SAU100546	5289	SAU1c0032_orf_2p	12235
S1M10000044D01	3357	SAU102880	5739	SAU1c0032_orf_1p	12224
S1M10000044D04	3358	SAU101793	5534	SAU1c0032_orf_14p	12218
S1M10000044D06	3359	SAU101300	5415	SAU1c0044_orf_113p	12557
S1M10000044D06	3359	SAU101365	5432	SAU1c0044_orf_112p	12556
S1M10000044D08	3360	SAU102270	5631	SAU1c0032_orf_65p	12253
S1M10000044D09	3361	SAU100131	5232	SAU1c0043_orf_156p	12517
S1M10000044D10	3362	SAU201197	5806	SAU2c0429_orf_2p	12938
S1M10000044D11	3363	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000044D12	3364	SAU102231	5614	SAU1c0043_orf_18p	12527
S1M10000044D12	3364	SAU102232	5615	SAU1c0043_orf_19p	12530
S1M10000044E01	3365	SAU101371	5435	SAU1c0033_orf_7p	12275
S1M10000044E02	3366	SAU102283	5634	SAU1c0006_orf_1p	12119
S1M10000044E06	3367	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000044E07	3368	SAU301829	5902	SAU3c1515_orf_7p	13162
S1M10000044E09	3369	SAU101320	5420	SAU1c0015_orf_16p	12128
S1M10000044E10	3370	SAU100497	5280	SAU1c0018_orf_3p	12140
S1M10000044E11	3371	SAU101270	5410	SAU1c0037_orf_89p	12365
S1M10000044F02	3372	SAU101632	5499	SAU1c0039_orf_3p	12407
S1M10000044F06	3373	SAU101756	5524	SAU1c0040_orf_82p	12445
S1M10000044F08	3374	SAU101262	5406	SAU1c0042_orf_113p	12488

TABLE IA

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
S1M10000044F10	3375	SAU101092	5381	SAU1c0028_orf_9p	12192
S1M10000044F10	3375	SAU202882	5855	SAU2c0381_orf_3p	12848
S1M10000044G02	3376	SAU102933	5744	SAU1c0039_orf_62p	12412
S1M10000044G05	3377	SAU101242	5404	SAU1c0044_orf_18p	12578
S1M10000044G08	3378	SAU102601	5707	SAU1c0041_orf_46p	12467
S1M10000044G08	3378	SAU102606	5711	SAU1c0041_orf_50p	12471
S1M10000044G10	3379	SAU101092	5381	SAU1c0028_orf_9p	12192
S1M10000044G10	3379	SAU202882	5855	SAU2c0381_orf_3p	12848
S1M10000044G11	3380	SAU101546	5475	SAU1c0037_orf_133p	12349
S1M10000044H06	3381	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000044H06	3381	SAU100965	5364	SAU1c0044_orf_87p	12642
S1M10000044H07	3382	SAU100595	5294	SAU1c0043_orf_62p	12547
S1M10000044H08	3383	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000044H09	3384	SAU100886	5349	SAU1c0018_orf_16p	12139
S1M10000044H09	3384	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000044H10	3385	SAU101573	5485	SAU1c0044_orf_212p	12587
S1M10000044H11	3386	SAU102578	5701	SAU1c0039_orf_61p	12411
S1M10000045A02	3387	SAU100866	5344	SAU1c0044_orf_100p	12553
S1M10000045A06	3388	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000045A07	3389	SAU102378	5653	SAU1c0040_orf_61p	12437
S1M10000045A08	3390	SAU102336	5646	SAU1c0045_orf_146p	12659
S1M10000045A12	3391	SAU201765	5833	SAU2c0309_orf_5p	12770
S1M10000045B01	3392	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000045B02	3393	SAU100546	5289	SAU1c0032_orf_2p	12235
S1M10000045B03	3394	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000045B07	3395	SAU101803	5543	SAU1c0032_orf_23p	12228
S1M10000045B10	3396	SAU200468	5781	SAU2c0429_orf_19p	12937
S1M10000045B11	3397	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000045B12	3398	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000045C02	3399	SAU100690	5309	#N/A	#N/A
S1M10000045C03	3400	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000045C04	3401	SAU102286	5636	SAU1c0038_orf_6p	12393
S1M10000045C04	3401	SAU102287	5637	SAU1c0038_orf_7p	12398
S1M10000045C05	3402	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000045C07	3403	SAU101573	5485	SAU1c0044_orf_212p	12587
S1M10000045C09	3404	SAU101744	5520	SAU1c0037_orf_94p	12367
S1M10000045C09	3404	SAU300191	5868	SAU3c0672_orf_1p	13037
S1M10000045D01	3405	SAU101893	5572	SAU1c0034_orf_32p	12282
S1M10000045D03	3406	SAU101599	5491	SAU1c0041_orf_5p	12478
S1M10000045D07	3407	SAU101491	5464	SAU1c0025_orf_20p	12165
S1M10000045D08	3408	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000045D09	3409	SAU101572	5484	SAU1c0044_orf_211p	12586
S1M10000045D10	3410	SAU100866	5344	SAU1c0044_orf_100p	12553
S1M10000045D11	3411	SAU101492	5465	SAU1c0025_orf_21p	12166
S1M10000045D11	3411	SAU101493	5466	SAU1c0025_orf_22p	12167
S1M10000045D12	3412	SAU101800	5540	SAU1c0032_orf_20p	12225
S1M10000045D12	3412	SAU101801	5541	#N/A	#N/A
S1M10000045E04	3413	SAU102132	5605	SAU1c0027_orf_19p	12177

TABLE IA

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000045E08	3415	SAU201752	5832	SAU2c0436_orf_19p	12963
S1M10000045E09	3416	SAU101794	5535	#N/A	#N/A
S1M10000045E10	3417	SAU101756	5524	SAU1c0040_orf_82p	12445
S1M10000045E11	3418	SAU100970	5365	SAU1c0043_orf_197p	12529
S1M10000045E12	3419	SAU100547	5290	SAU1c0032_orf_3p	12240
S1M10000045F04	3420	SAU102241	5617	SAU1c0043_orf_25p	12539
S1M10000045F05	3421	SAU100114	5228	SAU1c0043_orf_225p	12535
S1M10000045F08	3422	SAU200657	5789	#N/A	#N/A
S1M10000045F11	3423	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000045F12	3424	SAU101806	5546	SAU1c0032_orf_25p	12230
S1M10000045G03	3425	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000045G06	3426	SAU101400	5444	SAU1c0036_orf_35p	12326
S1M10000045G07	3427	SAU101561	5479	SAU1c0022_orf_4p	12149
S1M10000045G08	3428	SAU100690	5309	#N/A	#N/A
S1M10000045G10	3429	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000045G12	3430	SAU101400	5444	SAU1c0036_orf_35p	12326
S1M10000045H06	3431	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000045H10	3432	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000045H11	3433	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000046A03	3434	SAU202731	5850	#N/A	#N/A
S1M10000046A04	3435	SAU100062	5225	SAU1c0035_orf_98p	12309
S1M10000046A04	3435	SAU100231	5245	#N/A	#N/A
S1M10000046A06	3436	SAU101383	5438	SAU1c0022_orf_20p	12147
S1M10000046A08	3437	SAU200994	5802	SAU2c0428_orf_4p	12935
S1M10000046A09	3438	SAU100315	5260	SAU1c0037_orf_62p	12358
S1M10000046A11	3439	SAU100432	5271	SAU1c0040_orf_88p	12450
S1M10000046A11	3439	SAU100433	5272	SAU1c0040_orf_87p	12449
S1M10000046A12	3440	SAU101814	5551	SAU1c0032_orf_32p	12237
S1M10000046B01	3441	SAU102334	5645	SAU1c0045_orf_144p	12658
S1M10000046B03	3442	SAU101039	5373	SAU1c0043_orf_181p	12522
S1M10000046B04	3443	SAU101797	5537	SAU1c0032_orf_17p	12221
S1M10000046B05	3444	SAU101156	5386	SAU1c0036_orf_12p	12311
S1M10000046B07	3445	SAU100866	5344	SAU1c0044_orf_100p	12553
S1M10000046B08	3446	SAU101365	5432	SAU1c0044_orf_112p	12556
S1M10000046B09	3447	SAU100866	5344	SAU1c0044_orf_100p	12553
S1M10000046B11	3448	SAU102541	5697	SAU1c0045_orf_195p	12668
S1M10000046B12	3449	SAU101400	5444	SAU1c0036_orf_35p	12326
S1M10000046C02	3450	SAU200601	5787	#N/A	#N/A
S1M10000046C04	3451	SAU100118	5229	SAU1c0015_orf_13p	12125
S1M10000046C05	3452	SAU101159	5387	SAU1c0036_orf_46p	12331
S1M10000046C06	3453	SAU102585	5703	SAU1c0044_orf_289p	12611
S1M10000046C06	3453	SAU201773	5834	SAU2c0446_orf_4p	12996
S1M10000046C07	3454	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000046C08	3455	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000046C11	3456	SAU102144	5608	SAU1c0041_orf_15p	12459
S1M10000046C12	3457	SAU100313	5259	SAU1c0045_orf_153p	12661
S1M10000046C12	3457	SAU100359	5264	SAU1c0032_orf_35p	12239

TABLE IA

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
S1M10000046D01	3458	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000046D02	3459	SAU102144	5608	SAU1c0041_orf_15p	12459
S1M10000046D03	3460	SAU101857	5560	SAU1c0044_orf_156p	12569
S1M10000046D04	3461	SAU102433	5668	SAU1c0045_orf_37p	12701
S1M10000046D05	3462	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000046D08	3463	SAU101495	5467	SAU1c0037_orf_65p	12360
S1M10000046D09	3464	SAU100679	5305	SAU1c0018_orf_14p	12137
S1M10000046D10	3465	SAU101808	5548	SAU1c0032_orf_27p	12232
S1M10000046D11	3466	SAU100496	5279	SAU1c0041_orf_83p	12484
S1M10000046D11	3466	SAU301004	5882	SAU3c1255_orf_1p	13079
S1M10000046D12	3467	SAU100496	5279	SAU1c0041_orf_83p	12484
S1M10000046D12	3467	SAU301004	5882	SAU3c1255_orf_1p	13079
S1M10000046E01	3468	SAU101610	5492	SAU1c0044_orf_5p	12629
S1M10000046E02	3469	SAU101857	5560	SAU1c0044_orf_156p	12569
S1M10000046E04	3470	SAU101800	5540	SAU1c0032_orf_20p	12225
S1M10000046E04	3470	SAU101801	5541	#N/A	#N/A
S1M10000046E07	3471	SAU100521	5283	SAU1c0044_orf_250p	12600
S1M10000046E08	3472	SAU102283	5634	SAU1c0006_orf_1p	12119
S1M10000046E10	3473	SAU102283	5634	SAU1c0006_orf_1p	12119
S1M10000046F01	3474	SAU101028	5370	SAU1c0043_orf_7p	12552
S1M10000046F02	3475	SAU100546	5289	SAU1c0032_orf_2p	12235
S1M10000046F02	3475	SAU102880	5739	SAU1c0032_orf_1p	12224
S1M10000046F05	3476	SAU102671	5729	SAU1c0024_orf_9p	12161
S1M10000046F06	3477	SAU100702	5310	SAU1c0029_orf_34p	12196
S1M10000046F06	3477	SAU300825	5878	SAU3c1171_orf_1p	13068
S1M10000046F08	3478	SAU102297	5640	SAU1c0045_orf_41p	12704
S1M10000046F09	3479	SAU100517	5282	#N/A	#N/A
S1M10000046F10	3480	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000046F12	3481	SAU101365	5432	SAU1c0044_orf_112p	12556
S1M10000046G01	3482	SAU200752	5795	SAU2c0354_orf_5p	12809
S1M10000046G01	3482	SAU300975	5880	SAU3c1240_orf_3p	13075
S1M10000046G02	3483	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000046G03	3484	SAU100773	5326	SAU1c0038_orf_39p	12377
S1M10000046G04	3485	SAU100436	5273	SAU1c0023_orf_20p	12154
S1M10000046G07	3486	SAU101866	5564	SAU1c0036_orf_21p	12319
S1M10000046G09	3487	SAU102663	5727	SAU1c0024_orf_2p	12158
S1M10000046G10	3488	SAU101756	5524	SAU1c0040_orf_82p	12445
S1M10000046H01	3489	SAU101445	5452	SAU1c0038_orf_47p	12382
S1M10000046H01	3489	SAU101446	5453	SAU1c0038_orf_48p	12383
S1M10000046H10	3490	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000047A03	3491	SAU100157	5237	SAU1c0040_orf_81p	12444
S1M10000047A04	3492	SAU300572	5873	SAU3c1019_orf_1p	13051
S1M10000047A05	3493	SAU101805	5545	SAU1c0032_orf_24p	12229
S1M10000047A06	3494	SAU201775	5835	SAU2c0446_orf_4p	12996
S1M10000047A06	3494	SAU301030	5883	SAU3c1268_orf_1p	13080
S1M10000047A07	3495	SAU101807	5547	SAU1c0032_orf_26p	12231
S1M10000047A08	3496	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000047A09	3497	SAU101271	5411	SAU1c0037_orf_90p	12366

TABLE IA

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
S1M10000047A10	3498	SAU100751	5321	SAU1c0036_orf_59p	12335
S1M10000047A11	3499	SAU100131	5232	SAU1c0043_orf_156p	12517
S1M10000047A12	3500	SAU100300	5253	SAU1c0040_orf_90p	12451
S1M10000047B02	3501	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000047B04	3502	SAU101366	5433	SAU1c0033_orf_2p	12266
S1M10000047B05	3503	SAU101545	5474	SAU1c0037_orf_132p	12348
S1M10000047B06	3504	SAU200006	5770	SAU2c0157_orf_1p	12723
S1M10000047B08	3505	SAU101808	5548	SAU1c0032_orf_27p	12232
S1M10000047B09	3506	SAU100131	5232	SAU1c0043_orf_156p	12517
S1M10000047B10	3507	SAU101156	5386	SAU1c0036_orf_12p	12311
S1M10000047B12	3508	SAU101868	5565	SAU1c0036_orf_23p	12320
S1M10000047C01	3509	SAU100275	5252	SAU1c0036_orf_15p	12314
S1M10000047C02	3510	SAU101156	5386	SAU1c0036_orf_12p	12311
S1M10000047C03	3511	SAU200006	5770	SAU2c0157_orf_1p	12723
S1M10000047C04	3512	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000047C06	3513	SAU101815	5552	SAU1c0032_orf_33p	12238
S1M10000047C08	3514	SAU101808	5548	SAU1c0032_orf_27p	12232
S1M10000047C09	3515	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000047C11	3516	SAU201775	5835	SAU2c0446_orf_4p	12996
S1M10000047C11	3516	SAU301030	5883	SAU3c1268_orf_1p	13080
S1M10000047C12	3517	SAU101868	5565	SAU1c0036_orf_23p	12320
S1M10000047D02	3518	SAU101387	5440	SAU1c0038_orf_52p	12386
S1M10000047D03	3519	SAU101868	5565	SAU1c0036_orf_23p	12320
S1M10000047D04	3520	SAU100157	5237	SAU1c0040_orf_81p	12444
S1M10000047D05	3521	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000047D09	3522	SAU100921	5355	SAU1c0038_orf_76p	12396
S1M10000047D10	3523	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000047D11	3524	SAU103038	5757	#N/A	#N/A
S1M10000047D12	3525	SAU101175	5388	SAU1c0031_orf_1p	12213
S1M10000047E01	3526	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000047E02	3527	SAU100131	5232	SAU1c0043_orf_156p	12517
S1M10000047E03	3528	SAU102452	5676	SAU1c0045_orf_20p	12674
S1M10000047E04	3529	SAU101996	5584	SAU1c0040_orf_99p	12456
S1M10000047E05	3530	SAU101815	5552	SAU1c0032_orf_33p	12238
S1M10000047E06	3531	SAU101807	5547	SAU1c0032_orf_26p	12231
S1M10000047E08	3532	SAU102200	5611	SAU1c0045_orf_168p	12665
S1M10000047E09	3533	SAU100810	5333	SAU1c0037_orf_11p	12343
S1M10000047E10	3534	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000047E11	3535	SAU101156	5386	SAU1c0036_orf_12p	12311
S1M10000047E12	3536	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000047F02	3537	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000047F03	3538	SAU101242	5404	SAU1c0044_orf_18p	12578
S1M10000047F04	3539	SAU300572	5873	SAU3c1019_orf_1p	13051
S1M10000047F05	3540	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000047F06	3541	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000047F07	3542	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000047F08	3543	SAU101242	5404	SAU1c0044_orf_18p	12578
S1M10000047F09	3544	SAU100157	5237	SAU1c0040_orf_81p	12444

TABLE IA

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
S1M10000047F10	3545	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000047F11	3546	SAU101805	5545	SAU1c0032_orf_24p	12229
S1M10000047F12	3547	SAU101808	5548	SAU1c0032_orf_27p	12232
S1M10000047G01	3548	SAU101369	5434	SAU1c0033_orf_5p	12274
S1M10000047G02	3549	SAU100141	5236	SAU1c0032_orf_8p	12259
S1M10000047G04	3550	SAU101341	5424	SAU1c0044_orf_38p	12618
S1M10000047G05	3551	SAU100684	5306	SAU1c0044_orf_68p	12632
S1M10000047G05	3551	SAU100685	5307	SAU1c0044_orf_69p	12633
S1M10000047G06	3552	SAU100141	5236	SAU1c0032_orf_8p	12259
S1M10000047G07	3553	SAU101798	5538	SAU1c0032_orf_18p	12222
S1M10000047G08	3554	SAU101028	5370	SAU1c0043_orf_7p	12552
S1M10000047G09	3555	SAU100810	5333	SAU1c0037_orf_11p	12343
S1M10000047G10	3556	SAU102607	5712	SAU1c0041_orf_51p	12472
S1M10000047H03	3557	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000047H04	3558	SAU102200	5611	SAU1c0045_orf_168p	12665
S1M10000047H05	3559	SAU102452	5676	SAU1c0045_orf_20p	12674
S1M10000047H06	3560	SAU103038	5757	#N/A	#N/A
S1M10000047H07	3561	SAU200006	5770	SAU2c0157_orf_1p	12723
S1M10000047H08	3562	SAU101798	5538	SAU1c0032_orf_18p	12222
S1M10000047H09	3563	SAU102578	5701	SAU1c0039_orf_61p	12411
S1M10000047H11	3564	SAU101028	5370	SAU1c0043_orf_7p	12552
S1M10000048A02	3565	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000048A03	3566	SAU100866	5344	SAU1c0044_orf_100p	12553
S1M10000048A04	3567	SAU103038	5757	#N/A	#N/A
S1M10000048A05	3568	SAU101868	5565	SAU1c0036_orf_23p	12320
S1M10000048A06	3569	SAU100157	5237	SAU1c0040_orf_81p	12444
S1M10000048A07	3570	SAU101156	5386	SAU1c0036_orf_12p	12311
S1M10000048A09	3571	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000048A10	3572	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000048A11	3573	SAU101807	5547	SAU1c0032_orf_26p	12231
S1M10000048A12	3574	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000048B02	3575	SAU100608	5297	SAU1c0034_orf_69p	12293
S1M10000048B05	3576	SAU101028	5370	SAU1c0043_orf_7p	12552
S1M10000048B08	3577	SAU102452	5676	SAU1c0045_orf_20p	12674
S1M10000048B10	3578	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000048B11	3579	SAU103038	5757	#N/A	#N/A
S1M10000048B12	3580	SAU200916	5797	SAU2c0373_orf_4p	12838
S1M10000048B12	3580	SAU301620	5899	SAU3c1478_orf_2p	13140
S1M10000048C01	3581	SAU101028	5370	SAU1c0043_orf_7p	12552
S1M10000048C02	3582	SAU301465	5896	SAU3c1429_orf_4p	13121
S1M10000048C03	3583	SAU102200	5611	SAU1c0045_orf_168p	12665
S1M10000048C05	3584	SAU300998	5881	SAU3c1253_orf_3p	13077
S1M10000048C06	3585	SAU100684	5306	SAU1c0044_orf_68p	12632
S1M10000048C06	3585	SAU100685	5307	SAU1c0044_orf_69p	12633
S1M10000048C07	3586	SAU102452	5676	SAU1c0045_orf_20p	12674
S1M10000048C08	3587	SAU101632	5499	SAU1c0039_orf_3p	12407
S1M10000048C09	3588	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000048C11	3589	SAU101815	5552	SAU1c0032_orf_33p	12238

TABLE IA

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
S1M10000048D02	3590	SAU100123	5230	SAU1c0043_orf_189p	12526
S1M10000048D02	3590	SAU102001	5586	SAU1c0040_orf_102p	12424
S1M10000048D02	3590	SAU103159	5762	SAU1c0045_orf_204p	12670
S1M10000048D02	3590	SAU201827	5837	SAU2c0449_orf_21p	13002
S1M10000048D08	3591	SAU300572	5873	SAU3c1019_orf_1p	13051
S1M10000048D09	3592	SAU100141	5236	SAU1c0032_orf_8p	12259
S1M10000048D10	3593	SAU302950	5914	SAU3c1512_orf_12p	13160
S1M10000048D12	3594	SAU102599	5706	SAU1c0041_orf_45p	12466
S1M10000048D12	3594	SAU103191	5765	SAU1c0041_orf_44p	12465
S1M10000048E02	3595	SAU101028	5370	SAU1c0043_orf_7p	12552
S1M10000048E03	3596	SAU102200	5611	SAU1c0045_orf_168p	12665
S1M10000048E04	3597	SAU101545	5474	SAU1c0037_orf_132p	12348
S1M10000048E06	3598	SAU200006	5770	SAU2c0157_orf_1p	12723
S1M10000048E07	3599	SAU100959	5359	SAU1c0042_orf_102p	12485
S1M10000048E08	3600	SAU101807	5547	SAU1c0032_orf_26p	12231
S1M10000048E10	3601	SAU302950	5914	SAU3c1512_orf_12p	13160
S1M10000048F02	3602	SAU101387	5440	SAU1c0038_orf_52p	12386
S1M10000048F07	3603	SAU101175	5388	SAU1c0031_orf_1p	12213
S1M10000048F08	3604	SAU100157	5237	SAU1c0040_orf_81p	12444
S1M10000048F09	3605	SAU101793	5534	SAU1c0032_orf_14p	12218
S1M10000048F11	3606	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000048F11	3606	SAU301148	5888	#N/A	#N/A
S1M10000048F12	3607	SAU103038	5757	#N/A	#N/A
S1M10000048G02	3608	SAU102453	5677	SAU1c0045_orf_19p	12669
S1M10000048G03	3609	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000048G04	3610	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000048G05	3611	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000048G07	3612	SAU102006	5589	SAU1c0040_orf_107p	12427
S1M10000048G07	3612	SAU102007	5590	SAU1c0040_orf_108p	12428
S1M10000048G10	3613	SAU101793	5534	SAU1c0032_orf_14p	12218
S1M10000048G11	3614	SAU200006	5770	SAU2c0157_orf_1p	12723
S1M10000048H01	3615	SAU100608	5297	SAU1c0034_orf_69p	12293
S1M10000048H02	3616	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000048H03	3617	SAU101815	5552	SAU1c0032_orf_33p	12238
S1M10000048H04	3618	SAU102200	5611	SAU1c0045_orf_168p	12665
S1M10000048H05	3619	SAU100157	5237	SAU1c0040_orf_81p	12444
S1M10000048H07	3620	SAU100157	5237	SAU1c0040_orf_81p	12444
S1M10000048H08	3621	SAU100141	5236	SAU1c0032_orf_8p	12259
S1M10000048H09	3622	SAU100157	5237	SAU1c0040_orf_81p	12444
S1M10000048H10	3623	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000048H11	3624	SAU101271	5411	SAU1c0037_orf_90p	12366
K1M10000037D10	1077	ECO100078	10023	#N/A	#N/A
K1M10000002F02	1054	ECO100252	10052	#N/A	#N/A
K1M10000007F01	1057	ECO100397	10064	#N/A	#N/A
K1M10000007F01	1057	ECO100398	10065	#N/A	#N/A
K1M10000004F06	1056	ECO100990	10120	#N/A	#N/A
K1M10000019D06	1064	ECO100990	10120	#N/A	#N/A
K1M10000030C07	1070	ECO102108	10214	#N/A	#N/A

TABLE IA

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
K1M10000044G05	1086	ECO102262	10228	#N/A	#N/A
K1M10000036G08	1076	ECO102447	10247	#N/A	#N/A
K1M10000033E01	1075	ECO102539	10258	#N/A	#N/A
K1M10000043D05	1081	ECO102620	10266	#N/A	#N/A
K1M10000045D10	1088	ECO102620	10266	#N/A	#N/A
K1M10000003C01	1055	ECO103101	10315	#N/A	#N/A
K1M10000030E07	1071	ECO104120	10462	#N/A	#N/A
K1M10000045A07	1087	ECO104268	10475	#N/A	#N/A
S4M10000020F05	3721	ECO100449	#N/A	#N/A	#N/A
S4M10000026D04	3742	ECO100676	#N/A	#N/A	#N/A
S4M10000014D07	3706	ECO100757	#N/A	#N/A	#N/A
S4M10000015B11	3708	ECO100757	#N/A	#N/A	#N/A
S4M10000016A02	3710	ECO100757	#N/A	#N/A	#N/A
S4M10000022E12	3725	ECO100757	#N/A	#N/A	#N/A
S4M10000026E12	3744	ECO100757	#N/A	#N/A	#N/A
S4M10000035E03	3764	ECO100757	#N/A	#N/A	#N/A
S4M10000008H10	3693	ECO100758	10101	#N/A	#N/A
S4M10000014B05	3704	ECO100758	10101	#N/A	#N/A
S4M10000014D07	3706	ECO100758	10101	#N/A	#N/A
S4M10000015B11	3708	ECO100758	10101	#N/A	#N/A
S4M10000015E09	3709	ECO100758	10101	#N/A	#N/A
S4M10000016A02	3710	ECO100758	10101	#N/A	#N/A
S4M10000022E12	3725	ECO100758	10101	#N/A	#N/A
S4M10000029B12	3747	ECO100758	10101	#N/A	#N/A
S4M10000020G10	3722	ECO100796	10105	#N/A	#N/A
S4M10000023F01	3728	ECO101916	#N/A	#N/A	#N/A
S4M10000014H02	3707	ECO102028	#N/A	#N/A	#N/A
S4M10000012B06	3700	ECO102066	#N/A	#N/A	#N/A
S4M10000035D01	3762	ECO102066	#N/A	#N/A	#N/A
S4M10000024C06	3730	ECO102189	10224	#N/A	#N/A
S4M10000006C05	3689	ECO102282	#N/A	#N/A	#N/A
S4M10000037H09	3772	ECO102296	#N/A	#N/A	#N/A
S4M10000030G11	3751	ECO102302	#N/A	#N/A	#N/A
S4M10000026C10	3741	ECO102416	10245	#N/A	#N/A
S4M10000026E06	3743	ECO102416	10245	#N/A	#N/A
S4M10000036F07	3768	ECO102416	10245	#N/A	#N/A
S4M10000034A02	3756	ECO102526	#N/A	#N/A	#N/A
S4M10000006F08	3690	ECO102541	10259	#N/A	#N/A
S4M10000002G08	3684	ECO102730	#N/A	#N/A	#N/A
S4M10000026C10	3741	ECO102870	#N/A	#N/A	#N/A
S4M10000026E06	3743	ECO102870	#N/A	#N/A	#N/A
S4M10000036F07	3768	ECO102870	#N/A	#N/A	#N/A
S4M10000034H05	3759	ECO102900	#N/A	#N/A	#N/A
S4M10000006A08	3688	ECO102944	#N/A	#N/A	#N/A
S4M10000014D04	3705	ECO102986	10301	#N/A	#N/A
S4M10000022D12	3724	ECO103238	10354	#N/A	#N/A
S4M10000033F08	3753	ECO103238	10354	#N/A	#N/A
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TABLE IA

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S4M10000024B02	3729	ECO103280	#N/A	#N/A	#N/A
S4M10000020A04	3720	ECO103461	#N/A	#N/A	#N/A
S4M10000002B06	3681	ECO103666	#N/A	#N/A	#N/A
S4M10000019H06	3719	ECO103738	#N/A	#N/A	#N/A
S4M10000024H02	3736	ECO103738	#N/A	#N/A	#N/A
S4M10000030F07	3750	ECO103738	#N/A	#N/A	#N/A
S4M10000034H09	3760	ECO103738	#N/A	#N/A	#N/A
S4M10000032B12	3752	ECO103935	#N/A	#N/A	#N/A
S4M10000002B09	3682	ECO103936	#N/A	#N/A	#N/A
S4M10000037A10	3770	ECO103951	#N/A	#N/A	#N/A
S4M10000018D09	3711	ECO104080	#N/A	#N/A	#N/A
S4M10000035F09	3766	EFA101301	#N/A	EFA1c0040_orf_173p	#N/A
S4M10000035F09	3766	EFA102170	#N/A	EFA1c0040_orf_121p	#N/A
S4M10000001C01	3680	EFA103268	#N/A	EFA1c0010_orf_1p	10479
S4M10000036F07	3768	HPY200334	#N/A	#N/A	#N/A
S4M10000001C01	3680	HPY201116	11570	#N/A	#N/A
S4M10000037A10	3770	KPN100467	#N/A	KPN1c0583_orf_2p	#N/A
S4M10000030G11	3751	KPN101078	#N/A	KPN1c1190_orf_1p	#N/A
S4M10000024B02	3729	KPN101160	#N/A	KPN1c1224_orf_1p	#N/A
S4M10000032B12	3752	KPN101846	#N/A	KPN1c1681_orf_2p	#N/A
S4M10000006C05	3689	KPN102011	#N/A	KPN1c1862_orf_4p	#N/A
S4M10000035B01	3761	KPN102014	#N/A	KPN1c1786_orf_1p	11654
S4M10000012B06	3700	KPN102524	#N/A	#N/A	#N/A
S4M10000035D01	3762	KPN102524	#N/A	#N/A	#N/A
S4M10000002G04	3683	KPN102558	#N/A	KPN1c1982_orf_3p	#N/A
S4M10000002G08	3684	KPN102558	#N/A	KPN1c1982_orf_3p	#N/A
S4M10000008H10	3693	KPN103640	#N/A	KPN1c2761_orf_1p	#N/A
S4M10000014B05	3704	KPN103640	#N/A	KPN1c2761_orf_1p	#N/A
S4M10000014D07	3706	KPN103640	#N/A	KPN1c2761_orf_1p	#N/A
S4M10000015B11	3708	KPN103640	#N/A	KPN1c2761_orf_1p	#N/A
S4M10000015E09	3709	KPN103640	#N/A	KPN1c2761_orf_1p	#N/A
S4M10000016A02	3710	KPN103640	#N/A	KPN1c2761_orf_1p	#N/A
S4M10000022E12	3725	KPN103640	#N/A	KPN1c2761_orf_1p	#N/A
S4M10000026E12	3744	KPN103640	#N/A	KPN1c2761_orf_1p	#N/A
S4M10000035E03	3764	KPN103640	#N/A	KPN1c2761_orf_1p	#N/A
S4M10000008H10	3693	KPN103641	#N/A	KPN1c2761_orf_2p	11705
S4M10000014B05	3704	KPN103641	#N/A	KPN1c2761_orf_2p	11705
S4M10000014D07	3706	KPN103641	#N/A	KPN1c2761_orf_2p	11705
S4M10000015B11	3708	KPN103641	#N/A	KPN1c2761_orf_2p	11705
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S4M10000022E12	3725	KPN103641	#N/A	KPN1c2761_orf_2p	11705
S4M10000029B12	3747	KPN103641	#N/A	KPN1c2761_orf_2p	11705
S4M10000035E03	3764	KPN103641	#N/A	KPN1c2761_orf_2p	11705
S4M10000026C10	3741	KPN103871	#N/A	KPN1c2844_orf_2p	#N/A
S4M10000026E06	3743	KPN103871	#N/A	KPN1c2844_orf_2p	#N/A
S4M10000036F07	3768	KPN103871	#N/A	KPN1c2844_orf_2p	#N/A

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S4M10000024H02	3736	KPN104321	#N/A	KPN1c3011_orf_1p	#N/A
S4M10000030F07	3750	KPN104321	#N/A	KPN1c3011_orf_1p	#N/A
S4M10000034H09	3760	KPN104321	#N/A	KPN1c3011_orf_1p	#N/A
S4M10000035F02	3765	KPN104321	#N/A	KPN1c3011_orf_1p	#N/A
S4M10000002B06	3681	KPN104608	#N/A	KPN1c3070_orf_3p	#N/A
S4M10000018D09	3711	KPN105957	#N/A	KPN1c3587_orf_1p	#N/A
S4M10000024C06	3730	KPN106468	#N/A	KPN1c1186_orf_1p	11638
S4M10000009A05	3694	KPN106681	#N/A	#N/A	#N/A
S4M10000010D04	3696	KPN106681	#N/A	#N/A	#N/A
S4M10000011E08	3699	KPN106681	#N/A	#N/A	#N/A
S4M10000020A04	3720	KPN106813	#N/A	KPN1c2010_orf_1p	#N/A
S4M10000005G05	3685	KPN106840	#N/A	KPN1c2087_orf_1p	11664
S4M10000006F08	3690	KPN106840	#N/A	KPN1c2087_orf_1p	11664
S4M10000007G01	3691	KPN106840	#N/A	KPN1c2087_orf_1p	11664
S4M10000008C08	3692	KPN106840	#N/A	KPN1c2087_orf_1p	11664
S4M10000018E10	3712	KPN106840	#N/A	KPN1c2087_orf_1p	11664
S4M10000018F10	3713	KPN106840	#N/A	KPN1c2087_orf_1p	11664
S4M10000019G04	3717	KPN106840	#N/A	KPN1c2087_orf_1p	11664
S4M10000001C01	3680	SAU101756	#N/A	SAU1c0040_orf_82p	12445
S4M10000001C01	3680	SAU200931	#N/A	SAU2c0151_orf_1p	12722
S4M10000001C01	3680	SPN102008	#N/A	SPN1c0007_orf_92p	#N/A
S4M10000001C01	3680	SPN202419	#N/A	SPN2c0592_orf_1p	#N/A
S4M10000019H06	3719	STY000068	#N/A	STYc00048_orf_26p	#N/A
S4M10000024H02	3736	STY000068	#N/A	STYc00048_orf_26p	#N/A
S4M10000030F07	3750	STY000068	#N/A	STYc00048_orf_26p	#N/A
S4M10000034H09	3760	STY000068	#N/A	STYc00048_orf_26p	#N/A
S4M10000035F02	3765	STY000068	#N/A	STYc00048_orf_26p	#N/A
S4M10000026C10	3741	STY000225	#N/A	STYc00041_orf_40p	13740
S4M10000026E06	3743	STY000225	#N/A	STYc00041_orf_40p	13740
S4M10000036F07	3768	STY000225	#N/A	STYc00041_orf_40p	13740
S4M10000026D04	3742	STY000244	#N/A	STYc00041_orf_11p	#N/A
S4M10000034H05	3759	STY000244	#N/A	STYc00041_orf_11p	#N/A
S4M10000027E02	3746	STY000409	#N/A	STYc00053_orf_110p	#N/A
S4M10000025E02	3738	STY000498	#N/A	STYc00072_orf_46p	#N/A
S4M10000034A02	3756	STY000498	#N/A	STYc00072_orf_46p	#N/A
S4M10000034D06	3758	STY000625	#N/A	STYc00062_orf_63p	13784
S4M10000014D04	3705	STY000737	#N/A	STYc00054_orf_108p	13759
S4M10000013H02	3703	STY000753	#N/A	STYc00054_orf_91p	#N/A
S4M10000006A08	3688	STY000817	#N/A	STYc00054_orf_145p	#N/A
S4M10000036D07	3767	STY000817	#N/A	STYc00054_orf_145p	#N/A
S4M10000018D09	3711	STY000848	#N/A	STYc00101_orf_23p	#N/A
S4M10000014H02	3707	STY000968	#N/A	STYc00086_orf_86p	#N/A
S4M10000024G04	3734	STY000986	#N/A	#N/A	#N/A
S4M10000025H07	3740	STY000986	#N/A	#N/A	#N/A
S4M10000029D12	3748	STY000986	#N/A	#N/A	#N/A
S4M10000037A10	3770	STY001009	#N/A	STYc00080_orf_144p	#N/A
S4M10000035F09	3766	STY001185	#N/A	STYc00098_orf_2p	#N/A

TABLE IA

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S4M10000022H06	3727	STY001285	#N/A	#N/A	#N/A
S4M10000030D03	3749	STY001285	#N/A	#N/A	#N/A
S4M10000037E10	3771	STY001363	#N/A	STYc00034_orf_126p	#N/A
S4M10000002B06	3681	STY001380	#N/A	STYc00119_orf_3p	#N/A
S4M10000011D08	3698	STY001534	#N/A	#N/A	#N/A
S4M10000024C11	3731	STY001582	#N/A	#N/A	#N/A
S4M10000025A11	3737	STY001582	#N/A	#N/A	#N/A
S4M10000035F09	3766	STY001619	#N/A	#N/A	#N/A
S4M10000022D12	3724	STY001777	#N/A	STYc00187_orf_4p	13970
S4M10000033F08	3753	STY001777	#N/A	STYc00187_orf_4p	13970
S4M10000033G09	3755	STY001777	#N/A	STYc00187_orf_4p	13970
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S4M10000026C10	3741	STY001853	#N/A	STYc00180_orf_22p	#N/A
S4M10000026E06	3743	STY001853	#N/A	STYc00180_orf_22p	#N/A
S4M10000036F07	3768	STY001853	#N/A	STYc00180_orf_22p	#N/A
S4M10000020A04	3720	STY002064	#N/A	STYc00074_orf_163p	#N/A
S4M10000020A04	3720	STY002066	#N/A	#N/A	#N/A
S4M10000024B02	3729	STY002145	#N/A	STYc00074_orf_17p	#N/A
S4M10000010B05	3695	STY002525	#N/A	STYc00114_orf_159p	#N/A
S4M10000012B12	3701	STY002525	#N/A	STYc00114_orf_159p	#N/A
S4M10000022D04	3723	STY002525	#N/A	STYc00114_orf_159p	#N/A
S4M10000022G07	3726	STY002525	#N/A	STYc00114_orf_159p	#N/A
S4M10000024G01	3733	STY002525	#N/A	STYc00114_orf_159p	#N/A
S4M10000024G09	3735	STY002525	#N/A	STYc00114_orf_159p	#N/A
S4M10000025E05	3739	STY002525	#N/A	STYc00114_orf_159p	#N/A
S4M10000027C10	3745	STY002525	#N/A	STYc00114_orf_159p	#N/A
S4M10000034A09	3757	STY002525	#N/A	STYc00114_orf_159p	#N/A
S4M10000037H09	3772	STY002590	#N/A	STYc00114_orf_104p	#N/A
S4M10000002G04	3683	STY002623	#N/A	STYc00114_orf_90p	#N/A
S4M10000002G08	3684	STY002623	#N/A	STYc00114_orf_90p	#N/A
S4M10000033G05	3754	STY002638	#N/A	STYc00114_orf_15p	13870
S4M10000006A06	3687	STY002672	#N/A	STYc00114_orf_136p	#N/A
S4M10000010H04	3697	STY002711	#N/A	STYc00223_orf_1p	#N/A
S4M10000005H02	3686	STY002738	#N/A	STYc00223_orf_17p	#N/A
S4M10000012B06	3700	STY002826	#N/A	STYc00152_orf_12p	#N/A
S4M10000035D01	3762	STY002826	#N/A	STYc00152_orf_12p	#N/A
S4M10000018G03	3714	STY002889	#N/A	#N/A	#N/A
S4M10000018H04	3715	STY002889	#N/A	#N/A	#N/A
S4M10000019F05	3716	STY002889	#N/A	#N/A	#N/A
S4M10000019G05	3718	STY002889	#N/A	#N/A	#N/A
S4M10000037E10	3771	STY002959	#N/A	STYc00215_orf_11p	14011
S4M10000002B09	3682	STY003082	#N/A	STYc00238_orf_12p	#N/A
S4M10000032B12	3752	STY003084	#N/A	STYc00238_orf_13p	#N/A
S4M10000024C06	3730	STY003375	#N/A	STYc00183_orf_19p	13957
S4M10000012D02	3702	STY003377	#N/A	#N/A	#N/A
S4M10000030G11	3751	STY003384	#N/A	STYc00183_orf_130p	#N/A
S4M10000006F08	3690	STY003460	#N/A	STYc00339_orf_20p	14087

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S4M10000020G10	3722	STY004048	#N/A	STYc00207_orf_161p	13999
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S4M10000014B05	3704	STY004152	#N/A	STYc00207_orf_194p	14003
S4M10000015E09	3709	STY004152	#N/A	STYc00207_orf_194p	14003
S4M10000016A02	3710	STY004152	#N/A	STYc00207_orf_194p	14003
S4M10000022E12	3725	STY004152	#N/A	STYc00207_orf_194p	14003
S4M10000029B12	3747	STY004152	#N/A	STYc00207_orf_194p	14003
S4M10000035E03	3764	STY004152	#N/A	STYc00207_orf_194p	14003
S4M10000008H10	3693	STY004154	#N/A	STYc00207_orf_195p	#N/A
S4M10000014B05	3704	STY004154	#N/A	STYc00207_orf_195p	#N/A
S4M10000014D07	3706	STY004154	#N/A	STYc00207_orf_195p	#N/A
S4M10000015B11	3708	STY004154	#N/A	STYc00207_orf_195p	#N/A
S4M10000015E09	3709	STY004154	#N/A	STYc00207_orf_195p	#N/A
S4M10000016A02	3710	STY004154	#N/A	STYc00207_orf_195p	#N/A
S4M10000022E12	3725	STY004154	#N/A	STYc00207_orf_195p	#N/A
S4M10000026E12	3744	STY004154	#N/A	STYc00207_orf_195p	#N/A
S4M10000035E03	3764	STY004154	#N/A	STYc00207_orf_195p	#N/A
S4M10000005G05	3685	STY004239	#N/A	#N/A	#N/A
S4M10000007G01	3691	STY004239	#N/A	#N/A	#N/A
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S4M10000018E10	3712	STY004239	#N/A	#N/A	#N/A
S4M10000018F10	3713	STY004239	#N/A	#N/A	#N/A
S4M10000019G04	3717	STY004239	#N/A	#N/A	#N/A
S4M10000037A04	3769	STY005016	#N/A	#N/A	#N/A
K1M10000007F01	1057	SAU100968	#N/A	SAU1c0044_orf_90p	12643
K1M10000007F01	1057	SAU201145	#N/A	SAU2c0405_orf_7p	12884
K1M10000007F01	1057	SPN101971	#N/A	SPN1c0009_orf_54p	#N/A
K1M10000007F01	1057	SPN201024	#N/A	SPN2c0417_orf_4p	#N/A
K1M10000003C01	1055	STY000773	#N/A	STYc00054_orf_16p	13764
K1M10000023E09	1068	STY000886	#N/A	#N/A	#N/A
K1M10000023E10	1069	STY000886	#N/A	#N/A	#N/A
K1M10000007F01	1057	STY001430	#N/A	STYc00148_orf_11p	13915
K1M10000007F01	1057	STY001433	#N/A	STYc00148_orf_12p	13916
K1M10000036G08	1076	STY001867	#N/A	STYc00180_orf_50p	13948
K1M10000030C07	1070	STY002768	#N/A	#N/A	#N/A
K1M10000037D10	1077	STY002995	#N/A	STYc00215_orf_67p	14018
K1M10000044G05	1086	STY003357	#N/A	STYc00183_orf_91p	13963

TABLE IA

TABLE IC

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
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EFA100023	3807	4862
EFA100065	3808	4863
EFA100151	3809	4864
EFA100157	3810	4865
EFA100165	3811	4866
EFA100190	3812	4867
EFA100194	3813	4868
EFA100200	3814	4869
EFA100210	3815	4870
EFA100211	3816	4871
EFA100289	3817	4872
EFA100295	3818	4873
EFA100312	3819	4874
EFA100329	3820	4875
EFA100394	3821	4876
EFA100397	3822	4877
EFA100399	3823	4878
EFA100426	3824	4879
EFA100478	3825	4880
EFA100615	3826	4881
EFA100617	3827	4882
EFA100641	3828	4883
EFA100642	3829	4884
EFA100668	3830	4885
EFA100689	3831	4886
EFA100704	3832	4887
EFA100739	3833	4888
EFA100740	3834	4889
EFA100741	3835	4890
EFA100742	3836	4891
EFA100748	3837	4892
EFA100756	3838	4893
EFA100757	3839	4894
EFA100783	3840	4895
EFA100795	3841	4896
EFA100798	3842	4897
EFA100811	3843	4898
EFA100870	3844	4899
EFA100914	3845	4900
EFA100919	3846	4901
EFA100955	3847	4902
EFA100970	3848	4903
EFA100978	3849	4904
EFA100991	3850	4905
EFA101022	3851	4906
EFA101060	3852	4907

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
EFA101079	3853	4908
EFA101080	3854	4909
EFA101086	3855	4910
EFA101120	3856	4911
EFA101121	3857	4912
EFA101123	3858	4913
EFA101141	3859	4914
EFA101150	3860	4915
EFA101159	3861	4916
EFA101160	3862	4917
EFA101161	3863	4918
EFA101162	3864	4919
EFA101163	3865	4920
EFA101164	3866	4921
EFA101165	3867	4922
EFA101169	3868	4923
EFA101253	3869	4924
EFA101257	3870	4925
EFA101258	3871	4926
EFA101322	3872	4927
EFA101339	3873	4928
EFA101340	3874	4929
EFA101354	3875	4930
EFA101370	3876	4931
EFA101403	3877	4932
EFA101404	3878	4933
EFA101409	3879	4934
EFA101410	3880	4935
EFA101411	3881	4936
EFA101412	3882	4937
EFA101413	3883	4938
EFA101414	3884	4939
EFA101415	3885	4940
EFA101416	3886	4941
EFA101417	3887	4942
EFA101424	3888	4943
EFA101425	3889	4944
EFA101477	3890	4945
EFA101536	3891	4946
EFA101540	3892	4947
EFA101541	3893	4948
EFA101583	3894	4949
EFA101670	3895	4950
EFA101682	3896	4951
EFA101685	3897	4952
EFA101686	3898	4953
EFA101695	3899	4954
EFA101736	3900	4955
EFA101737	3901	4956

TABLE IA

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
EFA101753	3902	4957
EFA101765	3903	4958
EFA101790	3904	4959
EFA101791	3905	4960
EFA101792	3906	4961
EFA101795	3907	4962
EFA101797	3908	4963
EFA101799	3909	4964
EFA101833	3910	4965
EFA101868	3911	4966
EFA101872	3912	4967
EFA101873	3913	4968
EFA101892	3914	4969
EFA101924	3915	4970
EFA101925	3916	4971
EFA101963	3917	4972
EFA102006	3918	4973
EFA102022	3919	4974
EFA102023	3920	4975
EFA102051	3921	4976
EFA102091	3922	4977
EFA102110	3923	4978
EFA102183	3924	4979
EFA102185	3925	4980
EFA102186	3926	4981
EFA102201	3927	4982
EFA102205	3928	4983
EFA102253	3929	4984
EFA102282	3930	4985
EFA102326	3931	4986
EFA102338	3932	4987
EFA102350	3933	4988
EFA102351	3934	4989
EFA102352	3935	4990
EFA102353	3936	4991
EFA102389	3937	4992
EFA102453	3938	4993
EFA102501	3939	4994
EFA102502	3940	4995
EFA102503	3941	4996
EFA102518	3942	4997
EFA102541	3943	4998
EFA102542	3944	4999
EFA102549	3945	5000
EFA102551	3946	5001
EFA102554	3947	5002
EFA102655	3948	5003
EFA102656	3949	5004
EFA102698	3950	5005

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
EFA102728	3951	5006
EFA102736	3952	5007
EFA102764	3953	5008
EFA102774	3954	5009
EFA102780	3955	5010
EFA102788	3956	5011
EFA102802	3957	5012
EFA102813	3958	5013
EFA102915	3959	5014
EFA103021	3960	5015
EFA103033	3961	5016
EFA103038	3962	5017
EFA103039	3963	5018
EFA103062	3964	5019
EFA103081	3965	5020
EFA103174	3966	5021
EFA103210	3967	5022
EFA103268	3968	5023
EFA103295	3969	5024
EFA103348	3970	5025
EFA103365	3971	5026
EFA103375	3972	5027
EFA103504	3973	5028
EFA103508	3974	5029
EFA103571	3975	5030
EFA103786	3976	5031
KPN100432	3977	5032
KPN100854	3978	5033
KPN101022	3979	5034
KPN101026	3980	5035
KPN101729	3981	5036
KPN101750	3982	5037
KPN102057	3983	5038
KPN102638	3984	5039
KPN103882	3985	5040
KPN104183	3986	5041
KPN104281	3987	5042
KPN104430	3988	5043
KPN104538	3989	5044
KPN104716	3990	5045
KPN105722	3991	5046
KPN105779	3992	5047
KPN106044	3993	5048
KPN106659	3994	5049
KPN106840	3995	5050
KPN107626	3996	5051
KPN107776	3997	5052
PA0028	3998	5053
PA0120	3999	5054

TABLE IA

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
PA0129	4000	5055
PA0141	4001	5056
PA0221	4002	5057
PA0265	4003	5058
PA0321	4004	5059
PA0337	4005	5060
PA0353	4006	5061
PA0378	4007	5062
PA0401	4008	5063
PA0413	4009	5064
PA0414	4010	5065
PA0419	4011	5066
PA0423	4012	5067
PA0469	4013	5068
PA0472	4014	5069
PA0506	4015	5070
PA0600	4016	5071
PA0642	4017	5072
PA0650	4018	5073
PA0715	4019	5074
PA0788	4020	5075
PA0882	4021	5076
PA0934	4022	5077
PA0938	4023	5078
PA1019	4024	5079
PA1072	4025	5080
PA1115	4026	5081
PA1270	4027	5082
PA1301	4028	5083
PA1360	4029	5084
PA1365	4030	5085
PA1398	4031	5086
PA1462	4032	5087
PA1493	4033	5088
PA1547	4034	5089
PA1636	4035	5090
PA1684	4036	5091
PA1868	4037	5092
PA1876	4038	5093
PA1918	4039	5094
PA1986	4040	5095
PA2009	4041	5096
PA2083	4042	5097
PA2101	4043	5098
PA2108	4044	5099
PA2128	4045	5100
PA2147	4046	5101
PA2196	4047	5102
PA2197	4048	5103

TABLE IA

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
PA2222	4049	5104
PA2313	4050	5105
PA2398	4051	5106
PA2424	4052	5107
PA2461	4053	5108
PA2470	4054	5109
PA2488	4055	5110
PA2494	4056	5111
PA2584	4057	5112
PA2594	4058	5113
PA2634	4059	5114
PA2641	4060	5115
PA2671	4061	5116
PA2680	4062	5117
PA2684	4063	5118
PA2726	4064	5119
PA2742	4065	5120
PA3006	4066	5121
PA3011	4067	5122
PA3013	4068	5123
PA3041	4069	5124
PA3048	4070	5125
PA3068	4071	5126
PA3121	4072	5127
PA3153	4073	5128
PA3154	4074	5129
PA3160	4075	5130
PA3279	4076	5131
PA3280	4077	5132
PA3374	4078	5133
PA3479	4079	5134
PA3484	4080	5135
PA3522	4081	5136
PA3643	4082	5137
PA3703	4083	5138
PA3709	4084	5139
PA3716	4085	5140
PA3764	4086	5141
PA3845	4087	5142
PA3866	4088	5143
PA3876	4089	5144
PA3877	4090	5145
PA3931	4091	5146
PA3984	4092	5147
PA4024	4093	5148
PA4027	4094	5149
PA4037	4095	5150
PA4067	4096	5151
PA4070	4097	5152

TABLE IA

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
PA4081	4098	5153
PA4105	4099	5154
PA4124	4100	5155
PA4125	4101	5156
PA4158	4102	5157
PA4237	4103	5158
PA4242	4104	5159
PA4244	4105	5160
PA4245	4106	5161
PA4246	4107	5162
PA4247	4108	5163
PA4248	4109	5164
PA4249	4110	5165
PA4250	4111	5166
PA4251	4112	5167
PA4252	4113	5168
PA4253	4114	5169
PA4254	4115	5170
PA4256	4116	5171
PA4257	4117	5172
PA4258	4118	5173
PA4259	4119	5174
PA4262	4120	5175
PA4263	4121	5176
PA4264	4122	5177
PA4268	4123	5178
PA4269	4124	5179
PA4271	4125	5180
PA4272	4126	5181
PA4316	4127	5182
PA4332	4128	5183
PA4347	4129	5184
PA4363	4130	5185
PA4375	4131	5186
PA4413	4132	5187
PA4433	4133	5188
PA4473	4134	5189
PA4506	4135	5190
PA4512	4136	5191
PA4542	4137	5192
PA4576	4138	5193
PA4598	4139	5194
PA4665	4140	5195
PA4681	4141	5196
PA4709	4142	5197
PA4744	4143	5198
PA4771	4144	5199
PA4888	4145	5200
PA4942	4146	5201

TABLE IA

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
PA4997	4147	5202
PA5030	4148	5203
PA5076	4149	5204
PA5088	4150	5205
PA5193	4151	5206
PA5199	4152	5207
PA5207	4153	5208
PA5209	4154	5209
PA5248	4155	5210
PA5299	4156	5211
PA5316	4157	5212
PA5388	4158	5213
PA5393	4159	5214
PA5436	4160	5215
PA5443	4161	5216
PA5490	4162	5217
PA5493	4163	5218
PA5507	4164	5219
PA5567	4165	5220
SAU100040	4166	5221
SAU100053	4167	5222
SAU100056	4168	5223
SAU100059	4169	5224
SAU100062	4170	5225
SAU100077	4171	5226
SAU100112	4172	5227
SAU100114	4173	5228
SAU100118	4174	5229
SAU100123	4175	5230
SAU100128	4176	5231
SAU100131	4177	5232
SAU100133	4178	5233
SAU100139	4179	5234
SAU100140	4180	5235
SAU100141	4181	5236
SAU100157	4182	5237
SAU100158	4183	5238
SAU100162	4184	5239
SAU100175	4185	5240
SAU100182	4186	5241
SAU100186	4187	5242
SAU100198	4188	5243
SAU100227	4189	5244
SAU100231	4190	5245
SAU100242	4191	5246
SAU100246	4192	5247
SAU100251	4193	5248
SAU100265	4194	5249
SAU100266	4195	5250

TABLE IA

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
SAU100272	4196	5251
SAU100275	4197	5252
SAU100300	4198	5253
SAU100301	4199	5254
SAU100302	4200	5255
SAU100305	4201	5256
SAU100307	4202	5257
SAU100308	4203	5258
SAU100313	4204	5259
SAU100315	4205	5260
SAU100323	4206	5261
SAU100347	4207	5262
SAU100355	4208	5263
SAU100359	4209	5264
SAU100381	4210	5265
SAU100389	4211	5266
SAU100390	4212	5267
SAU100401	4213	5268
SAU100412	4214	5269
SAU100414	4215	5270
SAU100432	4216	5271
SAU100433	4217	5272
SAU100436	4218	5273
SAU100443	4219	5274
SAU100444	4220	5275
SAU100475	4221	5276
SAU100478	4222	5277
SAU100489	4223	5278
SAU100496	4224	5279
SAU100497	4225	5280
SAU100514	4226	5281
SAU100517	4227	5282
SAU100521	4228	5283
SAU100522	4229	5284
SAU100527	4230	5285
SAU100528	4231	5286
SAU100532	4232	5287
SAU100542	4233	5288
SAU100546	4234	5289
SAU100547	4235	5290
SAU100557	4236	5291
SAU100582	4237	5292
SAU100590	4238	5293
SAU100595	4239	5294
SAU100596	4240	5295
SAU100601	4241	5296
SAU100608	4242	5297
SAU100610	4243	5298
SAU100613	4244	5299

TABLE IA

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
SAU100617	4245	5300
SAU100633	4246	5301
SAU100646	4247	5302
SAU100658	4248	5303
SAU100659	4249	5304
SAU100679	4250	5305
SAU100684	4251	5306
SAU100685	4252	5307
SAU100689	4253	5308
SAU100690	4254	5309
SAU100702	4255	5310
SAU100710	4256	5311
SAU100714	4257	5312
SAU100731	4258	5313
SAU100733	4259	5314
SAU100734	4260	5315
SAU100736	4261	5316
SAU100738	4262	5317
SAU100741	4263	5318
SAU100745	4264	5319
SAU100747	4265	5320
SAU100751	4266	5321
SAU100752	4267	5322
SAU100767	4268	5323
SAU100770	4269	5324
SAU100771	4270	5325
SAU100773	4271	5326
SAU100776	4272	5327
SAU100778	4273	5328
SAU100793	4274	5329
SAU100794	4275	5330
SAU100799	4276	5331
SAU100808	4277	5332
SAU100810	4278	5333
SAU100813	4279	5334
SAU100831	4280	5335
SAU100836	4281	5336
SAU100838	4282	5337
SAU100839	4283	5338
SAU100843	4284	5339
SAU100845	4285	5340
SAU100858	4286	5341
SAU100859	4287	5342
SAU100865	4288	5343
SAU100866	4289	5344
SAU100879	4290	5345
SAU100880	4291	5346
SAU100882	4292	5347
SAU100885	4293	5348

TABLE IA

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
SAU100886	4294	5349
SAU100887	4295	5350
SAU100899	4296	5351
SAU100901	4297	5352
SAU100916	4298	5353
SAU100920	4299	5354
SAU100921	4300	5355
SAU100932	4301	5356
SAU100944	4302	5357
SAU100952	4303	5358
SAU100959	4304	5359
SAU100961	4305	5360
SAU100962	4306	5361
SAU100963	4307	5362
SAU100964	4308	5363
SAU100965	4309	5364
SAU100970	4310	5365
SAU100996	4311	5366
SAU101006	4312	5367
SAU101020	4313	5368
SAU101024	4314	5369
SAU101028	4315	5370
SAU101034	4316	5371
SAU101038	4317	5372
SAU101039	4318	5373
SAU101065	4319	5374
SAU101067	4320	5375
SAU101070	4321	5376
SAU101084	4322	5377
SAU101085	4323	5378
SAU101086	4324	5379
SAU101090	4325	5380
SAU101092	4326	5381
SAU101104	4327	5382
SAU101143	4328	5383
SAU101145	4329	5384
SAU101155	4330	5385
SAU101156	4331	5386
SAU101159	4332	5387
SAU101175	4333	5388
SAU101180	4334	5389
SAU101183	4335	5390
SAU101184	4336	5391
SAU101189	4337	5392
SAU101197	4338	5393
SAU101198	4339	5394
SAU101199	4340	5395
SAU101220	4341	5396
SAU101224	4342	5397

TABLE IA

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
SAU101226	4343	5398
SAU101231	4344	5399
SAU101235	4345	5400
SAU101236	4346	5401
SAU101239	4347	5402
SAU101240	4348	5403
SAU101242	4349	5404
SAU101247	4350	5405
SAU101262	4351	5406
SAU101265	4352	5407
SAU101266	4353	5408
SAU101267	4354	5409
SAU101270	4355	5410
SAU101271	4356	5411
SAU101275	4357	5412
SAU101286	4358	5413
SAU101293	4359	5414
SAU101300	4360	5415
SAU101301	4361	5416
SAU101302	4362	5417
SAU101310	4363	5418
SAU101311	4364	5419
SAU101320	4365	5420
SAU101327	4366	5421
SAU101339	4367	5422
SAU101340	4368	5423
SAU101341	4369	5424
SAU101343	4370	5425
SAU101344	4371	5426
SAU101346	4372	5427
SAU101347	4373	5428
SAU101350	4374	5429
SAU101351	4375	5430
SAU101360	4376	5431
SAU101365	4377	5432
SAU101366	4378	5433
SAU101369	4379	5434
SAU101371	4380	5435
SAU101381	4381	5436
SAU101382	4382	5437
SAU101383	4383	5438
SAU101385	4384	5439
SAU101387	4385	5440
SAU101389	4386	5441
SAU101398	4387	5442
SAU101399	4388	5443
SAU101400	4389	5444
SAU101408	4390	5445
SAU101421	4391	5446

TABLE IA

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
SAU101427	4392	5447
SAU101432	4393	5448
SAU101436	4394	5449
SAU101438	4395	5450
SAU101444	4396	5451
SAU101445	4397	5452
SAU101446	4398	5453
SAU101447	4399	5454
SAU101452	4400	5455
SAU101455	4401	5456
SAU101461	4402	5457
SAU101463	4403	5458
SAU101476	4404	5459
SAU101481	4405	5460
SAU101482	4406	5461
SAU101483	4407	5462
SAU101488	4408	5463
SAU101491	4409	5464
SAU101492	4410	5465
SAU101493	4411	5466
SAU101495	4412	5467
SAU101497	4413	5468
SAU101509	4414	5469
SAU101526	4415	5470
SAU101529	4416	5471
SAU101541	4417	5472
SAU101543	4418	5473
SAU101545	4419	5474
SAU101546	4420	5475
SAU101549	4421	5476
SAU101551	4422	5477
SAU101554	4423	5478
SAU101561	4424	5479
SAU101565	4425	5480
SAU101567	4426	5481
SAU101570	4427	5482
SAU101571	4428	5483
SAU101572	4429	5484
SAU101573	4430	5485
SAU101574	4431	5486
SAU101575	4432	5487
SAU101576	4433	5488
SAU101586	4434	5489
SAU101592	4435	5490
SAU101599	4436	5491
SAU101610	4437	5492
SAU101612	4438	5493
SAU101614	4439	5494
SAU101616	4440	5495

TABLE IA

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
SAU101622	4441	5496
SAU101624	4442	5497
SAU101630	4443	5498
SAU101632	4444	5499
SAU101637	4445	5500
SAU101641	4446	5501
SAU101651	4447	5502
SAU101652	4448	5503
SAU101653	4449	5504
SAU101655	4450	5505
SAU101663	4451	5506
SAU101664	4452	5507
SAU101674	4453	5508
SAU101679	4454	5509
SAU101681	4455	5510
SAU101682	4456	5511
SAU101685	4457	5512
SAU101717	4458	5513
SAU101724	4459	5514
SAU101726	4460	5515
SAU101727	4461	5516
SAU101728	4462	5517
SAU101736	4463	5518
SAU101737	4464	5519
SAU101744	4465	5520
SAU101751	4466	5521
SAU101752	4467	5522
SAU101754	4468	5523
SAU101756	4469	5524
SAU101771	4470	5525
SAU101772	4471	5526
SAU101777	4472	5527
SAU101781	4473	5528
SAU101782	4474	5529
SAU101784	4475	5530
SAU101790	4476	5531
SAU101791	4477	5532
SAU101792	4478	5533
SAU101793	4479	5534
SAU101794	4480	5535
SAU101795	4481	5536
SAU101797	4482	5537
SAU101798	4483	5538
SAU101799	4484	5539
SAU101800	4485	5540
SAU101801	4486	5541
SAU101802	4487	5542
SAU101803	4488	5543
SAU101804	4489	5544

TABLE IA

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
SAU101805	4490	5545
SAU101806	4491	5546
SAU101807	4492	5547
SAU101808	4493	5548
SAU101810	4494	5549
SAU101811	4495	5550
SAU101814	4496	5551
SAU101815	4497	5552
SAU101818	4498	5553
SAU101824	4499	5554
SAU101833	4500	5555
SAU101839	4501	5556
SAU101842	4502	5557
SAU101845	4503	5558
SAU101849	4504	5559
SAU101857	4505	5560
SAU101862	4506	5561
SAU101864	4507	5562
SAU101865	4508	5563
SAU101866	4509	5564
SAU101868	4510	5565
SAU101869	4511	5566
SAU101876	4512	5567
SAU101881	4513	5568
SAU101882	4514	5569
SAU101890	4515	5570
SAU101891	4516	5571
SAU101893	4517	5572
SAU101904	4518	5573
SAU101907	4519	5574
SAU101909	4520	5575
SAU101910	4521	5576
SAU101915	4522	5577
SAU101922	4523	5578
SAU101948	4524	5579
SAU101966	4525	5580
SAU101968	4526	5581
SAU101991	4527	5582
SAU101995	4528	5583
SAU101996	4529	5584
SAU101999	4530	5585
SAU102001	4531	5586
SAU102002	4532	5587
SAU102003	4533	5588
SAU102006	4534	5589
SAU102007	4535	5590
SAU102032	4536	5591
SAU102035	4537	5592
SAU102044	4538	5593

TABLE IA

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
SAU102046	4539	5594
SAU102049	4540	5595
SAU102054	4541	5596
SAU102059	4542	5597
SAU102067	4543	5598
SAU102068	4544	5599
SAU102102	4545	5600
SAU102113	4546	5601
SAU102116	4547	5602
SAU102117	4548	5603
SAU102129	4549	5604
SAU102132	4550	5605
SAU102142	4551	5606
SAU102143	4552	5607
SAU102144	4553	5608
SAU102162	4554	5609
SAU102165	4555	5610
SAU102200	4556	5611
SAU102201	4557	5612
SAU102222	4558	5613
SAU102231	4559	5614
SAU102232	4560	5615
SAU102233	4561	5616
SAU102241	4562	5617
SAU102242	4563	5618
SAU102246	4564	5619
SAU102247	4565	5620
SAU102252	4566	5621
SAU102256	4567	5622
SAU102257	4568	5623
SAU102259	4569	5624
SAU102260	4570	5625
SAU102261	4571	5626
SAU102262	4572	5627
SAU102264	4573	5628
SAU102265	4574	5629
SAU102268	4575	5630
SAU102270	4576	5631
SAU102280	4577	5632
SAU102281	4578	5633
SAU102283	4579	5634
SAU102284	4580	5635
SAU102286	4581	5636
SAU102287	4582	5637
SAU102292	4583	5638
SAU102294	4584	5639
SAU102297	4585	5640
SAU102298	4586	5641
SAU102308	4587	5642

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
SAU102318	4588	5643
SAU102333	4589	5644
SAU102334	4590	5645
SAU102336	4591	5646
SAU102340	4592	5647
SAU102345	4593	5648
SAU102350	4594	5649
SAU102352	4595	5650
SAU102355	4596	5651
SAU102356	4597	5652
SAU102378	4598	5653
SAU102380	4599	5654
SAU102388	4600	5655
SAU102389	4601	5656
SAU102390	4602	5657
SAU102392	4603	5658
SAU102394	4604	5659
SAU102396	4605	5660
SAU102401	4606	5661
SAU102407	4607	5662
SAU102417	4608	5663
SAU102418	4609	5664
SAU102420	4610	5665
SAU102422	4611	5666
SAU102423	4612	5667
SAU102433	4613	5668
SAU102434	4614	5669
SAU102437	4615	5670
SAU102440	4616	5671
SAU102447	4617	5672
SAU102448	4618	5673
SAU102449	4619	5674
SAU102450	4620	5675
SAU102452	4621	5676
SAU102453	4622	5677
SAU102460	4623	5678
SAU102469	4624	5679
SAU102473	4625	5680
SAU102474	4626	5681
SAU102476	4627	5682
SAU102479	4628	5683
SAU102480	4629	5684
SAU102481	4630	5685
SAU102485	4631	5686
SAU102486	4632	5687
SAU102487	4633	5688
SAU102498	4634	5689
SAU102502	4635	5690
SAU102503	4636	5691

TABLE IA

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
SAU102526	4637	5692
SAU102527	4638	5693
SAU102531	4639	5694
SAU102533	4640	5695
SAU102534	4641	5696
SAU102541	4642	5697
SAU102551	4643	5698
SAU102554	4644	5699
SAU102575	4645	5700
SAU102578	4646	5701
SAU102584	4647	5702
SAU102585	4648	5703
SAU102593	4649	5704
SAU102598	4650	5705
SAU102599	4651	5706
SAU102601	4652	5707
SAU102602	4653	5708
SAU102603	4654	5709
SAU102605	4655	5710
SAU102606	4656	5711
SAU102607	4657	5712
SAU102609	4658	5713
SAU102610	4659	5714
SAU102613	4660	5715
SAU102614	4661	5716
SAU102615	4662	5717
SAU102620	4663	5718
SAU102621	4664	5719
SAU102629	4665	5720
SAU102631	4666	5721
SAU102636	4667	5722
SAU102637	4668	5723
SAU102639	4669	5724
SAU102652	4670	5725
SAU102658	4671	5726
SAU102663	4672	5727
SAU102669	4673	5728
SAU102671	4674	5729
SAU102674	4675	5730
SAU102693	4676	5731
SAU102694	4677	5732
SAU102725	4678	5733
SAU102764	4679	5734
SAU102766	4680	5735
SAU102812	4681	5736
SAU102863	4682	5737
SAU102870	4683	5738
SAU102880	4684	5739
SAU102881	4685	5740

TABLE IA

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
SAU102883	4686	5741
SAU102905	4687	5742
SAU102909	4688	5743
SAU102933	4689	5744
SAU102935	4690	5745
SAU102936	4691	5746
SAU102939	4692	5747
SAU102942	4693	5748
SAU102944	4694	5749
SAU102979	4695	5750
SAU102983	4696	5751
SAU102992	4697	5752
SAU103010	4698	5753
SAU103024	4699	5754
SAU103025	4700	5755
SAU103037	4701	5756
SAU103038	4702	5757
SAU103042	4703	5758
SAU103077	4704	5759
SAU103115	4705	5760
SAU103144	4706	5761
SAU103159	4707	5762
SAU103169	4708	5763
SAU103175	4709	5764
SAU103191	4710	5765
SAU103198	4711	5766
SAU103204	4712	5767
SAU103226	4713	5768
SAU103232	4714	5769
SAU200006	4715	5770
SAU200028	4716	5771
SAU200030	4717	5772
SAU200058	4718	5773
SAU200059	4719	5774
SAU200088	4720	5775
SAU200157	4721	5776
SAU200242	4722	5777
SAU200297	4723	5778
SAU200345	4724	5779
SAU200392	4725	5780
SAU200468	4726	5781
SAU200558	4727	5782
SAU200561	4728	5783
SAU200564	4729	5784
SAU200565	4730	5785
SAU200593	4731	5786
SAU200601	4732	5787
SAU200628	4733	5788
SAU200657	4734	5789

TABLE IA

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
SAU200685	4735	5790
SAU200721	4736	5791
SAU200725	4737	5792
SAU200731	4738	5793
SAU200740	4739	5794
SAU200752	4740	5795
SAU200914	4741	5796
SAU200916	4742	5797
SAU200928	4743	5798
SAU200934	4744	5799
SAU200949	4745	5800
SAU200960	4746	5801
SAU200994	4747	5802
SAU201167	4748	5803
SAU201168	4749	5804
SAU201184	4750	5805
SAU201197	4751	5806
SAU201225	4752	5807
SAU201236	4753	5808
SAU201301	4754	5809
SAU201333	4755	5810
SAU201375	4756	5811
SAU201380	4757	5812
SAU201381	4758	5813
SAU201385	4759	5814
SAU201403	4760	5815
SAU201469	4761	5816
SAU201486	4762	5817
SAU201506	4763	5818
SAU201508	4764	5819
SAU201513	4765	5820
SAU201539	4766	5821
SAU201541	4767	5822
SAU201558	4768	5823
SAU201571	4769	5824
SAU201611	4770	5825
SAU201615	4771	5826
SAU201620	4772	5827
SAU201621	4773	5828
SAU201654	4774	5829
SAU201666	4775	5830
SAU201743	4776	5831
SAU201752	4777	5832
SAU201765	4778	5833
SAU201773	4779	5834
SAU201775	4780	5835
SAU201810	4781	5836
SAU201827	4782	5837
SAU201929	4783	5838

TABLE IA

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
SAU201952	4784	5839
SAU201961	4785	5840
SAU201971	4786	5841
SAU202006	4787	5842
SAU202039	4788	5843
SAU202126	4789	5844
SAU202174	4790	5845
SAU202176	4791	5846
SAU202186	4792	5847
SAU202267	4793	5848
SAU202708	4794	5849
SAU202731	4795	5850
SAU202736	4796	5851
SAU202756	4797	5852
SAU202781	4798	5853
SAU202872	4799	5854
SAU202882	4800	5855
SAU202930	4801	5856
SAU202945	4802	5857
SAU202968	4803	5858
SAU203001	4804	5859
SAU203007	4805	5860
SAU203196	4806	5861
SAU203293	4807	5862
SAU203296	4808	5863
SAU203524	4809	5864
SAU300110	4810	5865
SAU300131	4811	5866
SAU300156	4812	5867
SAU300191	4813	5868
SAU300269	4814	5869
SAU300335	4815	5870
SAU300338	4816	5871
SAU300455	4817	5872
SAU300572	4818	5873
SAU300617	4819	5874
SAU300713	4820	5875
SAU300719	4821	5876
SAU300732	4822	5877
SAU300825	4823	5878
SAU300868	4824	5879
SAU300975	4825	5880
SAU300998	4826	5881
SAU301004	4827	5882
SAU301030	4828	5883
SAU301054	4829	5884
SAU301080	4830	5885
SAU301118	4831	5886
SAU301133	4832	5887

PathoSeq Gene Locus	Nucleotide SeqID	Protein SeqID
SAU301148	4833	5888
SAU301223	4834	5889
SAU301230	4835	5890
SAU301268	4836	5891
SAU301275	4837	5892
SAU301357	4838	5893
SAU301363	4839	5894
SAU301433	4840	5895
SAU301465	4841	5896
SAU301472	4842	5897
SAU301592	4843	5898
SAU301620	4844	5899
SAU301758	4845	5900
SAU301773	4846	5901
SAU301829	4847	5902
SAU301869	4848	5903
SAU301898	4849	5904
SAU302060	4850	5905
SAU302513	4851	5906
SAU302626	4852	5907
SAU302685	4853	5908
SAU302698	4854	5909
SAU302699	4855	5910
SAU302805	4856	5911
SAU302901	4857	5912
SAU302931	4858	5913
SAU302950	4859	5914
SAU302956	4860	5915

WHAT IS CLAIMED IS:

1. A purified or isolated nucleic acid sequence comprising a nucleotide sequence consisting essentially of one of SEQ ID NOs: 8-3795, wherein expression of said nucleic acid inhibits proliferation of a cell.

2. A purified or isolated nucleic acid comprising a fragment of one of SEQ ID NOs.: 8-3795, said fragment selected from the group consisting of fragments comprising at least 10, at least 20, at least 25, at least 30, at least 50 and more than 50 consecutive nucleotides of one of SEQ ID NOs: 8-3795.

3. A purified or isolated antisense nucleic acid comprising a nucleotide sequence complementary to at least a portion of an intragenic sequence, intergenic sequence, sequences spanning at least a portion of two or more genes, 5' noncoding region, or 3' noncoding region within an operon comprising a proliferation-required gene whose activity or expression is inhibited by an antisense nucleic acid comprising the nucleotide sequence of one of SEQ ID NOs.: 8-3795.

4. A purified or isolated nucleic acid comprising a nucleotide sequence having at least 70% identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, fragments comprising at least 25 consecutive nucleotides of SEQ ID NOs.: 8-3795, the nucleotide sequences complementary to SEQ ID NOs.: 8-3795 and the sequences complementary to fragments comprising at least 25 consecutive nucleotides of SEQ ID NOs.: 8-3795 as determined using BLASTN version 2.0 with the default parameters.

5. A vector comprising a promoter operably linked to a nucleic acid encoding a polypeptide whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence of any one of SEQ ID NOs.: 8-3795.

6. A purified or isolated polypeptide comprising a polypeptide whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence of any one of SEQ ID NOs.: 8-3795, or a fragment selected from the group consisting of fragments comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of one of the said polypeptides.

7. A purified or isolated polypeptide comprising a polypeptide having at least 25% amino acid identity to a polypeptide whose expression is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, or at least 25% amino acid identity to a fragment comprising at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of a polypeptide whose expression is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 as determined using FASTA version 3.0t78 with the default parameters.

8. A method of producing a polypeptide, comprising introducing a vector comprising a promoter operably linked to a nucleic acid comprising a nucleotide sequence encoding a

polypeptide whose expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 8-3795 into a cell.

9. A method of inhibiting proliferation of a cell in an individual comprising inhibiting the activity or reducing the amount of a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 or inhibiting the activity or reducing the amount of a nucleic acid encoding said gene product.

10. A method for identifying a compound which influences the activity of a gene product required for proliferation, said gene product comprising a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, said method comprising:

contacting said gene product with a candidate compound; and

determining whether said compound influences the activity of said gene product.

11. A method for identifying a compound or nucleic acid having the ability to reduce the activity or level of a gene product required for proliferation, said gene product comprising a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, said method comprising:

(a) contacting a target gene or RNA encoding said gene product with a candidate compound or nucleic acid; and

(b) measuring an activity of said target.

12. A method for identifying a compound which reduces the activity or level of a gene product required for proliferation of a cell, wherein the activity or expression of said gene product is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, said method comprising the steps of:

(a) providing a sublethal level of an antisense nucleic acid comprising a nucleotide sequence complementary to a nucleic acid comprising a nucleotide sequence encoding said gene product in a cell to reduce the activity or amount of said gene product in said cell, thereby producing a sensitized cell;

(b) contacting said sensitized cell with a compound; and

(c) determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a cell which does not contain said antisense nucleic acid.

13. A method for inhibiting cellular proliferation comprising introducing an effective amount of a compound with activity against a gene whose activity or expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 or a compound with activity against the product of said gene into a population of cells expressing said gene.

14. A composition comprising an effective concentration of an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, or a proliferation-inhibiting portion thereof in a pharmaceutically acceptable carrier.

15. A method for inhibiting the activity or expression of a gene in an operon required for proliferation wherein the activity or expression of at least one gene in said operon is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 8-3795, said method comprising contacting a cell in a cell population with an antisense nucleic acid complementary to at least a portion of said operon.

16. A method for identifying a gene which is required for proliferation of a cell comprising:

(a) contacting a cell with an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, wherein said cell is a cell other than the organism from which said nucleic acid was obtained;

(b) determining whether said nucleic acid inhibits proliferation of said cell; and

(c) identifying the gene in said cell which encodes the mRNA which is complementary to said antisense nucleic acid or a portion thereof.

17. A method for identifying a compound having the ability to inhibit proliferation of a cell comprising:

(a) identifying a homolog of a gene or gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs. 8-3795 in a test cell, wherein said test cell is not the cell from which said nucleic acid was obtained ;

(b) identifying an inhibitory nucleic acid sequence which inhibits the activity of said homolog in said test cell;

(c) contacting said test cell with a sublethal level of said inhibitory nucleic acid, thus sensitizing said cell;

(d) contacting the sensitized cell of step (c) with a compound; and

(e) determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a cell which does not contain said inhibitory nucleic acid.

18. A method of identifying a compound having the ability to inhibit proliferation comprising:

(a) contacting a test cell with a sublethal level of a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs. 8-3795 or a portion thereof which inhibits the proliferation of the cell from which said nucleic acid was obtained, thus sensitizing said test cell;

(b) contacting the sensitized test cell of step (a) with a compound; and

(c) determining the degree to which said compound inhibits proliferation of said sensitized test cell relative to a cell which does not contain said nucleic acid.

19. A method for identifying a compound having activity against a biological pathway required for proliferation comprising:

(a) sensitizing a cell by providing a sublethal level of an antisense nucleic acid complementary to a nucleic acid encoding a gene product required for proliferation, wherein the activity or expression of said gene product is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, in said cell to reduce the activity or amount of said gene product;

(b) contacting the sensitized cell with a compound; and

(c) determining the degree to which said compound inhibits the growth of said sensitized cell relative to a cell which does not contain said antisense nucleic acid.

20. A method for identifying a compound having the ability to inhibit cellular proliferation comprising:

(a) contacting a cell with an agent which reduces the activity or level of a gene product required for proliferation of said cell, wherein said gene product is a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795;

(b) contacting said cell with a compound; and

(c) determining whether said compound reduces proliferation of said contacted cell by acting on said gene product.

21. A method for identifying the biological pathway in which a proliferation-required gene or its gene product lies, wherein said gene or gene product comprises a gene or gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 8-3795, said method comprising:

(a) providing a sublethal level of an antisense nucleic acid which inhibits the activity of said proliferation-required gene or gene product in a test cell;

(b) contacting said test cell with a compound known to inhibit growth or proliferation of a cell, wherein the biological pathway on which said compound acts is known; and

(c) determining the degree to which said proliferation of said test cell is inhibited relative to a cell which was not contacted with said compound.

22. A method for determining the biological pathway on which a test compound acts comprising:

(a) providing a sublethal level of an antisense nucleic acid complementary to a proliferation-required nucleic acid in a first cell, wherein the activity or expression of said proliferation-required nucleic acid is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 8-3795 and wherein the

biological pathway in which said proliferation-required nucleic acid or a protein encoded by said proliferation-required nucleic acid lies is known,

(b) contacting said first cell with said test compound; and

(c) determining the degree to which said test compound inhibits proliferation of said first cell relative to a cell which does not contain said antisense nucleic acid.

23. A purified or isolated nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 8-3795.

24. A compound which interacts with a gene or gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence of one of SEQ ID NOs.: 8-3795 to inhibit proliferation.

25. A compound which interacts with a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence of one of SEQ ID NOs.: 8-3795 to inhibit proliferation.

26. A method for manufacturing an antibiotic comprising the steps of:

screening one or more candidate compounds to identify a compound that reduces the activity or level of a gene product required for proliferation, said gene product comprising a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795; and

manufacturing the compound so identified.

27. A purified or isolated nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, fragments comprising at least 25 consecutive nucleotides of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, the nucleotide sequences complementary to SEQ ID NOs.:3796-3800, 3806-4860, 5916-10012, and the nucleotide sequences complementary to fragments comprising at least 25 consecutive nucleotides of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012 as determined using BLASTN version 2.0 with the default parameters.

28. A method of inhibiting proliferation of a cell comprising inhibiting the activity or reducing the amount of a gene product in said cell or inhibiting the activity or reducing the amount of a nucleic acid encoding said gene product in said cell, wherein said gene product is selected from the group consisting of a gene product having having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID

NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 8-3795.

29. A method for identifying a compound which influences the activity of a gene product required for proliferation comprising:

contacting a candidate compound with a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795; and

determining whether said candidate compound influences the activity of said gene product.

30. A method for identifying a compound or nucleic acid having the ability to reduce the activity or level of a gene product required for proliferation comprising:

(a) providing a target that is a gene or RNA, wherein said target comprises a nucleic acid that encodes a gene product selected from the group consisting of a gene

product having having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleic acid identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795;

(b) contacting said target with a candidate compound or nucleic acid; and

(c) measuring an activity of said target.

31. A method for identifying a compound which reduces the activity or level of a gene product required for proliferation of a cell comprising:

(a) providing a sublethal level of an antisense nucleic acid complementary to a nucleic acid encoding said gene product in a cell to reduce the activity or amount of said gene product in said cell, thereby producing a sensitized cell, wherein said gene product is selected from the group consisting of a gene product having having at least 70% nucleic acid identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a

nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795;

(b) contacting said sensitized cell with a compound; and

(c) determining the degree to which said compound inhibits the growth of said sensitized cell relative to a cell which does not contain said antisense nucleic acid.

32. A method for inhibiting cellular proliferation comprising introducing a compound with activity against a gene product or a compound with activity against a gene encoding said gene product into a population of cells expressing said gene product, wherein said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795.

33. A preparation comprising an effective concentration of an antisense nucleic acid in a pharmaceutically acceptable carrier wherein said antisense nucleic acid is selected from the group consisting of a nucleic acid comprising a sequence having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 or a proliferation-inhibiting portion thereof, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, and a nucleic acid

comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions.

34. A method for inhibiting the activity or expression of a gene in an operon which encodes a gene product required for proliferation comprising contacting a cell in a cell population with an antisense nucleic acid comprising at least a proliferation-inhibiting portion of said operon in an antisense orientation, wherein said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795.

35. A method for identifying a gene which is required for proliferation of a cell comprising:

(a) contacting a cell with an antisense nucleic acid selected from the group consisting of a nucleic acid at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 or a proliferation-inhibiting portion thereof, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, wherein said cell is a cell other than the organism from which said nucleic acid was obtained;

(b) determining whether said nucleic acid inhibits proliferation of said cell; and

(c) identifying the gene in said cell which encodes the mRNA which is complementary to said antisense nucleic acid or a portion thereof.

36. A method for identifying a compound having the ability to inhibit proliferation of a cell comprising:

(a) identifying a homolog of a gene or gene product whose activity or level is inhibited by an antisense nucleic acid in a test cell, wherein said test cell is not the microorgaism from which the antisense nucleic acid was obtained, wherein said antisense nucleic acid is selected from the group consisting of a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs. 8-3795, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions;

(b) identifying an inhibitory nucleic acid sequence which inhibits the activity of said homolog in said test cell;

(c) contacting said test cell with a sublethal level of said inhibitory nucleic acid, thus sensitizing said cell;

(d) contacting the sensitized cell of step (c) with a compound; and

(e) determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a cell which does not express said inhibitory nucleic acid.

37. A method of identifying a compound having the ability to inhibit proliferation comprising:

(a) sensitizing a test cell by contacting said test cell with a sublethal level of an antisense nucleic acid, wherein said antisense nucleic acid is selected from the group consisting of a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs. 8-3795 or a portion thereof which inhibits the proliferation of the cell from which said nucleic acid was obtained, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditionst;

(b) contacting the sensitized test cell of step (a) with a compound; and

(c) determining the degree to which said compound inhibits proliferation of said sensitized test cell relative to a cell which does not contain said antisense nucleic acid.

38. A method for identifying a compound having activity against a biological pathway required for proliferation comprising:

(a) sensitizing a cell by providing a sublethal level of an antisense nucleic acid complementary to a nucleic acid encoding a gene product required for proliferation, wherein said gene product is selected from the group consisting of a gene product having at

least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795;

(b) contacting the sensitized cell with a compound; and

(c) determining the extent to which said compound inhibits the growth of said sensitized cell relative to a cell which does not contain said antisense nucleic acid.

39. A method for identifying a compound having the ability to inhibit cellular proliferation comprising:

(a) contacting a cell with an agent which reduces the activity or level of a gene product required for proliferation of said cell, wherein said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795

under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795;

(b) contacting said cell with a compound; and

(c) determining the degree to which said compound reduces proliferation of said contacted cell relative to a cell which was not contacted with said agent.

40. A method for identifying the biological pathway in which a proliferation-required gene product or a gene encoding a proliferation-required gene product lies comprising:

(a) providing a sublethal level of an antisense nucleic acid which inhibits the activity or reduces the level of said gene encoding a proliferation-required gene product or said said proliferation-required gene product in a test cell, wherein said proliferation-required gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795;

(b) contacting said test cell with a compound known to inhibit growth or proliferation of a cell, wherein the biological pathway on which said compound acts is known; and

(c) determining the degree to which said compound inhibits proliferation of said test cell relative to a cell which does not contain said antisense nucleic acid.

41. A method for determining the biological pathway on which a test compound acts comprising:

(a) providing a sublethal level of an antisense nucleic acid complementary to a proliferation-required nucleic acid in a cell, thereby producing a sensitized cell, wherein said antisense nucleic acid is selected from the group consisting of a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795 or a proliferation-inhibiting portion thereof,a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions and wherein the biological pathway in which said proliferation-required nucleic acid or a protein encoded by said proliferation-required polypeptide lies is known,

(b) contacting said cell with said test compound; and

(c) determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a cell which does not contain said antisense nucleic acid.

42. A compound which inhibits proliferation by interacting with a gene encoding a gene product required for proliferation or with a gene product required for proliferation, wherein said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795.

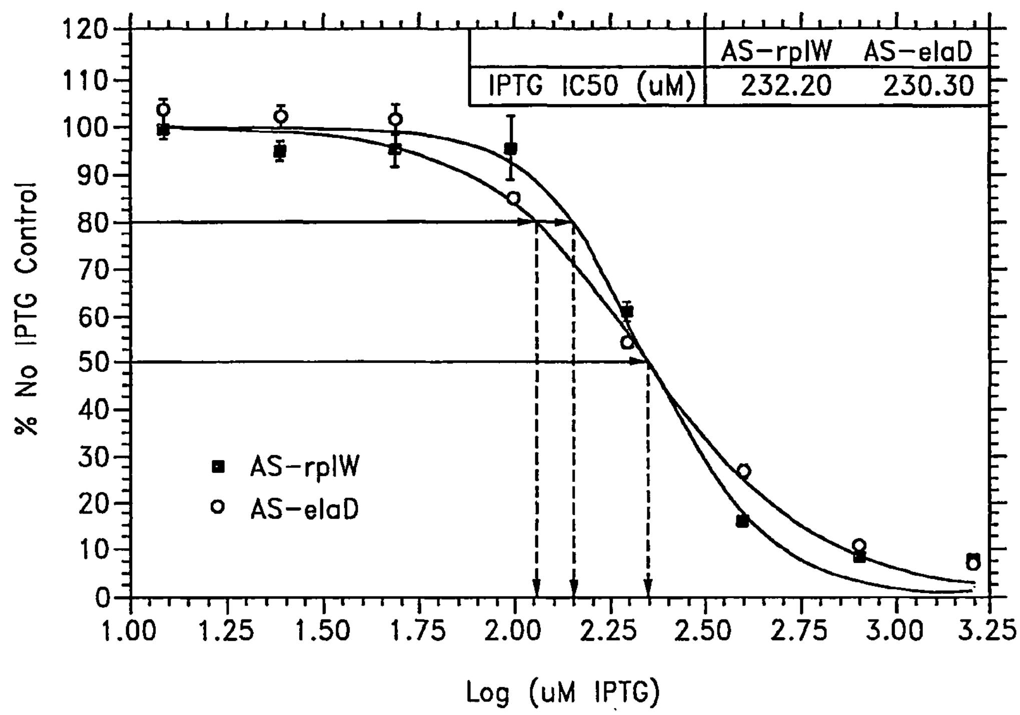
43. A method for manufacturing an antibiotic comprising the steps of:

screening one or more candidate compounds to identify a compound that reduces the activity or level of a gene product required for proliferation wherein said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795 ; and

manufacturing the compound so identified.

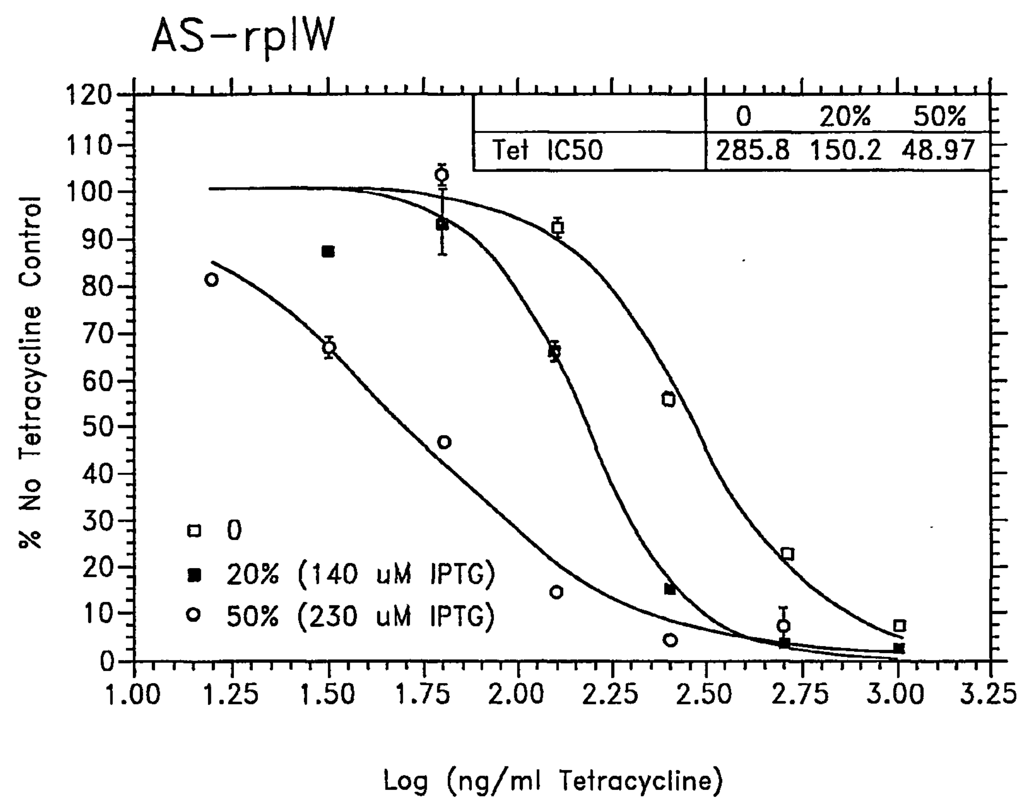
44. A method for inhibiting proliferation of a cell in a subject comprising administering an effective amount of a compound that reduces the activity or level of a gene product required for proliferation of said cell, wherein said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose

activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795.



AS-rplW
AS-elaD
IPTG IC50 (uM)
232.20
230.30
% No IPTG Control
Log (uM IPTG)
AS-rplW
AS-elaD
0
10
20
30
40
50
60
70
80
90
100
110
120
1.00
1.25
1.50
1.75
2.00
2.25
2.50
2.75
3.00
3.25

FIG. 1



AS-rplW
| | 0 | 20% | 50% |
Tet IC50 | 285.8 | 150.2 | 48.97
% No Tetracycline Control
120
110
100
90
80
70
60
50
40
30
20
10
0
1.00 1.25 1.50 1.75 2.00 2.25 2.50 2.75 3.00 3.25
0
20% (140 uM IPTG)
50% (230 uM IPTG)
Log (ng/ml Tetracycline)

FIG.2A

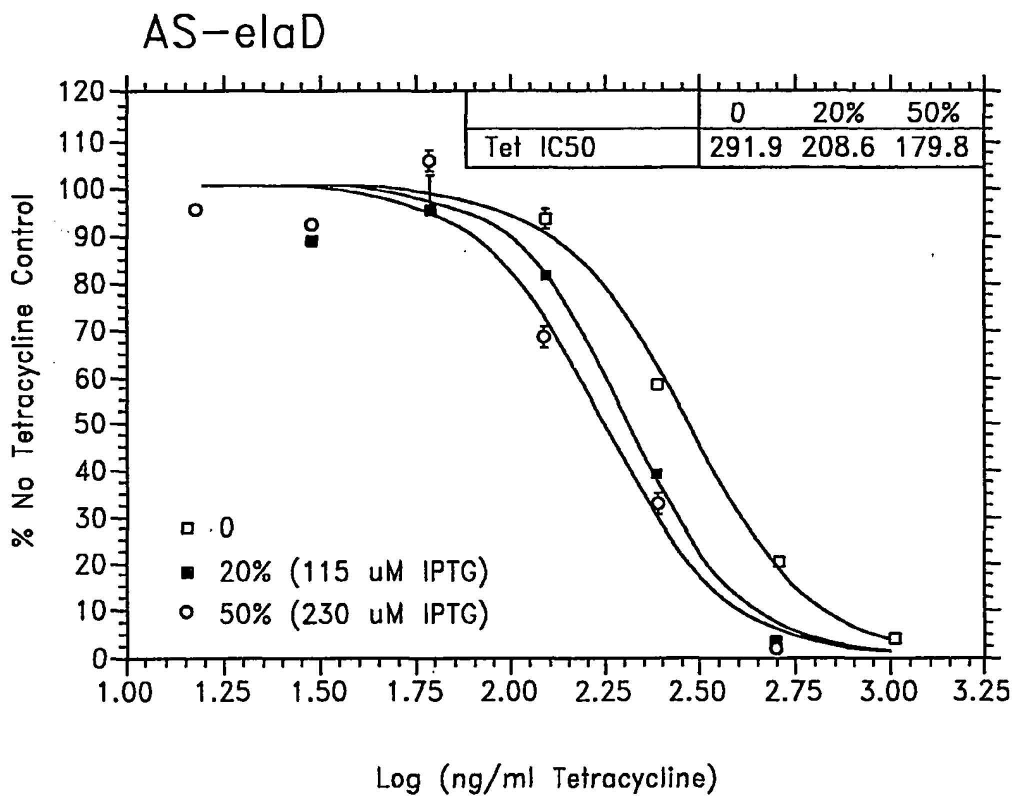

AS-elaD
| | 0 | 20% | 50% |
Tet IC50 291.9 208.6 179.8
120
110
100
90
80
70
60
50
40
30
20
10
0
% No Tetracycline Control
1.00 1.25 1.50 1.75 2.00 2.25 2.50 2.75 3.00 3.25
Log (ng/ml Tetracycline)
0
20% (115 uM IPTG)
50% (230 uM IPTG)

FIG.2B

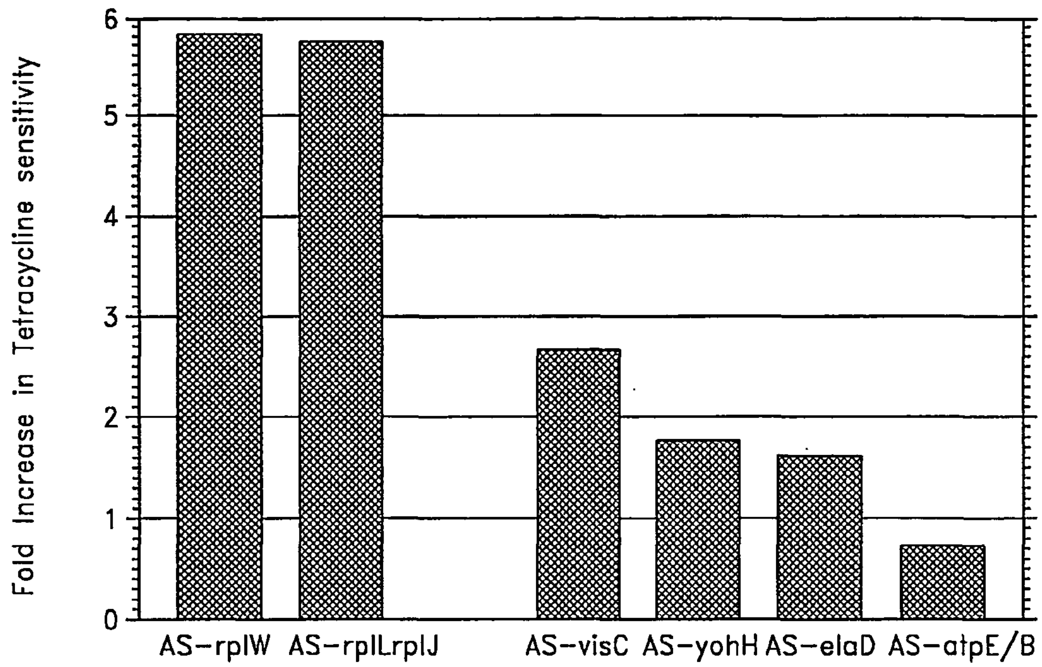

Fold Increase in Tetracycline sensitivity
0
1
2
3
4
5
6
AS-rplW
AS-rplLrplJ
AS-visC
AS-yohH
AS-elaD
AS-atpE/B

FIG. 3

THE SELECTIVE SENSITIZATION TO AN ANTIBIOTIC INHIBITING GYRASE B SUBUNIT ACTIVITY FOLLOWING THE INDUCTION OF AN ANTISENSE CONSTRUCT TO THE B SUBUNIT OF GYRASE.

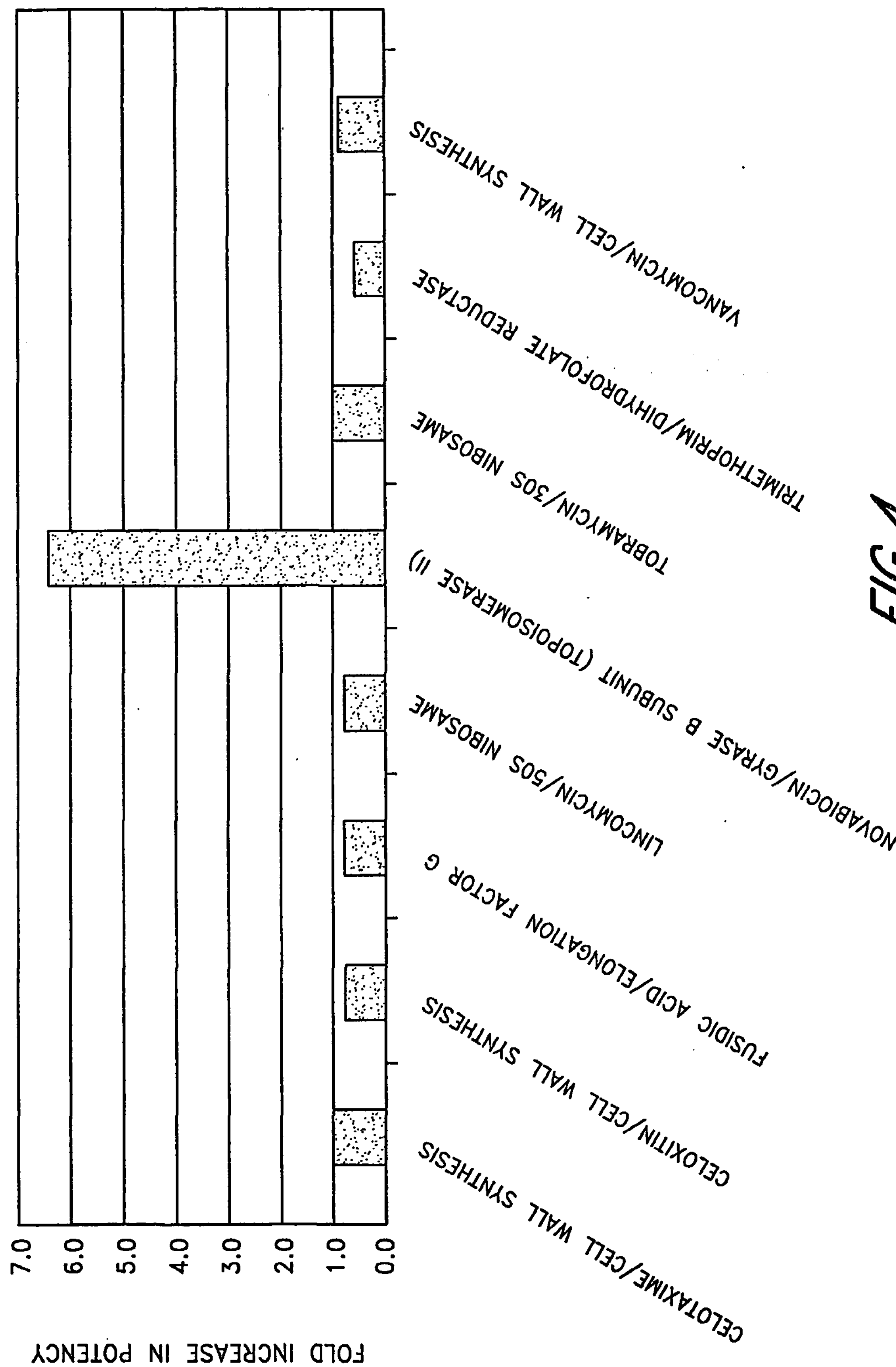


FIG. 4

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60/253,625	27 November 2000 (27.11.2000)	US
60/257,931	22 December 2000 (22.12.2000)	US
60/269,308	16 February 2001 (16.02.2001)	US

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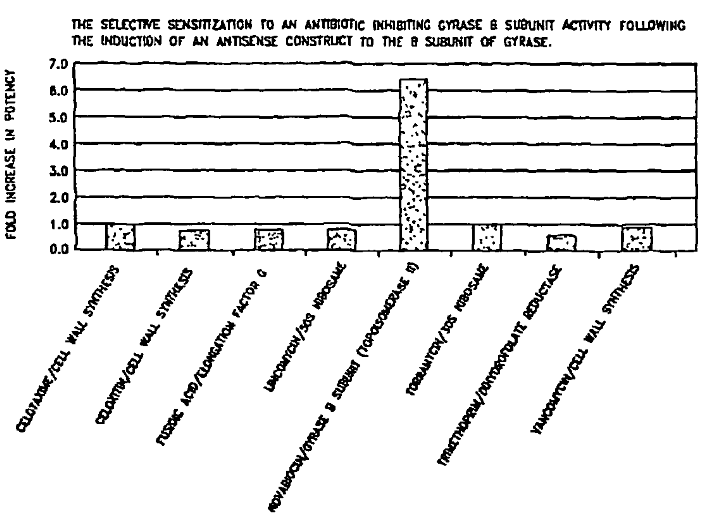
[Continued on next page]

(54) Title: IDENTIFICATION OF ESSENTIAL GENES IN PROKARYOTES



(57) Abstract: The sequences of antisense nucleic acids which inhibit the proliferation of prokaryotes are disclosed. Cell-based assays which employ the antisense nucleic acids to identify and develop antibiotics are also disclosed. The antisense nucleic acids can also be used to identify proteins required for proliferation, express these proteins or portions thereof, obtain antibodies capable of specifically binding to the expressed proteins, and to use those expressed proteins as a screen to isolate candidate molecules for rational drug discovery programs. The nucleic acids can also be used to screen for homologous nucleic acids that are required for proliferation in cells other than *Staphylococcus aureus, Salmonella typhimurium, Klebsiella pneumoniae,* and *Pseudomonas aeruginosa*. The nucleic acids of the present invention can also be used in various assay systems to screen for proliferation required genes in other organisms.

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